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Causes and Consequences of Plant Genome Evolution

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Causes and Consequences of Plant Genome Evolution

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by

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ABSTRACT OF THE DISSERTATION

Causes and Consequences of Plant Genome Evolution

by

Christopher James Fiscus

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Dr. Daniel Koenig, Chairperson

Genome evolution is responsible for generating phenotypic differences between individuals, which has cumulated in the extraordinary variation in organism development, morphology, and life history present in the tree of life. Genomes vary in size, structure, and content and this variation is especially apparent among plants, who as sessile organisms must adapt rapidly to face environmental stress. In this dissertation, I examine the causes and consequences of plant genome evolution in three disparate species to understand the patterns by which these lineages have undergone genome evolution while adapting to their respective ranges. In Chapter 1, I develop a novel method to summarize genomes from high-throughput sequencing reads and apply the method to describe genome content evolution in over 1,000 resequenced *Arabidopsis thaliana* genomes. In Chapter 2, I examine the subgenome evolution of the recent allopolyploid *Capsella bursa-pastoris* and describe the genetic factors that enabled this species to colonize every continent except for Antarctica. In Chapter 3, I develop a resource for genome-wide association mapping in *Vigna unguiculata* (cowpea) and demonstrate the effectiveness of this utility by mapping the genetic basis of previously unknown seed pigmentation phenotypes. Overall, the work in this dissertation contributes insight into the genetic and environmental factors affecting plant genome evolution.

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Introduction

During the last 500 million years land plants have diversified and evolved to occupy nearly every environment on planet Earth [1]. As a result, plants have evolved incredible variation in morphology, development, and life history, the basis of which is encoded in the genome. Plant genomes are surprisingly diverse in size, structure, and content. For instance, plant genomes range over 2,400 fold in size due to differences in the amount of non-coding DNA, ranging from the 61 Mbp (1C) genome of *Genlisea tuberosa* [2] to the 149 Gbp (1C) genome of *Paris japonica* [3]. Plants are incredibly tolerant of polyploidy, in which more than two sets of chromosomes are inherited per individual, with estimates of polyploidy occuring in up to 80% of flowering plants [4,5]. The content of plant genomes also varies considerably, with gene numbers ranging from about 12,000 in the ancestor of all flowering plants [6] to tens of thousands in the octoploid strawberry [7]. Despite considerable efforts over the last century to understand the mechanisms and effects of plant genome evolution [8], our understanding of these processes remains poor.

Causes and classes of genomic variation

All genomic variation begins as randomly occurring mutations. Mutations are generated by the lack of perfect fidelity of the molecular machinery governing DNA replication and DNA repair [9] and by the activity of transposable elements [10]. The incidence of mutation across genomes is non-uniform, with certain sequences, such as short tandem repeats, more susceptible to experiencing mutation due to the interaction of their sequence motifs with molecular machinery (e.g. replication slippage). Once a mutation has occurred, its fate in a population is determined by its effect on fitness and on the demographic processes acting on the population [11]. Since mutations occur in a single individual and must occur in a cell lineage that produces gametes to be inherited, most mutations that have ever occurred have been lost.

Below the species level, variation in genomes is generally divided into three main classes according to the nature and size of the variation. The smallest and most frequent variations are single nucleotide polymorphisms (SNPs), which are single base-pair substitutions between two or more sequences. SNPs are classified by whether they are transitions (i.e. purine to purine, pyrimidine to pyrimidine) or transversions (i.e. purine to pyrimidine or vice versa), with the former being much more common. If they occur in coding regions, SNPs are called synonymous if they do not alter the protein coding sequence of a gene and nonsynonymous if they alter protein coding sequence. Historically, SNPs were genotyped by amplifying short genomic sequences followed by Sanger sequencing of the amplicons [12]. In the modern era, SNPs are typically genotyped using microarrays, in which the segregating variation must be defined *a priori* or by using a variety of sequencing-based approaches dependent on aligning sequencing reads to a genome assembly.

The second class of genomic variation are short insertions or deletions, called “indels.” Indels are typically defined as being between 1 bp and 10,000 bp long, with the majority of observed indels < 1,000 bp [13]. Although less common than SNPs, indels have been of considerable interest to geneticists due to their associations with human disease [14,15]. The detection of indels has been historically more challenging than SNPs, with numerous approaches based on *de novo* assembly of unmapped short reads, analyzing coverage differences across the genome, and analyzing patterns of discordant or split reads (reviewed [16,17]).

The final class of genomic variation is structural variants, which includes very large insertions and deletions, duplications, and inversions. When large indels or duplications span genes, they produce copy number variants. Structural variants are the least common form of genomic variation and due to their size, affect many loci [18]. Structural variants have been linked to differences in gene expression [19] and patterns of recombination [20]. Structural variants are typically detected by aligning long reads to genomes or by pairwise alignment of genome assemblies (reviewed [21]).

In addition to the classes of variation described previously, genomic variation between species can consist of differences in karyotype, ploidy, and genome size. Spontaneous mutations affecting karyotype or ploidy have been linked with rapid speciation due to reproductive barriers caused by nondisjunction [5].

Discovering the consequences of genomic variation

The ability to link causal genetic variation to variation in phenotype is paramount for understanding the consequences of genomic variation. Since comparisons across species can span millions of years of evolution, efforts to map the consequences of genomic variation have focused on mapping the genetic basis of phenotypic variation between individuals of a species. The modern methods for linking phenotypic variation to genotypic variation is quantitative trait locus (QTL) mapping wherein a cohort of individuals are genotyped and phenotyped and a linear model is fit to predict the effects of alleles at a locus on phenotypic variation. Although this procedure sounds trivial, it can be complicated by population structure in the mapping cohort, lack of power to detect rare variants affecting a trait, and lack of power to detect small effect alleles [22].

In this dissertation, I examine the causes and consequences of plant genome evolution through three separate lines of inquiry in various experimental systems:

Chapter 1 presents a novel method to summarize genomes using high-throughput sequencing reads and examines the genetic basis of genome content variation across the species range of *Arabidopsis thaliana*.

Chapter 2 focuses on the evolution of subgenomes in the allotetraploid *Capsella bursa-pastoris*, a successful colonizer with a cosmopolitan distribution that formed from the hybridization of two progenitor species about 120,000 years ago.

Chapter 3 examines population structure and describes genome-wide association mapping in *Vigna unguiculata* (cowpea), an important drought tolerant crop species endemic to West Africa.

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Chapter 1: The genetic control of rapid genome content divergence in *Arabidopsis thaliana*

Abstract

Repetitive sequences compose the majority of eukaryotic genomes and vary widely in both copy number and sequence content. Attempts to understand the evolution of repetitive sequences and their role in shaping genome content variation have been hindered by the lack of high-quality genome assemblies with resolved repeats. Here, we employ a novel K-mer based approach to study variation in genome content in 1,142 resequenced *Arabidopsis thaliana* genomes. We use our approach to study repeat evolution in this species and identify hundreds of repetitive sequences with copy number variation. We then map the genetic basis of this variation to both cis and trans-acting loci using genome wide association (GWAS). Furthermore, we use a meta-GWAS approach to identify loci associated with copy number variation of different types of repeats, suggesting that these loci are involved in modulating the rate of genome content evolution. Finally, we show that loci associated with repeat copy number change are under strong purifying selection. Overall, our work provides insight into the genetic basis of genome content variation in plant genomes.

Introduction

Despite conservation of genomic sequence involved in essential biological processes [1], genome content variation exists across scales, even between individuals within a population. The lack of correlation between genome size and organismal complexity, called the C-value enigma [2], is a longstanding conundrum that was “solved” with the discovery of non-coding DNA [3]. While it is now understood that genome content variation in eukaryotes is primarily due to copy number increases or decreases of repetitive sequences [4], the forces driving the evolution of genome size and content have been debated for quite some time.

Numerous hypotheses have been proposed to attempt to explain the role of natural selection acting on genome size variation [2] while an alternative view posits that genome size evolves through a tradeoff between the rate of sequence deletions and insertions [5]. A prerequisite of the mutational equilibrium model is that mutation rates vary between lineages and over evolutionary time. However, the molecular changes that modulate rates of insertion and deletion remain poorly understood, limiting our understanding of the evolutionary pressures that drive directed shifts in genome content.

The model plant *Arabidopsis thaliana* has a compact 150 Mbp genome [6] with over 10% of variation in genome content between accessions [7]. Compared to its closest ancestor *Arabidopsis lyrata*, from which it is diverged < 6 million years ago [8,9], the *A. thaliana* genome is relatively repeat poor, with the majority of repetitive sequences occupying the centromere and pericentromere [10,11]. Population level surveys of variation in structural variants [12], single nucleotide polymorphisms (SNPs) and short indels [13,14] as well as repeat [6,7,15] and gene copy number [13,16] have been conducted previously in this system. Despite these efforts to catalog genomic variation in *A. thaliana*, the genetic basis of variation in the rate of genome content change remains elusive.

Efforts to catalog sequence differences segregating between individuals have historically relied upon variant calling and coverage-based approaches in which high-throughput sequencing reads from diverse individuals are mapped to a single reference genome. The strength of variant calling pipelines is their ability to detect small changes in conserved sequences, but variation in sequences absent from the reference genome are inaccessible to this method. For example, a study of genome variation in *A. thaliana* identified sequences up to 9 Mb in length present in individual genomes but missing from the Col-0 reference genome [7]. Alternatively, coverage-based approaches have been used to estimate copy number variation of genes and repeats. Repetitive sequences are largely missing or collapsed into single representative sequences in many first generation reference genomes [17], and may be found in various sequence contexts, hindering their detection by coverage differences.

To circumvent the limitations of variant calling or coverage-based approaches, we developed a K-mer based method to detect differences in genome content between individual genomes. K-mers are short sequences of length K that can be rapidly identified and counted in sequencing reads without the need for a genome assembly and have been successfully used to compare genomes in other systems such as maize [18]. We use this method to catalog genome content variation in over 1,000 accessions of *A. thaliana* and identify extensive copy number variation of repetitive sequences. We next map the genetic basis of sequence abundance variation and use a “meta-GWA” approach to identify alleles affecting the rate of genome content variation. Finally, we explore the evolutionary dynamics of variants affecting sequence copy number, and show that the frequency of these variants appears to be under selection.

Results

A pipeline for describing sequence abundance with K-mers

We set out to develop a pipeline to estimate genome content from sequencing reads produced on Illumina instruments using K-mers. The pipeline begins with unfiltered whole genome sequencing reads, removes poor quality sequences, organeller sequences, and corrects likely base calling errors. K-mers are then counted from the remaining sequences and the resulting counts are normalized for differences in sequencing depth, GC content, and biases introduced across sequencing center instruments to create genome content profiles (GCPs) for each sample (Figure 1.1A). GCPs can be thought of as a compressed representation of the content of a specific genome that can be compared without alignment between samples. GCPs can also be used to estimate the abundance of a specific sequence or genome compartment. For example, the abundance of a centromere associated repeat could be estimated by calculating the median count of k-mers that occur in that repeat from a specific GCP.

Optimizing K to characterize genome content

The first step in building a database of *A. thaliana* GCPs was to choose an appropriate length of K-mer. GCPs built with very small K would not discriminate between different sequences in the genome (lacking specificity), while very large values of K can fail to identify divergent or fragmented copies of related sequences and would generate very large datasets (lacking sensitivity). We set out to determine the smallest value of K that could differentiate repetitive sequences from non-repetitive sequences in the TAIR10 genome assembly. At values of K < 10, we have no power to assign K-mers to either the non-repetitive or repetitive bin and by K = 15 nearly all K-mers in non-repetitive sequence and the majority of K-mers in repetitive sequence are unique to their respective bins (Figure 1.1B, top). We also compared the abundance of K-mers in the bins by K and found that by K = 14 over half of non-repetitive sequences were at an abundance of 1 (Figure 1.1B, bottom). Given our desire to keep K as small as possible due to the fact that each increase in K makes the number of K-mers grow exponentially, we decided to use a value of K = 12 for further analyses since it appears to be the minimum value wherein we start to gain the specificity to identify repetitive sequences.

Our approach is intended to estimate sequence abundance in a genome from Illumina reads. To demonstrate that 12-mer abundances in sequencing reads provide an accurate summary of a given genome, we compared the 12-mer profiles produced by our pipeline for sequencing reads at ~23 X coverage from accession Col-0 [14] with the corresponding 12-mer profile of the TAIR10 reference genome. 12-mer abundances in the reference and Illumina sequences were well correlated ($R^2 = 0.86$), and the large majority of 12-mers were distributed around a slope of 1 (Figure 1.1C). However, a subset of K-mers were found in higher abundance in the Illumina sample than in the reference genome as indicated by a strong positive skew in the distribution of residuals from a linear model fit (Figure 1.S1). These 12-mers were strongly enriched in repetitive sequences, suggesting that this discrepancy arises from repeats that were collapsed during the reference genome assembly [17].

Given the strong relationship between 12-mer abundance in sequencing reads compared to the assembly, we sought to determine the degree to which this relationship is dependent on sequencing coverage. To do this, we compared the correlation between 12-mer abundances in simulated reads from the TAIR10 assembly and sampled reads from the Illumina resequencing data for various coverages from 0.1 X to 10 X. As expected, the Spearman's correlation drops precipitously at ultra low coverages < 1 X (Figure 1.S2).

We next asked whether GCPs built with 12-mers could be used to accurately estimate the abundance of specific sequences in the *A. thaliana* genome. Annotated transposon abundance estimates using our approach were positively, though imperfectly, correlated with the actual occurrence of repeats in the reference genome ($R^2 = 0.66$, Figure 1.1D). Based on these observations, we selected K = 12 as a reasonable compromise between dataset size and ability to discriminate the repetitive sequence abundance.

Together these analyses indicate that 12-mer GCPs can reproduce abundance differences between sequences in a genome, and may facilitate relatively accurate estimates of the abundance of very repetitive sequences not resolved in draft or even high quality genome assemblies.

A species-wide description of genome content

We summarized the genomes of 1,319 natural collections of *Arabidopsis thaliana* by counting the abundance of 12-mers in whole-genome sequencing reads [14,19,20] (Table 1.S1). After filtering low quality and near-identical samples (Figure 1.S3), the dataset represents 1,043 *A. thaliana* genomes with the normalized abundances of 8,390,656 discrete 12-mers. We then used each GCP to estimate the abundance of known repetitive sequences (Table 1.S2) in each of the 1,043 genomes. For purposes of comparison, we also estimated the abundance of a set of genes that are expected to be under strong selective pressure to remain as a single copy [1]. Repetitive sequences had much higher copy number variability than BUSCOs (Figure 1.2A). Overall, copy number variability of sequences scaled according to their abundance in the genome, with the sequences at the highest copy number having the highest copy number variability.

To map regions of the genome that showed usually high variation in content, we calculated the standardized range (sR) of abundance across all accessions in 100 KB windows. The standardized range in our scan spans two orders of magnitude with highly variable regions constrained to genomic regions that are repeat-rich and gene-poor (Figure 1.2B, Figure 1.S5). The most variable windows correspond to known cytological features including the pericentromere and centromere on all five chromosomes, the nucleolar organizer region (rDNA) on chromosome 2 (NOR4 is missing from the reference genome), and the heterochromatic knobs on chromosomes 4 (hk4S) and 5 (hk5L). In addition to heterochromatic regions of the genome, highly variable regions included a cluster of pre-tRNA genes on chromosome 1, clusters of cysteine-rich repeat secretory genes on chromosomes 3 and 4, and the RPP5 NBS-LRR disease resistance gene cluster on chromosome 4 which is known to vary substantially between accessions [21].

Genetic mapping of repeat abundance

Our analyses suggested that genome content variation might arise through changes in repeat-dense, heterochromatic parts of the genome. But, the dispersed nature of many repeats makes it difficult to definitively pinpoint variable sequences. To map the location of variable repetitive sequences in the genome, we treated the abundance of each repeat like a phenotype in a genome wide association (GWA) study. Significant single nucleotide polymorphisms (SNPs) in each GWA are potentially linked to variation in the repeat of interest. A total of 384 of the 659 tested repeats had one or more significant variants per a Bonferroni threshold. These included 167 / 348 retrotransposons, 111 / 166 DNA transposons, all 22 satellites, and 84 / 121 simple repeats.

Significant associations were strongly clustered in the genome in repeat-rich regions, especially in centromeric and pericentromeric regions for all repeat classes (Figure 1.3). Per a Bonferroni adjusted threshold, we identified 76 retrotransposons, 19 DNA transposons, 15 satellites, and 14 simple repeats with significant SNPs enriched in centromeres (Table 1.S3). Sequences with enrichment of significant SNPs within the centromere were non-randomly distributed across transposon superfamilies and satellite and simple repeat subclasses. Of the retrotransposons tested, 46% of Copia superfamily transposons and 75% of Gypsy superfamily transposons were enriched for significant SNPs in the centromeres. Also enriched in the centromere were DNA transposons of the En/Spm superfamily except ATENSPM1, ATHAT1 of the hAT superfamily, and some MuDR and VANDAL superfamily transposons. We did not identify any centromeric enrichment for retrotransposons of the L1 or SADHU superfamilies or DNA transposons of the helitron, mariner/Tc1, and pogo superfamilies. All satellites save for rDNA repeats and ATCLUST1 were enriched for centromeric SNPs. The GATCGATCGATC tetramer and some penta- and hexa- mers were also enriched for centromeric SNPs.

An enrichment of significant SNPs in centromeric regions does not indicate cis regulation of sequence abundance variation *per se.* To demonstrate that the significant hits within centromeres are indicative of genuine cis hits and can be localized to specific centromeres, we partitioned the GWA by whether they were significantly enriched for centromeric SNPs and compared the distribution of significant SNPs and sequence annotations across chromosome arms and centromeres. For sequences enriched for centromeric SNPs we observed that the proportion of significant SNPs within a centromere is correlated with the proportion of sequence annotations within the same centromere, suggesting that centromeric significant SNPs represent cis-acting variants associated with sequence abundance variation (Figure 1.S6).

We further examined the localization of repetitive sequences to specific centromeres. In general, for transposons, there was a mixture of Copia and Gypsy superfamily LTR retrotransposons localized to all five centromeres, VANDAL superfamily DNA transposons localized to the centromeres on chromosomes 1-3, MuDR superfamily DNA transposons localized to the centromeres in chromosomes 2-5, and En/Spm superfamily DNA transposons localized to the centromeres on chromosomes 1-2. Notable sequences with sequence abundance variation localized to centromere 1 included a number of Copia transposons including ONSEN (ATCOPIA78), Gypsy transposons of the ATHILA8A family, satellite ATREP18 which contains the major telomere repeat, and centromere satellite variants from clusters 5 and 6. We localized abundance variation in AtSB5, a SINE Non-LTR retrotransposon, and ATMSAT1, a mini-satellite, to centromere on chromosome 2. Of note localized to centromere on chromosome 3 were all families of autonomous ARNOLD MuDR superfamily DNA transposons, and centromere satellite variant AR3. Centromere 4 was marked with variation in abundance of ATHAT1, the only hAT superfamily DNA transposon localized to a centromere, and numerous centromere satellite variants (AT12, COLAR12, cluster 2, cluster 3), as well as the major knob repeat of hk4S (ATENSAT1). Aside from transposons described previously, the only notable sequences localized to centromere 5 were variants of the hk5L knob repeat (Table 1.S4).

Putative mutator alleles regulate copy number change of repetitive sequences in trans

The observation that differences in repeat content between genomes are explained by the differential abundance of multiple classes of repetitive sequences suggests a common genetic basis of repeat expansions and contractions. Since the molecular basis of repeat evolution is variable across repeat classes, alleles that affect the abundance of multiple repetitive sequences likely are modulating the mutation rate and are thus referred hereafter as “putative mutator alleles.” To discover putative mutator alleles, we produced meta-analyses of the GWA mapping sequence abundance variation, partitioned by sequence class. After filtering sequences with correlated abundance and GWA with evidence of extensive p-value inflation, the three meta-GWA analyses consisted of 88 retrotransposons, 31 DNA transposons, and 60 simple repeats (Figure 1.4).

Given the complexity of statistical power differences across the meta-GWA caused by different numbers of input GWA, we set a hard threshold and considered the top 0.1% of variants in each meta-analysis to be “focal variants.” There was considerable overlap between the focal variants from the meta-GWA, with 915 of 2749

(33%) variants focal in two and 314 variants focal in all three sets (11%). GO analysis of variants focal in two or three meta-GWA revealed an enrichment for numerous processes involved in DNA replication and repair such as nuclear DNA replication, DNA strand elongation involved in DNA replication, DNA methylation on cytosine, DNA replication initiation, double-strand break repair via break-induced replication, and mismatch repair (Table 1.S5). We also manually examined the meta-GWA peaks shared between all three analyses and found focal variation linked to non-synonymous variation in multiple genes involved in DNA replication, recombination, and repair such as *AT1G49250*, which encodes an ATP-dependent DNA ligase, *PDS5B (AT1G77600)*, which encodes a mitotic sister chromatid cohesion protein, *FAS2 (AT5G64630)*, which has been linked to increased frequency of homologous recombination, and *AT1G14460*, an AAA-type ATPase family protein that is part of the DNA polymerase III complex. Meta-GWA peaks for the two analyses of transposons were linked to non-synonymous variation in *AT5G51795*, a DNA/RNA binding protein with Kin17 conserved region and *TOP1 (AT5G55310)*, encoding DNA topoisomerase I beta. We also identified linked variation shared in two or more classes near recombination acting *AtRAD51 (AT5G20850)*, *AtBRCA2B (AT5G01630)*, and *CMT3 (AT1G69770)*, a chromomethylase that acts to methylate cytosines in non-CG context. A full list of shared focal meta-GWA variants and candidate loci is listed in Table 1.S6.

On average, minor alleles were associated with more increases than decreases in sequence copy number abundance across all three sequence classes (Figure 1.S7). Considered in a pairwise fashion, the majority of minor alleles at shared focal variants had a consistent (i.e. non antagonistic) effect on both sequence classes, although we were able to detect some alleles with antagonistic relationships (Figure 1.S8). The proportion of variants in the four effect classes did not vary significantly across comparisons.

Evolutionary dynamics of potential mutator alleles

To understand the evolutionary dynamics of putative mutator alleles, we calculated site frequency spectrums for these loci at both the species-wide and admixture group levels. Focal meta-GWA variants were enriched for low frequency derived alleles (Figure 1.5A). The strength of the enrichment for alleles that were focal across one or two groups is similar to the enrichment of low frequency derived alleles in putatively causal variants from GWAS from the AraGWAS database [22]. Focal variants shared across all three sequence classes had an even stronger enrichment for low frequency derived alleles. These data suggest that variants associated with sequence abundance variation are subject to strong purifying selection at a species wide level, with the strength of selection even stronger for variants affecting all three sequence classes.

We further examined the site frequency spectrum partitioned by population group for focal sites across all three meta-GWA analyses to determine whether the pattern of enrichment for low frequency derived alleles was present across all admixture groups. While the pattern is similar across most population groups, some groups such as North Sweden, Asia, and Relict are instead enriched for intermediate or high frequency derived alleles indicating that the pattern is not universal across the species range (Figure 1.5B). Increased frequency of derived alleles at focal meta-GWA sites in some groups could be due to either differential selection experienced by individuals on the fringe of the species range or due to reduced selection efficacy due to differences in effective population size. To test the latter hypothesis, we compared the number of sequences with copy number change to the ratio of mean derived allele frequency for nonsynonymous vs synonymous sites. We found a strong correlation (Spearman's rho 0.73, p =0.031, Figure 1.5C) between the number of sequences with copy number change and the frequency of nonsynonymous sites compared to synonymous sites. This result suggests that differences in effective population size (as approximated by the frequency of nonsynonymous to synonymous variation) reasonably explains copy number proliferation of repetitive sequences in Eurasian *A. thaliana*.

Discussion

A K-mer based method to estimate sequence copy number

In this work, we present a novel K-mer based approach to estimate sequence copy number from high-throughput sequencing reads and apply the method to study genome content variation in a species-wide survey of *A. thaliana*. The premise of the method is to use high-throughput sequencing reads to profile a genome while avoiding the complexities of genome assembly. As such, the method is useful to study sequences that present difficulties when assembling genomes from short reads such as repeats [17], but has the disadvantage of being unable to localize a sequence in a genome. While we have entered the era of complete (i.e. telomere-to-telomere) genome assemblies [23], these assemblies take considerable resources to produce and will likely be infeasible for population-scale genomic variation studies for some time. Until then, our method will remain relevant to study variation in genomes using newly generated short reads or the extensive library of high-throughput sequencing reads in public databases such as NCBI SRA.

One important consideration when running the pipeline is the choice of the length of K-mer to use. While we described a method here to choose K and settled on K = 12 for this work, we admit that the choice of K is somewhat arbitrary and could affect the accuracy of the sequence copy number estimates. While we had success in mapping variation in genome content with K = 12, our K-mer based estimates of repeat abundance are imperfectly correlated with annotated repeat abundance. Our choice was somewhat motivated by the fact that each increase in K increases the size of the dataset exponentially and increases the number of singletons (i.e. K-mers with abundance of 1). Future work with larger K and simultaneous filtering of singleton K-mers to reduce the dataset size might provide more accurate estimates and increase the power of subsequent analysis.

To produce copy number estimates from genome content profiles, the method is also dependent on providing reference sequences from which the K-mer hash table is derived. The sequence abundance is then estimated by calculating the median abundance of constitutive overlapping K-mers. The assumption being made is that the sequence whose abundance is being estimated is conserved across genome content profiles. While the method is able to handle sequences with variation coded by IUPAC nucleotide ambiguity codes, the current implementation generates all possible K-mers encoded by the ambiguity code and then substitutes the median value of the possible K-mers for the K-mer with ambiguity when calculating the abundance estimate. If there are multiple ambiguous nucleotides within a single K-mer, the number of K-mers considered is quite large, costing performance. An improved implementation of the pipeline could substitute a weighting scheme to better handle conserved and variable sequences within a reference sequence.

A major issue with the approach is that K-mer profiles seem to be especially sensitive to technical biases in sequencing. We discovered this effect by doing a principal component analysis of 12-mer profiles and realized that samples clustered according to sequencing center (Figure 1.S9). We investigated this issue by attempting to isolate the variable responsible for the technical bias (e.g. GC content differences between libraries, organellar contamination, high or low abundance 12-mers) but were unsuccessful. In particular, in the 1001 Genomes dataset, population group and sequencing center were confounded, making it impossible to distinguish between biological and technical variation. In the end, we dealt with this issue by fitting a linear model to coarsely remove the effect of sequencing center with the understanding that we were also likely removing some biological variation from the dataset. Our recommendation for further use is to avoid the issue of technical sequencing bias by applying the pipeline only to samples sequenced as part of the same sequencing experiment at least where population and experiment are not confounded.

Genome content variation in A. thaliana

Our results indicate that genome content variation in *A. thaliana* is mostly explained by copy number variation of repetitive sequences present in the centromere and pericentromere. Compared to chromosome arms, the centromere and pericentromere of the *A. thaliana* genome are especially repeat rich, probably due to the effect of strong purifying selection acting against repeat proliferation in gene-rich regions [15,24]. Given that centromeres essentially act as large tracts of linked variation, it remains to be seen whether the patterns of genomic variation in *A. thaliana* are best explained by proliferation and loss of individual repeat families or distribution of centromeric haplotypes. We did observe that the abundances of some repeats across classes were positively or negatively correlated but our K-mer method does not give us the power to localize sequences in proximity to one another. Previous work has shown that centromeres are rearrangement hotspots in this species [25], which is counter to the notion that centromeres are devoid of variation and rarely experience recombination.

The family-level genome-wide mapping for transposon copy number variation was strikingly similar to the results of previous efforts based on coverage-based copy number estimates in a smaller cohort [15]. However, while our GWA had many of the same peaks, there were slight differences between the mapping results that can probably be attributed to differences in genetic heterogeneity between mapping cohorts [26].

The meta-GWA analyses uncovered many candidate loci associated with copy number changes across repeat classes. While we were not able to identify the candidate genes under all peaks (Figure 1.4), many of the genes that we were able to identify are involved in DNA replication or DNA repair. Further, we showed that these sites are experiencing strong purifying selection at the species level, despite being associated with both copy number increase and decrease. Taken together, our results suggest that natural variation affecting genes involved in mutational processes are implicated in repeat copy number variation and that changes in repeat copy number are strongly deleterious in *A. thaliana.* This is in opposition to the view that repeat copy number increase is deleterious while copy number loss is neutral or under positive selection.

The work presented here provides insight into the molecular and evolutionary processes governing genome content variation in a plant species and provides many avenues for future research. In particular, the contribution of centromeric haplotypes to genome content variation in eukaryotic genomes remains mostly unexplored. Current long read sequencing technologies and the construction of complete genomes will yield better descriptions of the previously inaccessible repeat-rich compartments of the genome. Finally, molecular characterization of the candidates presented here will increase our understanding of the mechanisms affecting plant genome evolution.

Material and Methods

Genome annotation

TAIR10 genome assembly was annotated with RepeatMasker 4.1.1 [27] using the Dfam 3.2 library [28] and specifying “-species arabidopsis”.

BUSCO 3.02 [1,29] was run on the TAIR10 genome assembly using Eudicotyledons OrthoDB release 10 [30]. Augustus 3.3 [31] was used as a dependency for the BUSCO pipeline.

Genome content profiles

Sequencing reads from 1319 previously sequenced accessions of *Arabidopsis thaliana* (studies PRJNA273563 [14], PRJEB19780 [19], and SRP062811 [20]) were downloaded from the European Nucleotide Archive. The reads were adapter and quality trimmed with

Trimmomatic 0.36 [32] to remove sequencing adapters, low quality sequence on read ends (quality < 20), low quality sequence in sliding windows (clip at quality < 20 in 4 bp sliding window), the first 20 base pairs of each read, and reads less than 36 base pairs long. A custom adapter file containing all Illumina single end (SE) or paired end (PE) adapter sequences was used to trim adapters from SE or PE reads, respectively. Trimmed reads were then error corrected with BayesHammer [33] as implemented in SPAdes 3.15.0 [34]. Error-corrected reads were then mapped to both the TAIR10 reference genome and the organellar genomes [35] separately with bwa 0.7.17 [36,37]. Alignment statistics were calculated with samtools 1.9 [38]. To reduce contamination from reads originating from the organellar genomes, reads that did not map to the organellar genomes were extracted from the alignments with bedtools 2.27.0 [39]. Canonical 12 mers (i.e. sequences and reverse complements were binned together) were counted in the unaligned reads using jellyfish 2.2.9 [40].

To remove samples that likely contained contamination, samples in which less than 90% of processed reads mapped to the TAIR10 reference genome were excluded from further analysis. Samples with coverage less than 1X based on coverage estimates produced using the sum of raw K-mer abundances found in the library divided by the approximate size of the genome (150 Mbp) were also subsequently disqualified. To remove libraries with extremes of GC content, which are likely due to PCR-bias during library preparation [41], samples with extreme GC content were filtered according to the 1.5 IQR rule.

To enable the comparison of 12-mer profiles between accessions, 12-mer counts for each sample were normalized according to a two step process. First, to correct for

GC content bias due to variable library preparation across samples, raw 12-mer counts were transformed such that the proportion of counts that fell into GC bins defined by the GC content of each 12-mer sequence was constant across samples. As a “reference sample” for the transformation, the proportion of counts attributed to each GC bin was calculated using the median count for each 12-mer across accessions. For each sample, the proportion of counts attributed to each GC bin was tabulated and a weight was calculated as the ratio of the proportion of the “reference sample” counts in each GC bin to the proportion of the sample counts in each GC bin. Sample counts were then transformed by multiplying the raw counts by the corresponding weights of each GC bin. Samples with extreme Spearman’s correlation between GC-normalized 12-mer count and 12-mer GC content were also filtered according to the 1.5 IQR rule.

To normalize for coverage differences, GC transformed counts were normalized by quantile-quantile normalization using limma v. 3.44.3 R package [42]. To reduce the impact of technical biases on 12-mer profiles, we removed the effect of sequencing center by fitting a linear model.

Finally, near-isogenic accessions were filtered from the dataset. Genetic distance was calculated using published genotypes [14] with plink 1.9 [43] and the distance matrix was hierarchically clustered and static tree cut at a height of 100000 in R [44]. For each cluster defined by the tree cut, one sample was randomly selected to be retained for further analysis and the remaining samples were filtered.

K-mer analyses of TAIR10 assembly

Canonical 5 - 20 mers were counted in repetitive and non-repetitive sequences of the TAIR10 genome assembly [35] using jellyfish 2.2.9 [40]. Designation of sequence as repetitive or non-repetitive was based on the RepeatMasker annotation described previously. From these K-mer counts, the number of unique K-mers and the median K-mer abundance per 100 Mbp were calculated.

To demonstrate that 12-mer profiles generated using the pipeline from sequencing reads reflect 12-mer profiles from genome assemblies, canonical 12-mers were calculated using jellyfish as described above for the TAIR10 assembly and compared to normalized 12-mer counts produced by the software pipeline described above and depicted in Figure 1.1A. Linear model was fit to log-transformed 12-mer counts using R [44].

To explore how coverage affects the relationship between the respective 12-mer profiles generated from sequencing reads and genome assemblies, Spearman's correlation was calculated between 12-mer profiles generated from Col-0 whole genome sequencing reads [14] and the TAIR10 assembly. For the sequencing reads, both empirical and simulated data were considered at coverages of 20, 10, 5, 2.5, 1, 0.5, 0.25, and 0.1X. Seqtk 1.2-r95 [45] was used for sampling of empirical data and wgsim 1.9 [38] was used to simulate 100bp reads from the TAIR10 assembly.

Sequence abundance estimation with genome content profiles

The abundance of annotated sequences were estimated in each genome content profile by extracting the overlapping 12-mers that compose the feature and calculating the median count of these representative 12-mers. This value was then transformed to an abundance estimate according to the following exponential equation: 2^x, where x is the median count of representative 12-mers. For all sequences besides the genomic windows, the abundance estimates were normalized by the median abundance estimate for complete single copy BUSCO genes within each sample. The *A. thaliana* Repbase 23.10 library [46] was used and supplemented with a 5S rDNA sequence from GenBank (GenBank M65137.1), a 45S rDNA sequence [47], and consensus sequences of each of the six 180bp centromere satellite variants described by [48]. Consensus sequences for each of the centromere satellite variant clusters was determined by further clustering sequences from each cluster with vsearch 2.9.1 [49] with a 75% identity threshold. The centroid that represented the greatest number of sequences per cluster was then used as the representative sequence for that cluster.

Statistical analysis for copy number change across admixture groups

To test for copy number change between admixture groups, the median of abundance estimates per sequence per group were compared to the respective median of abundance estimates from accessions of the Africa group. Wilcox-Mann-Whitney U tests were run using R [44]. Significance was determined using a Bonferroni adjusted threshold at the group level ($\alpha = 0.05 \; / 11$).

Sequence abundance variability across accessions

The standardized range (sR), defined as the range divided by the median of sequence abundance across accessions, was used to estimate sequence abundance variability.

Variant filtering and genome-wide association

Published variant calls from the 1001 Genomes Project [14] were filtered with bcftools 1.8 [38] and plink 1.9 [43] to retain biallelic sites called in 95% of individuals with a minimum minor allele frequency of 0.01 and minimum quality of 30.

Sequence abundance was treated as a molecular phenotype and mapped using genome-wide association with a mixed-linear model with GEMMA 0.98 [50]. Only sequences with a sR greater than the 99th percentile of sR across BUSCO genes were included in the analysis. A centered relatedness matrix was used to correct for population structure. K-mer sequence abundance estimates were $\log_2$-transformed prior to analysis. Bonferroni threshold (/N, where N is the number of variants) was used to determine significant variants for individual studies.

To determine if significant SNPs were enriched in the pericentromere and centromere, one-sided Fisher's Exact tests were applied to 2 X 2 contingency tables describing whether SNPs were significant or not or found within the pericentromere and centromere or chromosome arms. Only GWA with 10 or more significant SNPs were included in this analysis. Coordinates for the pericentromeres and centromeres are attributed to [51]. A Bonferroni threshold was used to determine significance for these tests.

GWA with enrichment for significant SNPs in the pericentromere and centromere were considered to be localized to a specific centromere if they had at least half of their significant SNPs present within the centromere.

The effect of an allele on sequence abundance was calculated by taking the harmonic mean of sequence abundance across individuals possessing the allele and comparing the value to the respective mean for individuals with the alternative allele.

Meta-analyses of genome-wide association of sequence abundance variation

Meta-GWAS analyses were performed separately for retrotransposons, DNA transposons, and simple repeats by combining p-values from genome-wide association likelihood ratio tests using Fisher's method per the following equation: 2 = -2i = 1klog (pi) [52] where *k* is the number of studies included in the meta-analysis and p_i is the p-value for a variant in study *i.* Individual studies with excess significant variants per Bonferroni threshold and studies in which the K-mer based sequence abundance estimates were strongly correlated (Spearman's rho > 0.60) were excluded from analysis.

To correct for test statistic inflation across studies included in the meta-analyses, the genomic inflation factor, , was calculated and used to correct the chi-squared values. was calculated as follows: = median (2 observed) / median (2 expected) where the median expected 2value is the value at the 0.5 / k quantile of observed values. Focal variants were considered to be the set of SNPs with the top 0.1% of 2value per meta-analysis.

Gene ontology enrichment analysis

Gene ontology enrichment analysis was done with topGO 2.46.0 [53] using the "weight01" algorithm and Fisher's exact test. Genes of interest were considered to be genes within

10 KB of focal meta-GWA SNPs for all three meta-GWA analyses. Genes were considered to be significantly enriched if $p < 0.05$.

Evolutionary analyses

Allele frequencies were calculated using plink 1.9 [43]. Alleles were assigned ancestral or derived state based on an alignment of the TAIR10 assembly to the *Arabidopsis lyrata* v.1 assembly [10] using minimap2 v. 2.17 [54] using the “asm10” parameter. Only sites with segregating ancestral and derived alleles in *A. thaliana* were considered for further analysis. Variants were classified as nonsynonymous or synonymous based on annotating the 1001 Genomes VCF using the Araport11 annotation [55] and Variant Effect Predictor v. 103.1 [56]. Associated variants from AraGWAS [57] were accessed on 2021-09-01 and consisted of 44,680 significant associations across 462 studies.

Sequences with copy number change were identified by testing whether the median sequence abundance per group was different from the median abundance in Africa, the presumed progenitor to all other groups, using Wilcoxon-Mann Whitney U test in R [44]. Bonferroni-adjusted alpha of 0.05 was used to determine significance.

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Figures and Tables

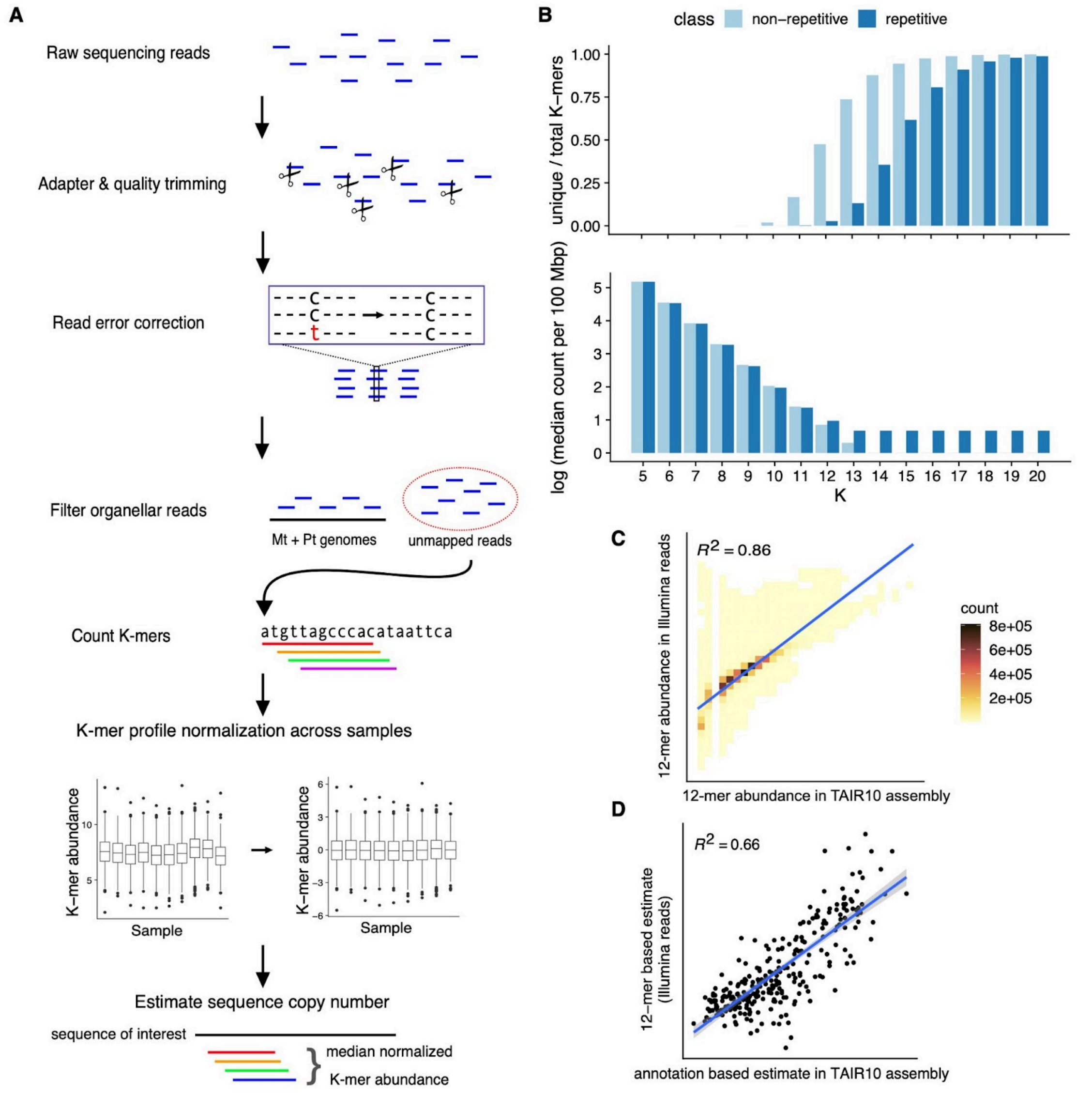

Figure 1.1 K-mer based approach to assess copy number variation from high-throughput sequencing reads.

A) Schematic of software pipeline to produce sequence copy number estimates from K-mers. B) The number of unique K-mers (top) and median K-mer abundance (bottom) for repetitive and non-repetitive sequences in the TAIR10 genome assembly. Both statistics are normalized by bin size. C) Relationship between 12-mer based abundance in Illumina reads compared to the reference genome for Col-0. D) Relationship between 12-mer based and annotation based copy number estimates for annotated transposons in the TAIR10 assembly.

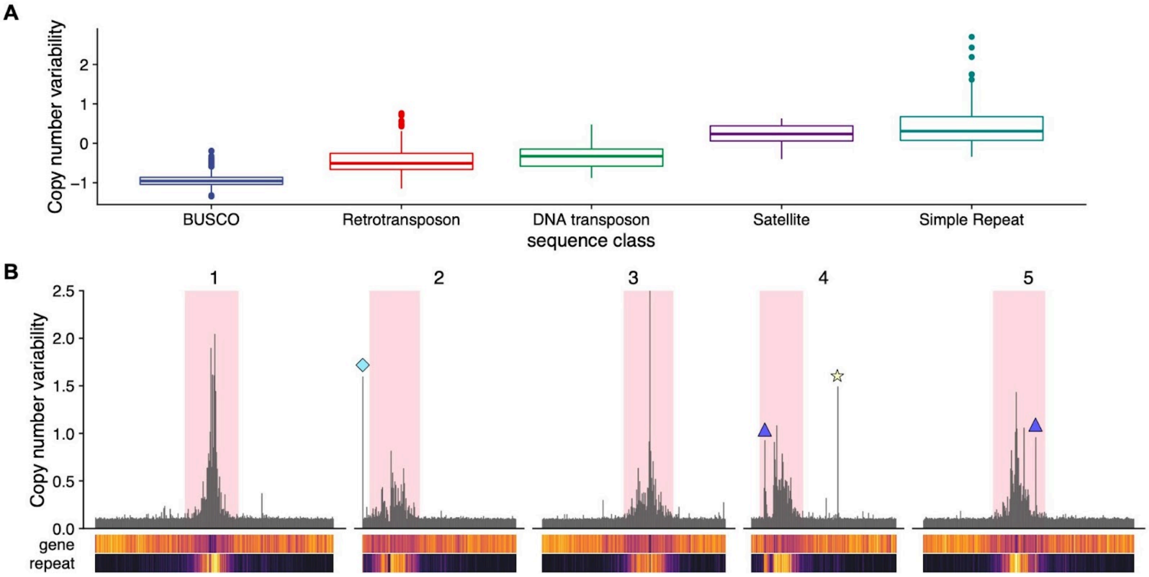

Figure 1.2 Genome content variation in A. thaliana is driven by repetitive sequences.

A) Tukey's box plots depicting the distribution of standardized copy number variability of annotated sequences by sequence class. BUSCO refers to conserved single copy genes. B) Standardized copy number variability in non-overlapping 100 KB windows across the A. thaliana Col-0 reference sequence. Shaded regions denote centromere and pericentromeric regions. Diamond = NOR2, triangles = knobs, star = cluster of cystein rich repeat proteins. All Y axes on log10 scale.

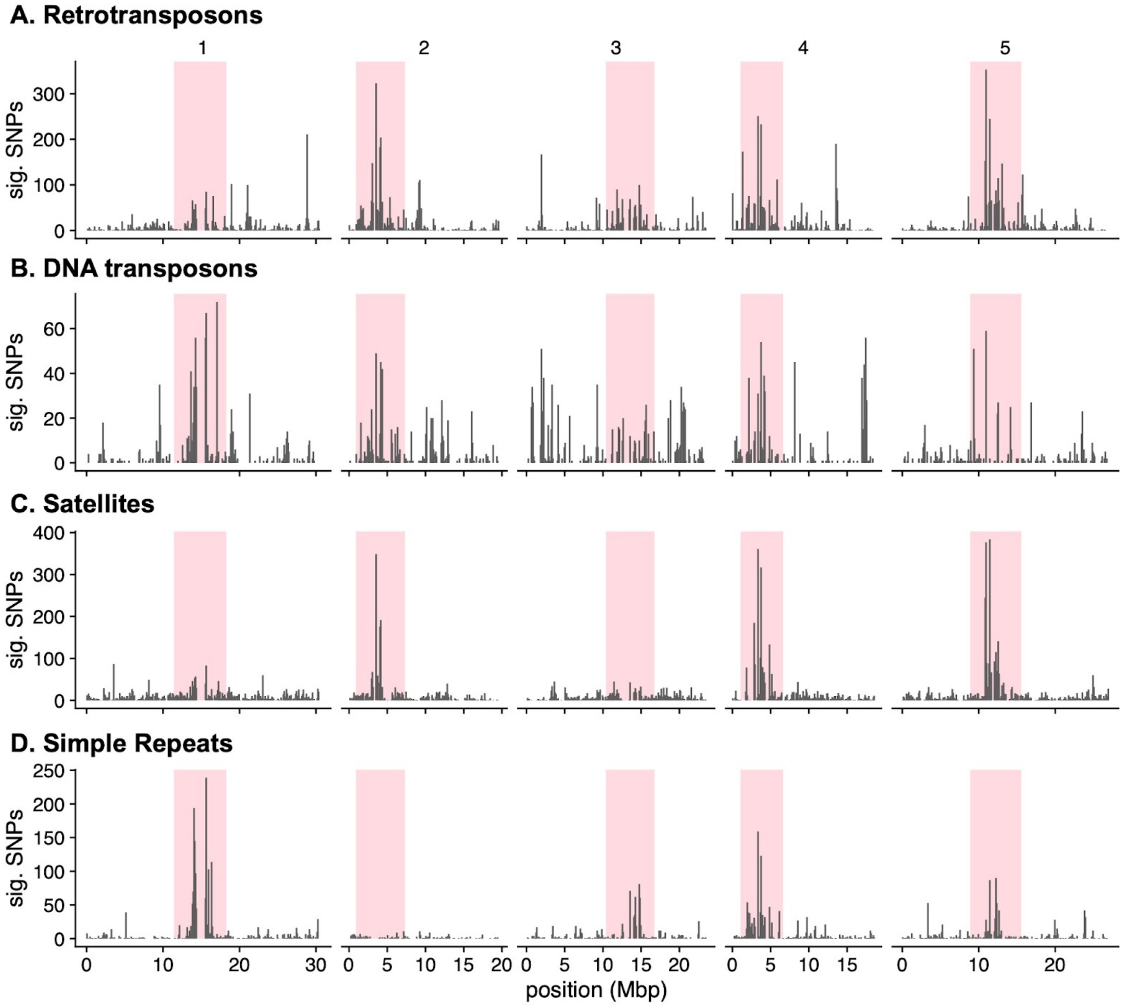

Figure 1.3 Summary of significant SNPs for copy number variation GWA.

Number of unique significant SNPs per 100 KB genomic window for GWA of copy number variation of A) Retrotranposons, B) DNA transposons, C) Satellites and D) Simple Repeats. Highlighted regions denote the centromere and pericentromere.

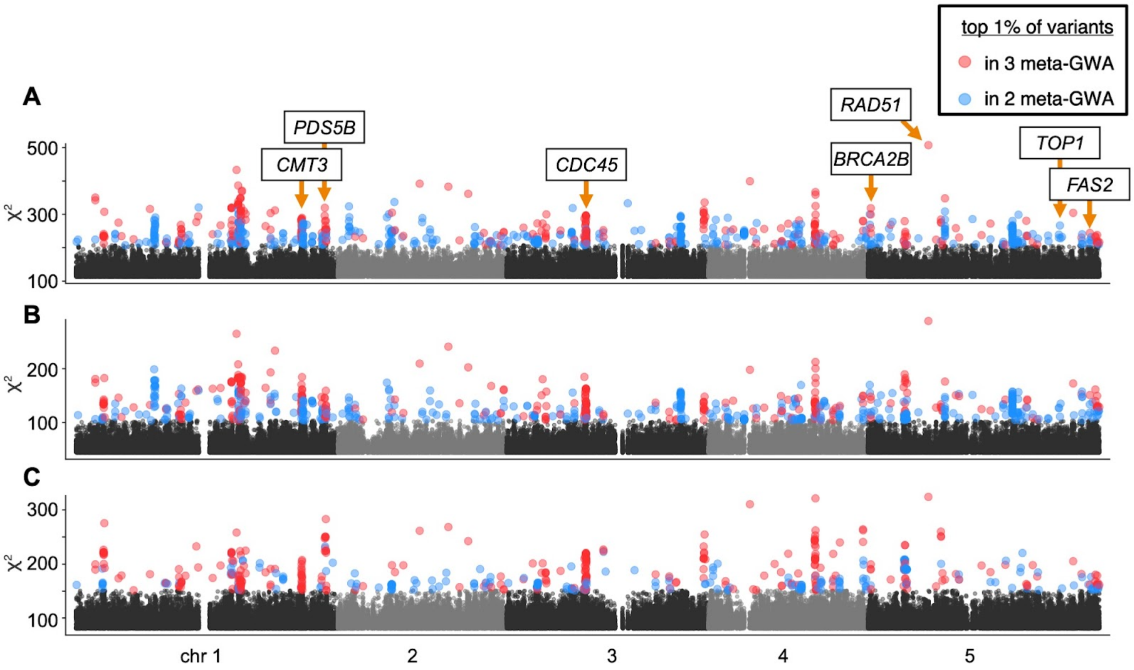

Figure 1.4 Meta-GWA of copy number variation of repetitive sequences.

Manhattan plots depicting meta-GWA analyses for variation in abundance of A) retrotransposons, B) DNA transposons, and C) simple repeats. Blue points are focal SNPs in two meta-analyses while red SNPs are focal SNPs in all three meta-analyses. Select candidates are labeled using orange arrows.

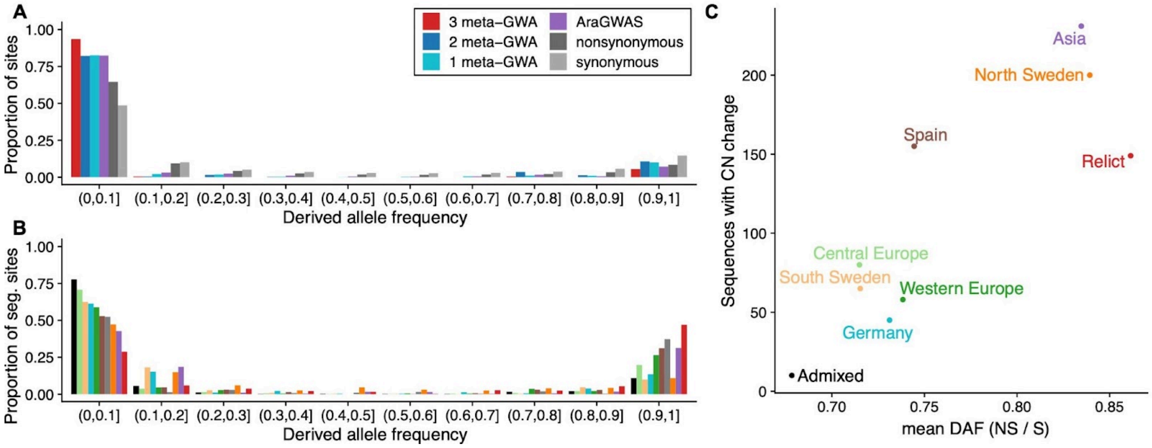

Figure 1.5 Evolutionary dynamics of potential mutator alleles.

A) Site frequency spectrum of focal SNPs from meta-GWA analyses compared to significant SNPs in AraGWAS database. B) Site frequency spectrum of SNPs focal in all three meta-GWA analyses by population group. C) The relationship between the number of sequences with copy number change and ratio of mean derived allele frequency for nonsynonymous vs. synonymous sites.

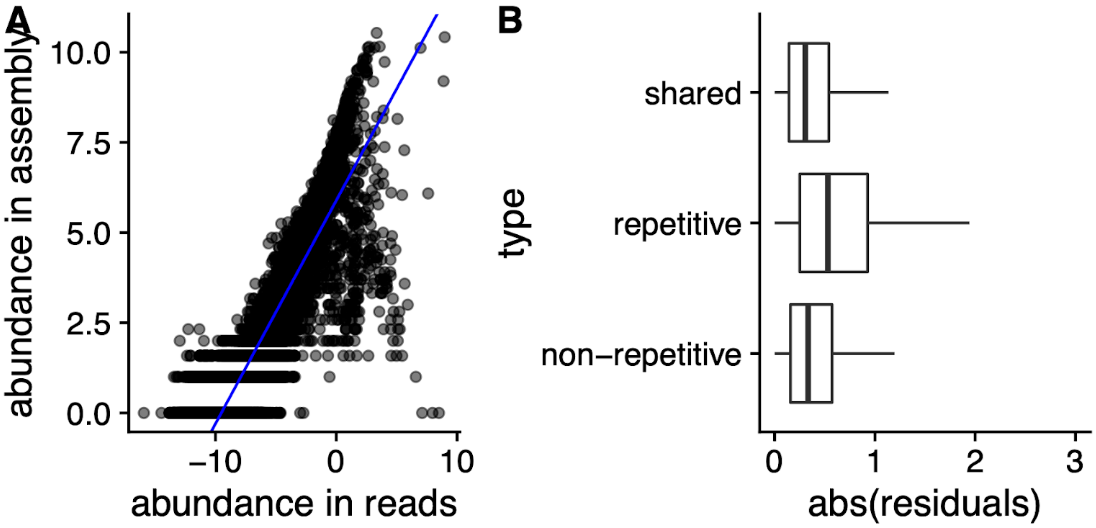

Figure 1.S1 Linear regression of 12-mer abundances from the TAIR10 genome assembly and sequencing reads.

A) Abundance of 100,000 random 12-mers on the log scale. Blue line represents the regression line calculated from all data. B) Magnitude of residuals partitioned by K-mers unique to repetitive or non-repetitive sequences or found in both bins (shared).

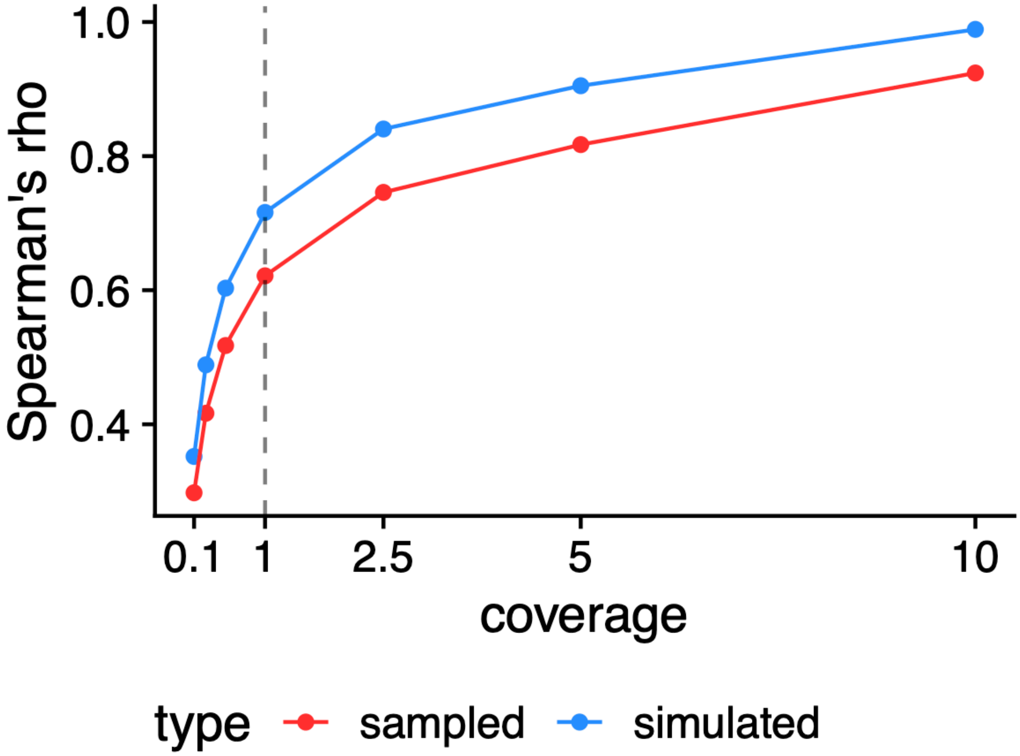

Figure 1.S2 Correlation between 12-mer profiles from TAIR10 genome assembly and sampled and simulated reads.

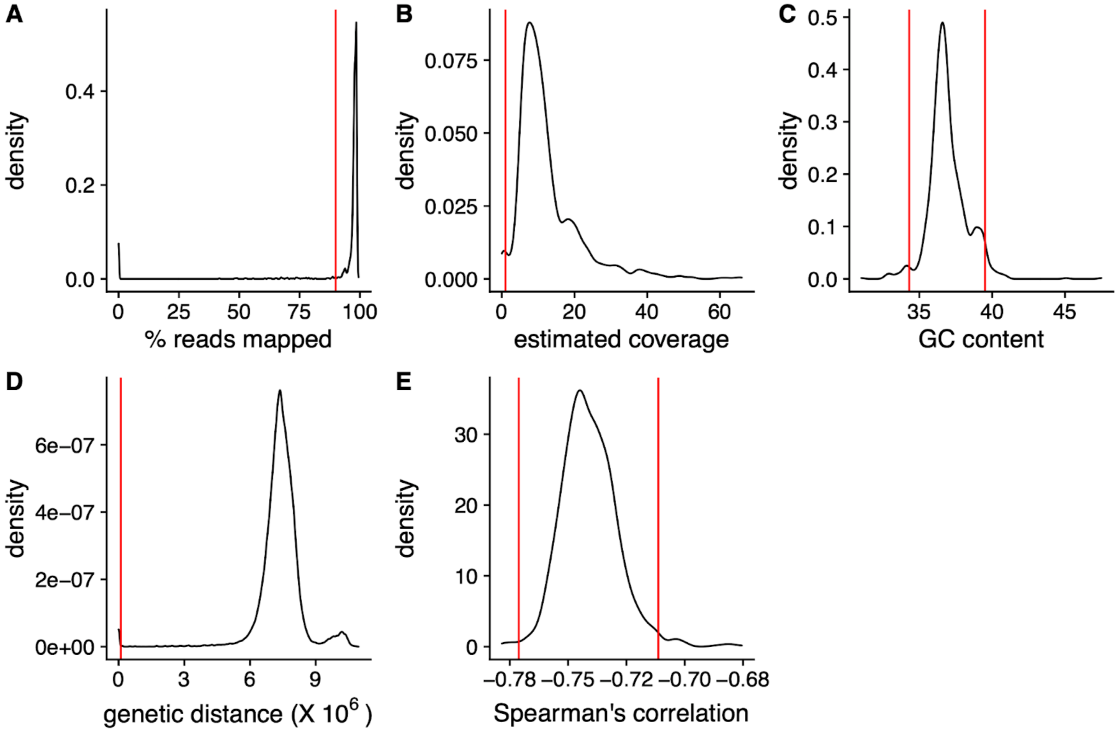

Figure 1.S3 K-mer counting software pipeline filters.

Distributions of A) proportion of reads mapped to TAIR10 genome per sequencing run, B) coverage estimated from 12-mer counts, C) GC content per sequencing run, D) Pairwise genetic distance (allele counts) and E) Spearman's correlation between GC content and 12-mer abundance. Vertical red lines indicate hard filtering thresholds. In A,B, and D samples with values less than the threshold were filtered. In C and E samples outside of the range denoted by the vertical lines were filtered.

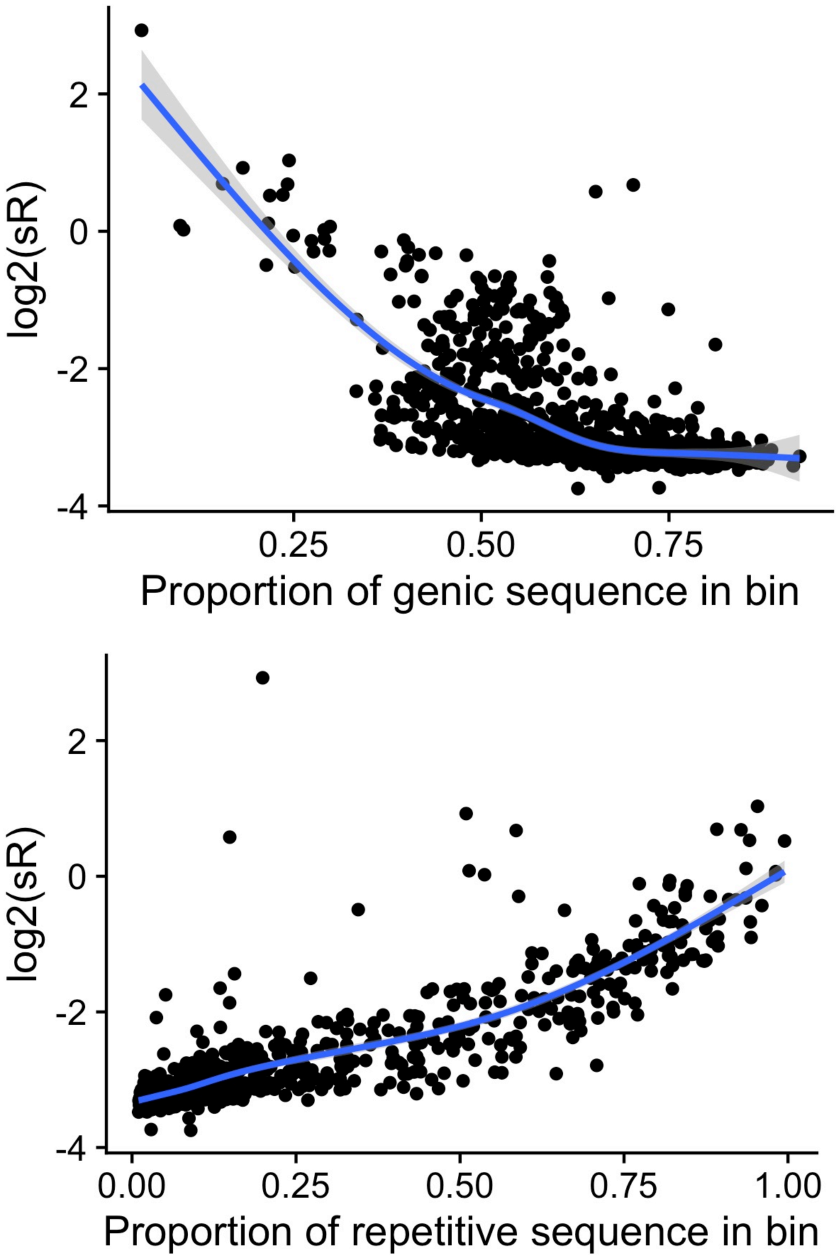

Figure 1.S4 Genome content variability on the log scale as a function of proportion of genic or repetitive sequence per 100 KB genomic window.

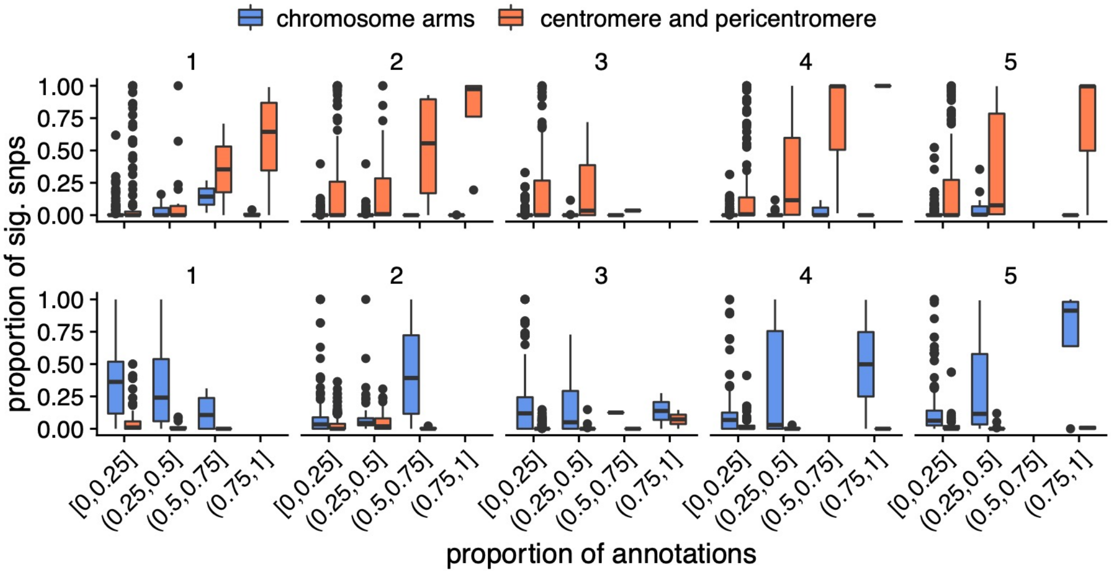

Figure 1.S5 Sequences in centromeres map to their respective loci.

Tukey's box plots showing the proportion of significant SNPs per sequence by quartile bins describing proportions of annotations for sequences with enrichment for significant SNPs in the pericentromere and centromere (top) and sequences that are not enriched for significant SNPs in the pericentromere and centromere (bottom). Boxplots are divided by whether the significant SNPs are in the centromere and pericentromere (orange) or in the chromosome arms (blue).

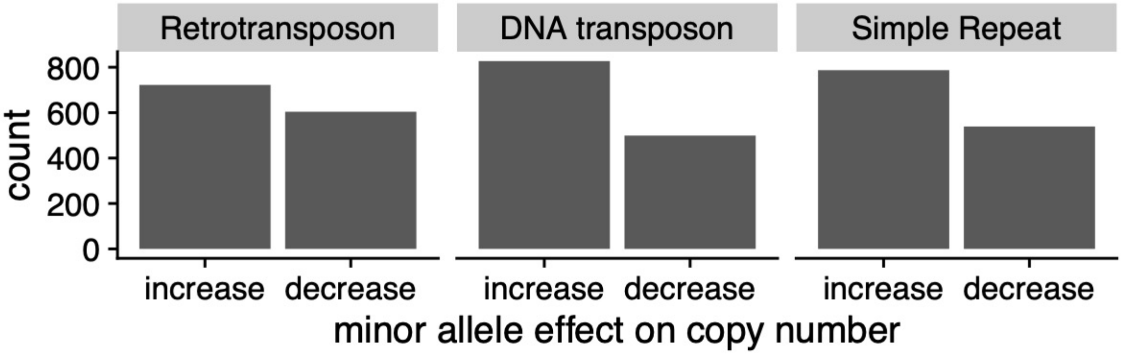

Figure 1.S6 Effect of minor alleles at focal sites on sequence copy number.

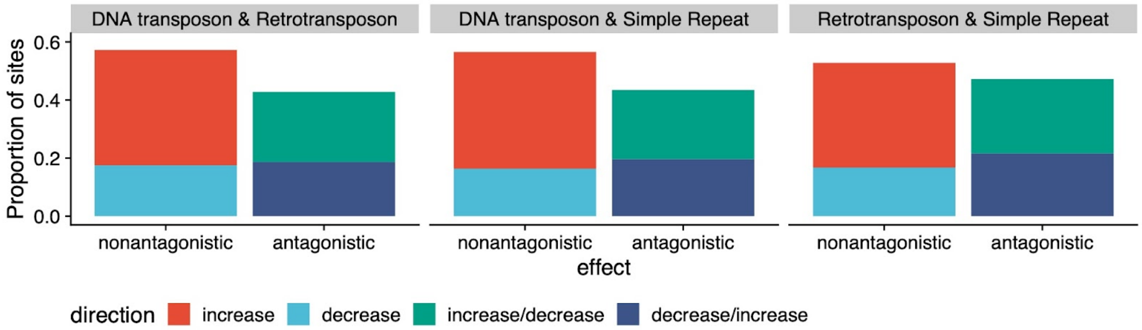

Figure 1.S7 Effect of minor alleles at focal sites on sequence copy number for focal alleles across groups considered pairwise.

Antagonistic effects are listed by the first sequence class / second sequence class.

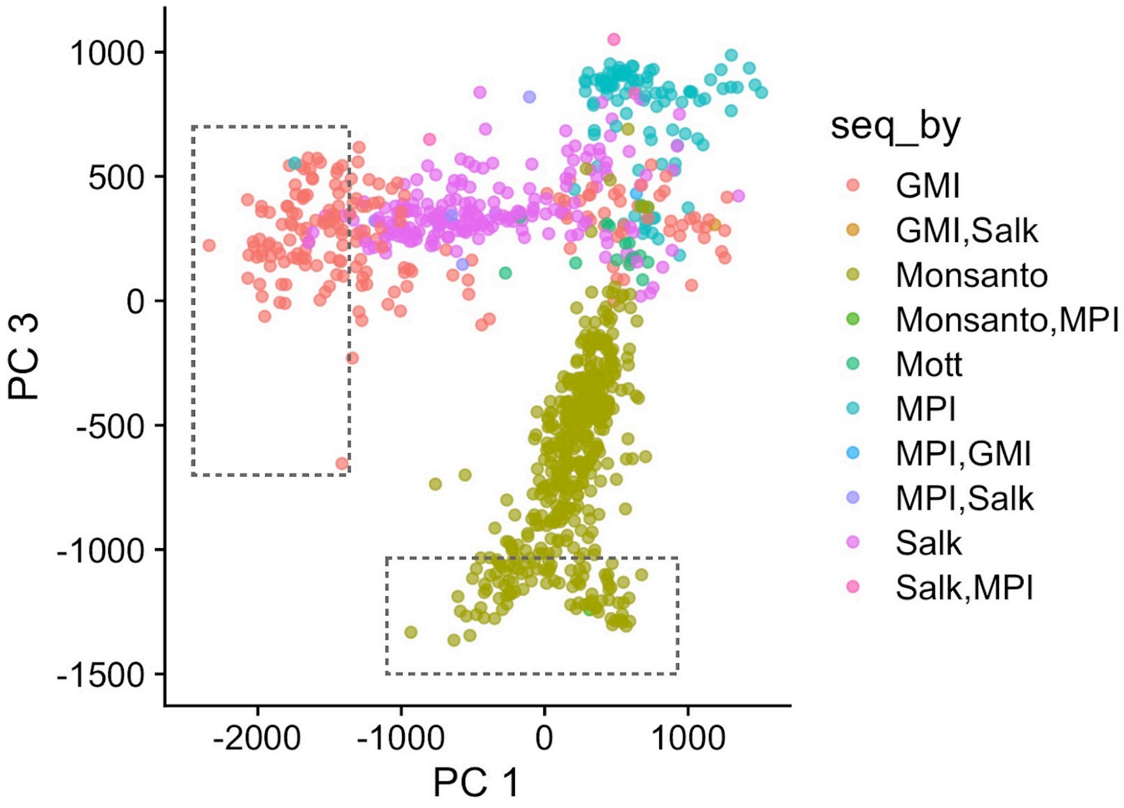

Figure 1.S8 Principal component analysis of 12-mer profiles before fitting model to remove effect of sequencing center.

PC 1 vs. PC 3 shown and samples are colored according to where they were sequenced.

Table 1.S1 Sample list

ID	**Name**	**CS id**	**Group**	**Latitude**	**Longitude**	**Seq. by**	**NCBI accession**	**Instrument**	**GCP**	**meta-GWA**
88	CYR	CS76790	Western Europe	47.40	0.68	Monsanto	SRR1945435	HiSeq 2000	Y	Y
108	LDV-18	CS77013	Western Europe	48.52	-4.07	Monsanto	SRR1945436	HiSeq 2000	Y	Y
139	LDV-46	CS77014	Western Europe	48.52	-4.07	Monsanto	SRR1945437	HiSeq 2000	N	N
159	MAR2-3	CS77070	Western Europe	47.35	3.93	Monsanto	SRR1945438	HiSeq 2000	Y	Y
265	PYL-6	CS77198	Admixed	44.65	-1.17	Monsanto	SRR1945439	HiSeq 2000	Y	Y
350	TOU-A1-88	CS77382	Western Europe	46.67	4.12	Monsanto	SRR1945440	HiSeq 2000	Y	Y
351	TOU-A1-89	CS77383	Western Europe	46.67	4.12	Monsanto	SRR1945441	HiSeq 2000	Y	Y
403	Zdarec3	CS78873	Central Europe	49.37	16.27	Monsanto	SRR1945442	HiSeq 2000	Y	Y
410	Doubravnik7	CS76808	Central Europe	49.42	16.35	Monsanto	SRR1945443	HiSeq 2000	Y	Y
424	Draha2	CS76812	Central Europe	49.41	16.28	Monsanto	SRR1945444	HiSeq 2000	Y	Y
428	Borky1	CS76718	Central Europe	49.40	16.23	Monsanto	SRR1945445	HiSeq 2000	Y	Y
430	Gr-1	CS76496	Central Europe	47	15.50	Salk	SRR1945446	HiSeq 2000	Y	Y
470	BRR4	CS78943	Germany	40.83	-87.74	MPI	SRR1945447	HiSeq 2000	N	N
476	BRR12	CS78944	Germany	40.83	-87.74	MPI	SRR1945448	HiSeq 2000	N	N
484	BRR23	CS78945	Germany	40.83	-87.74	MPI	SRR1945449	HiSeq 2000	N	N
504	BRR57	CS78946	Germany	40.83	-87.74	MPI	SRR1945450	HiSeq 2000	N	N
506	BRR60	CS78947	Germany	40.83	-87.74	MPI	SRR1945451	HiSeq 2000	N	N
531	BRR107	CS78948	Germany	40.83	-87.74	MPI	SRR1945452	HiSeq 2000	N	N

544	LI-WP-039	CS78949	Germany	40.91	-73.21	MPI	SRR1945453	HiSeq 2000	N	N
546	LI-WP-041	CS78950	Germany	40.91	-73.21	MPI	SRR1945454	HiSeq 2000	N	N
628	LI-OF-061	CS78951	Western Europe	40.78	-72.91	MPI	SRR1945455	HiSeq 2000	Y	Y
630	LI-OF-065	CS77036	Western Europe	40.78	-72.91	Monsanto	SRR1945456	HiSeq 2000	Y	Y
680	LI-RR-096	CS78952	Germany	40.94	-72.86	MPI	SRR1945457	HiSeq 2000	N	N
681	LI-RR-097	CS78953	Germany	40.94	-72.86	MPI	SRR1945458	HiSeq 2000	N	N
685	LI-EF-011	CS78954	Germany	40.91	-73.15	MPI	SRR1945459	HiSeq 2000	N	N
687	LI-EF-018	CS78955	Germany	40.91	-73.15	MPI	SRR1945460	HiSeq 2000	N	N
728	LI-SET-019	CS78956	Germany	40.94	-73.11	MPI	SRR1945461	HiSeq 2000	N	N
742	LI-SET-036	CS78957	Germany	40.94	-73.11	MPI	SRR1945462	HiSeq 2000	N	N
763	Kar-1	CS76522	Asia	42.30	74.37	Salk	SRR1945463	HiSeq 2000	Y	Y
765	Sus-1	CS76607	Asia	42.18	73.40	Salk	SRR1945464	HiSeq 2000	Y	Y
766	Dja-1	CS76473	Asia	42.58	73.63	Salk	SRR1945465	HiSeq 2000	Y	Y
768	Zal-1	CS76634	Asia	42.80	76.35	Salk	SRR1945466	HiSeq 2000	Y	Y
772	Neo-6	CS76560	Asia	37.35	72.47	Salk	SRR1945467	HiSeq 2000	Y	Y
801	KYC-33	CS76992	Germany	37.92	-84.46	Monsanto	SRR1945468	HiSeq 2000	N	N
853	MIA-1	CS78958	Germany	41.80	-86.67	MPI	SRR1945469	HiSeq 2000	N	N
854	MIA-5	CS78959	Germany	41.80	-86.67	MPI	SRR1945470	HiSeq 2000	N	N
867	MIC-20	CS78960	Germany	41.83	-86.44	MPI	SRR1945471	HiSeq 2000	N	N
868	MIC-24	CS78961	Germany	41.83	-86.44	MPI	SRR1945472	HiSeq 2000	N	N
870	MIC-31	CS77082	Germany	41.83	-86.44	Monsanto	SRR1945473	HiSeq 2000	Y	Y
915	LIN S-5	CS77040	Germany	41.90	-71.44	Monsanto	SRR1945474	HiSeq 2000	N	N
932	CHA-41	CS76765	Western Europe	42.36	-71.14	Monsanto	SRR1945475	HiSeq 2000	Y	Y
991	Ale-Stenar-41-1	CS76651	South Sweden	55.38	14.05	GMI	SRR1945476	HiSeq 2000	Y	Y
992	Ale-Stenar-44-4	CS76652	South Sweden	55.38	14.05	GMI	SRR1945477	Genome Analyzer IIx	Y	Y
997	Ale-Stenar-56-14	CS76653	South Sweden	55.38	14.05	GMI	SRR1945478	Genome Analyzer IIx	Y	Y
1002	Ale-Stenar-64-24	CS76654	South Sweden	55.38	14.05	GMI	SRR1945479	Genome Analyzer IIx	Y	Y

1006	Ale-Stenar-77-31	CS77636	South Sweden	55.38	14.05	GMI	SRR1945480	HiSeq 2000	Y	Y
1061	Brösarp-11-135	CS76727	South Sweden	55.72	14.13	GMI	SRR1945481	HiSeq 2000	Y	Y
1062	Brösarp-15-138	CS76728	South Sweden	55.72	14.13	GMI	SRR1945482	HiSeq 2000	Y	Y
1063	Brösarp-21-140	CS76729	South Sweden	55.72	14.13	GMI	SRR1945483	HiSeq 2000	Y	Y
1066	Brösarp-34-145	CS76730	South Sweden	55.72	14.13	GMI	SRR1945484	Genome Analyzer IIx	Y	Y
1070	Brösarp-45-153	CS77643	South Sweden	55.72	14.13	GMI	SRR1945485	Genome Analyzer IIx	Y	Y
1158	Aledal-6-49	CS76656	South Sweden	56.70	16.52	GMI	SRR1945486	HiSeq 2000	Y	Y
1166	Aledal-14-73	CS77651	South Sweden	56.70	16.52	GMI	SRR1945487	HiSeq 2000	Y	Y
1254	Tos-82-387	CS77379	North Sweden	59.43	17.02	GMI	SRR1945488	HiSeq 2000	Y	Y
1257	Tos-95-393	CS77380	North Sweden	59.43	17.02	GMI	SRR1945489	HiSeq 2000	N	N
1313	Ängsö-59-422	CS77658	Admixed	59.57	16.87	GMI	SRR1945490	HiSeq 2000	Y	Y
1317	Ängsö-74-430	CS76665	Admixed	59.57	16.87	GMI	SRR1945491	HiSeq 2000	Y	Y
1552	Sku-30	CS77251	North Sweden	63.08	18.37	GMI	SRR1945492	HiSeq 2000	N	N
1612	Brn-10	CS78962	Germany	41.90	-86.58	MPI	SRR1945493	HiSeq 2000	N	N
1622	Brn-24	CS78963	Germany	41.90	-86.58	MPI	SRR1945494	HiSeq 2000	N	N
1651	DuckLkSP38	CS78964	Germany	43.34	-86.40	MPI	SRR1945495	HiSeq 2000	N	N
1652	DuckLkSP40	CS78965	Germany	43.34	-86.40	MPI	SRR1945496	HiSeq 2000	N	N
1676	Haz-2	CS78966	Germany	41.88	-86.61	MPI	SRR1945497	HiSeq 2000	N	N
1684	Haz-10	CS78967	Germany	41.88	-86.61	MPI	SRR1945498	HiSeq 2000	N	N
1739	KBS-Mac-68	CS78968	Germany	42.41	-85.40	MPI	SRR1945499	HiSeq 2000	N	N
1741	KBS-Mac-74	CS78969	Germany	42.41	-85.40	MPI	SRR1945500	HiSeq 2000	N	N

1756	Ker-4	CS78970	Germany	42.18	-86.36	MPI	SRR1945501	HiSeq 2000	N	N
1757	Ker-5	CS78971	Germany	42.18	-86.36	MPI	SRR1945502	HiSeq 2000	N	N
1793	L-R-5	CS78972	Germany	41.85	-86.67	MPI	SRR1945503	HiSeq 2000	N	N
1797	L-R-10	CS78973	Germany	41.85	-86.67	MPI	SRR1945504	HiSeq 2000	N	N
1819	Lak-12	CS78974	Germany	41.80	-86.67	MPI	SRR1945505	HiSeq 2000	N	N
1820	Lak-13	CS78975	Germany	41.80	-86.67	MPI	SRR1945506	HiSeq 2000	N	N
1829	Mdn-1	CS77077	Germany	42.05	-86.51	Monsanto	SRR1945507	HiSeq 2000	Y	Y
1834	Mdn-8	CS78976	Germany	42.05	-86.51	MPI	SRR1945508	HiSeq 2000	N	N
1835	Mdn-10	CS78977	Germany	42.05	-86.51	MPI	SRR1945509	HiSeq 2000	Y	Y
1851	MNF-Pot-10	CS78978	Germany	43.60	-86.27	MPI	SRR1945510	HiSeq 2000	N	N
1852	MNF-Pot-15	CS78979	Germany	43.60	-86.27	MPI	SRR1945511	HiSeq 2000	Y	Y
1853	MNF-Pot-21	CS77099	Germany	43.60	-86.27	Monsanto	SRR1945512	HiSeq 2000	N	N
1872	MNF-Pot-75	CS77100	Germany	43.60	-86.27	Monsanto	SRR1945513	HiSeq 2000	Y	Y
1890	MNF-Riv-21	CS77101	Asia	43.51	-86.19	Monsanto	SRR1945514	HiSeq 2000	N	N
1925	MNF-Che-2	CS77096	Germany	43.53	-86.18	Monsanto	SRR1945515	HiSeq 2000	Y	Y
1942	MNF-Che-47	CS78980	Germany	43.53	-86.18	MPI	SRR1945516	HiSeq 2000	N	N
1943	MNF-Che-49	CS78981	Germany	43.53	-86.18	MPI	SRR1945517	HiSeq 2000	N	N
1954	MNF-Jac-12	CS77097	Germany	43.52	-86.17	Monsanto	SRR1945518	HiSeq 2000	N	N
2016	MNF-Pin-39	CS77098	Admixed	43.54	-86.18	Monsanto	SRR1945519	HiSeq 2000	Y	Y
2017	MNF-Pin-40	CS78982	Germany	43.54	-86.18	MPI	SRR1945520	HiSeq 2000	N	N
2031	Map-8	CS78983	Germany	42.17	-86.41	MPI	SRR1945521	HiSeq 2000	N	N
2053	Map-35	CS78984	Germany	42.17	-86.41	MPI	SRR1945522	HiSeq 2000	N	N
2057	Map-42	CS77732	Germany	42.17	-86.41	MPI	SRR1945523	HiSeq 2000	Y	Y
2081	MuskSP-68	CS78985	Germany	43.25	-86.34	MPI	SRR1945524	HiSeq 2000	N	N
2091	MuskSP-83	CS78986	Germany	43.25	-86.34	MPI	SRR1945525	HiSeq 2000	N	N
2106	MSGA-10	CS78987	Germany	43.27	-86.09	MPI	SRR1945526	HiSeq 2000	N	N
2108	MSGA-12	CS78988	Germany	43.27	-86.09	MPI	SRR1945527	HiSeq 2000	N	N
2141	MSGA-61	CS78989	Germany	43.27	-86.09	MPI	SRR1945528	HiSeq 2000	N	N
2159	Paw-13	CS78990	Germany	42.15	-86.43	MPI	SRR1945529	HiSeq 2000	N	N
2166	Paw-20	CS78991	Germany	42.15	-86.43	MPI	SRR1945530	HiSeq 2000	N	N
2171	Paw-26	CS77164	Germany	42.15	-86.43	Monsanto	SRR1945531	HiSeq 2000	Y	Y
2191	Pent-7	CS78992	Germany	43.76	-86.39	MPI	SRR1945532	HiSeq 2000	N	N
2202	Pent-23	CS77168	Admixed	43.76	-86.39	Monsanto	SRR1945533	HiSeq 2000	N	N

2212	Pent-46	CS78993	Germany	43.76	-86.39	MPI	SRR1945534	HiSeq 2000	N	N
2239	Riv-25	CS78994	Germany	42.18	-86.38	MPI	SRR1945535	HiSeq 2000	N	N
2240	Riv-26	CS78995	Germany	42.18	-86.38	MPI	SRR1945536	HiSeq 2000	N	N
2276	SLSP-31	CS77254	Admixed	43.67	-86.50	Monsanto	SRR1945537	HiSeq 2000	N	N
2278	SLSP-35	CS77255	Germany	43.67	-86.50	Monsanto	SRR1945538	HiSeq 2000	Y	Y
2285	SLSP-69	CS78996	Germany	43.67	-86.50	MPI	SRR1945539	HiSeq 2000	N	N
2286	SLSP-67	CS78997	Germany	43.67	-86.50	MPI	SRR1945540	HiSeq 2000	N	N
2317	Ste-40	CS77278	Admixed	42.03	-86.51	Monsanto	SRR1945541	HiSeq 2000	N	N
2370	Yng-4	CS78998	Germany	41.87	-86.65	MPI	SRR1945542	HiSeq 2000	N	N
2412	Yng-53	CS78999	Germany	41.87	-86.65	MPI	SRR1945543	HiSeq 2000	N	N
4779	UKSW06-179	CS78808	Western Europe	50.40	-4.90	Monsanto	SRR1945544	HiSeq 2000	N	N
4807	UKSW06-207	CS78809	Western Europe	50.40	-4.90	Monsanto	SRR1945545	HiSeq 2000	Y	Y
4826	UKSW06-226	CS78810	Western Europe	50.40	-4.90	Monsanto	SRR1945546	HiSeq 2000	N	N
4840	UKSW06-240	CS79000	Western Europe	50.40	-4.90	MPI	SRR1945547	HiSeq 2000	Y	Y
4857	UKSW06-257	CS79001	Western Europe	50.30	-4.90	MPI	SRR1945548	HiSeq 2000	N	N
4884	UKSW06-285	CS78811	Western Europe	50.30	-4.90	Monsanto	SRR1945549	HiSeq 2000	Y	Y
4900	UKSW06-302	CS78812	Western Europe	50.30	-4.80	Monsanto	SRR1945550	HiSeq 2000	N	N
4939	UKSW06-341	CS79002	Western Europe	50.40	-4.70	MPI	SRR1945551	HiSeq 2000	N	N
4958	UKSW06-360	CS78814	Western Europe	50.50	-4.50	Monsanto	SRR1945552	HiSeq 2000	Y	Y
5023	UKSE06-118	CS78799	Western Europe	51.30	0.50	Monsanto	SRR1945553	HiSeq 2000	N	N
5104	UKSE06-252	CS78800	Germany	51.30	0.50	Monsanto	SRR1945554	HiSeq 2000	N	N
5151	UKSE06-325	CS78801	Admixed	52.20	-1.70	Monsanto	SRR1945555	HiSeq 2000	Y	Y

5165	UKSE06-362	CS78802	Admixed	51.30	0.40	Monsanto	SRR1945556	HiSeq 2000	N	N
5210	UKSE06-432	CS78803	Western Europe	51.20	0.30	Monsanto	SRR1945557	HiSeq 2000	Y	Y
5236	UKSE06-470	CS78804	Western Europe	51.20	0.40	Monsanto	SRR1945558	HiSeq 2000	N	N
5249	UKSE06-491	CS79003	Western Europe	51.20	0.30	MPI	SRR1945559	HiSeq 2000	N	N
5253	UKSE06-500	CS78805	Western Europe	51.10	0.60	Monsanto	SRR1945560	HiSeq 2000	Y	Y
5276	UKSE06-533	CS78806	Western Europe	51.30	1.10	Monsanto	SRR1945561	HiSeq 2000	Y	Y
5279	UKSE06-541	CS79004	Western Europe	51.30	1.10	MPI	SRR1945562	HiSeq 2000	Y	Y
5349	UKSE06-639	CS78807	Western Europe	51.10	0.40	Monsanto	SRR1945563	HiSeq 2000	Y	Y
5353	UKNW06-003	CS78792	Western Europe	54.50	-3	Monsanto	SRR1945564	HiSeq 2000	Y	Y
5395	UKNW06-102	CS79005	Western Europe	54.40	-3	MPI	SRR1945565	HiSeq 2000	N	N
5486	UKNW06-233	CS78794	Germany	54.60	-3.30	Monsanto	SRR1945566	HiSeq 2000	Y	Y
5577	UKNW06-403	CS78797	Western Europe	54.70	-3.40	Monsanto	SRR1945567	HiSeq 2000	Y	Y
5644	UKNW06-481	CS78798	Western Europe	54.40	-2.90	Monsanto	SRR1945568	HiSeq 2000	Y	Y
5651	UKNW06-488	CS79006	Western Europe	54.40	-2.90	MPI	SRR1945569	HiSeq 2000	Y	Y
5717	Bra-1	CS79007	Western Europe	54.60	-3.20	MPI	SRR1945570	HiSeq 2000	N	N
5718	UKID11	CS79008	Western Europe	57	-3.40	MPI	SRR1945571	HiSeq 2000	N	N
5720	Cal-2	CS78781	Admixed	53.30	-1.60	Monsanto	SRR1945572	HiSeq 2000	Y	Y

5726	Cnt-1	CS78782	Western Europe	51.30	1.10	Monsanto	SRR1945573	HiSeq 2000	Y	Y
5741	For-2	CS78783	Western Europe	56.60	-4.10	Monsanto	SRR1945574	HiSeq 2000	Y	Y
5748	Kil-0	CS78784	Germany	56	-4.40	Monsanto	SRR1945575	HiSeq 2000	Y	Y
5757	Mc-1	CS78785	Admixed	54.60	-2.30	Monsanto	SRR1945576	HiSeq 2000	Y	Y
5768	UKID63	CS78786	Admixed	54.10	-1.50	Monsanto,MPI	SRR1945577	HiSeq 2000	Y	Y
5772	Set-1	CS78787	Admixed	54.10	-2.30	Monsanto	SRR1945578	HiSeq 2000	Y	Y
5776	UKID71	CS79009	Western Europe	52.90	-1.30	MPI	SRR1945579	HiSeq 2000	N	N
5779	UKID74	CS78789	Western Europe	51	-3.10	Monsanto	SRR1945580	HiSeq 2000	Y	Y
5784	Ty-1	CS78790	Admixed	56.40	-5.20	Monsanto	SRR1945581	HiSeq 2000	Y	Y
5798	UKID93	CS79010	Western Europe	53.10	-3.30	MPI	SRR1945582	HiSeq 2000	Y	Y
5800	UKID96	CS78791	Germany	57.40	-5.50	Monsanto	SRR1945583	HiSeq 2000	Y	Y
5811	UKID107	CS78778	Admixed	52.90	-3.10	Monsanto	SRR1945584	HiSeq 2000	Y	Y
5822	UKID116	CS78780	Admixed	56.73	-5.98	Monsanto	SRR1945585	HiSeq 2000	Y	Y
5830	App1-12	CS76667	South Sweden	56.33	15.97	GMI	SRR1945586	Genome Analyzer IIx	Y	Y
5831	App1-14	CS76668	South Sweden	56.33	15.97	GMI	SRR1945587	Genome Analyzer IIx	Y	Y
5832	App1-16	CS76669	South Sweden	56.33	15.97	GMI	SRR1945588	Genome Analyzer IIx	N	N
5836	Boo2-3	CS77906	South Sweden	55.86	13.51	GMI	SRR1945589	Genome Analyzer IIx	Y	Y
5837	Bor-1	CS76453	Central Europe	49.40	16.23	Salk	SRR1945590	HiSeq 2000	Y	Y
5856	Dör-10	CS76806	North Sweden	63.02	17.49	GMI	SRR1945591	Genome Analyzer IIx	Y	Y
5860	Dra-3	CS77913	North Sweden	62.68	18.02	GMI	SRR1945592	HiSeq 2000	Y	Y
5865	Dra1-4	CS76809	South Sweden	55.76	14.12	GMI	SRR1945593	HiSeq 2000	Y	Y

5867	Dra2-1	CS76810	South Sweden	55.76	14.12	GMI	SRR1945594	Genome Analyzer IIx	Y	Y
5874	DraII-6	CS76814	Central Europe	49.41	16.28	Monsanto	SRR1945595	HiSeq 2000	Y	Y
5890	DraIV 1-8	CS76817	Central Europe	49.41	16.28	Monsanto	SRR1945596	HiSeq 2000	Y	Y
5893	DraIV 1-11	CS76816	Central Europe	49.41	16.28	Monsanto	SRR1945597	HiSeq 2000	Y	Y
5907	DraIV 2-9	CS76818	Central Europe	49.41	16.28	Monsanto	SRR1945598	HiSeq 2000	Y	Y
5921	DraIV 3-7	CS76819	Central Europe	49.41	16.28	Monsanto	SRR1945599	HiSeq 2000	Y	Y
5950	DraIV 5-12	CS76820	Central Europe	49.41	16.28	Monsanto	SRR1945600	HiSeq 2000	Y	Y
5984	DraIV 6-13	CS76822	Central Europe	49.41	16.28	Monsanto	SRR1945601	HiSeq 2000	Y	Y
5993	DraIV 6-22	CS76823	Central Europe	49.41	16.28	Monsanto	SRR1945602	HiSeq 2000	Y	Y
6008	Duk	CS76824	Central Europe	49.10	16.20	Salk	SRR1945603	HiSeq 2000	Y	Y
6009	Eden-1	CS76826	North Sweden	62.88	18.18	GMI	SRR1945604	Genome Analyzer IIx	Y	Y
6010	Eden-5	CS78000	North Sweden	62.88	18.18	GMI	SRR1945605	Genome Analyzer IIx	Y	Y
6011	Eden-6	CS76828	North Sweden	62.88	18.18	GMI	SRR1945606	HiSeq 2000	Y	Y
6012	Eden-7	CS76829	North Sweden	62.88	18.18	GMI	SRR1945607	Genome Analyzer IIx	Y	Y
6013	Eden-9	CS76830	North Sweden	62.88	18.18	GMI	SRR1945608	Genome Analyzer IIx	Y	Y
6016	Eds-1	CS76834	North Sweden	62.90	18.40	GMI	SRR1945609	Genome Analyzer IIx	N	N
6017	Eds-9	CS76835	North Sweden	62.90	18.40	GMI	SRR1945610	Genome Analyzer IIx	Y	Y

6019	Fjä1-2	CS76860	South Sweden	56.06	14.29	GMI	SRR1945611	Genome Analyzer IIx	Y	Y
6020	Fjä1-5	CS76861	South Sweden	56.06	14.29	GMI	SRR1945612	Genome Analyzer IIx	Y	Y
6021	Fjä2-4	CS76862	South Sweden	56.06	14.29	GMI	SRR1945613	Genome Analyzer IIx	Y	Y
6022	Fjä2-6	CS78009	South Sweden	56.06	14.29	GMI	SRR1945614	Genome Analyzer IIx	Y	Y
6023	Fly2-1	CS76863	South Sweden	55.75	13.37	GMI	SRR1945615	Genome Analyzer IIx	Y	Y
6024	Fly2-2	CS76864	South Sweden	55.75	13.37	GMI	SRR1945616	Genome Analyzer IIx	Y	Y
6025	Gro-3	CS76889	North Sweden	62.64	17.73	GMI	SRR1945617	Genome Analyzer IIx	Y	Y
6030	Grön-5	CS76893	North Sweden	62.81	18.19	GMI	SRR1945618	Genome Analyzer IIx	N	N
6034	Hov1-7	CS76932	South Sweden	56.10	13.74	GMI	SRR1945619	Genome Analyzer IIx	Y	Y
6035	Hov1-10	CS76931	South Sweden	56.10	13.74	GMI	SRR1945620	Genome Analyzer IIx	Y	Y
6036	Hov3-2	CS76934	South Sweden	56.10	13.74	GMI	SRR1945621	Genome Analyzer IIx	Y	Y
6038	Hov3-5	CS76935	South Sweden	56.10	13.74	GMI	SRR1945622	Genome Analyzer IIx	Y	Y
6039	Hovdala-2	CS76937	Admixed	56.10	13.74	GMI	SRR1945623	Genome Analyzer IIx	N	N
6040	Kni-1	CS76970	South Sweden	55.66	13.40	GMI	SRR1945624	Genome Analyzer IIx	Y	Y
6041	Lis-3	CS77044	South Sweden	56.03	14.78	GMI	SRR1945625	Genome Analyzer IIx	Y	Y
6042	Lom1-1	CS77048	Admixed	56.09	13.90	GMI	SRR1945626	Genome Analyzer IIx	Y	Y
6043	Löv-1	CS77049	North Sweden	62.80	18.08	GMI	SRR1945627	Genome Analyzer IIx	N	N

6046	Löv-5	CS77050	North Sweden	62.80	18.08	GMI	SRR1945628	Genome Analyzer IIx	N	N
6064	Nyl-2	CS77136	North Sweden	62.95	18.28	GMI	SRR1945629	Genome Analyzer IIx	Y	Y
6069	Nyl-7	CS77137	North Sweden	62.95	18.28	GMI	SRR1945630	Genome Analyzer IIx	Y	Y
6070	Omn-1	CS77145	North Sweden	62.93	18.34	GMI	SRR1945631	Genome Analyzer IIx	Y	Y
6071	Omn-5	CS77146	North Sweden	62.93	18.34	GMI	SRR1945632	Genome Analyzer IIx	Y	Y
6073	ÖMö1-7	CS77147	South Sweden	56.15	15.82	GMI	SRR1945633	Genome Analyzer IIx	Y	Y
6074	Ör-1	CS77150	South Sweden	56.46	16.13	GMI	SRR1945634	Genome Analyzer IIx	Y	Y
6076	Rev-2	CS77215	South Sweden	55.69	13.45	GMI	SRR1945635	Genome Analyzer IIx	N	N
6077	Rev-3	CS78030	South Sweden	55.69	13.45	GMI	SRR1945636	HiSeq 2000	Y	Y
6085	Sparta-1	CS77260	South Sweden	55.71	13.21	GMI	SRR1945637	Genome Analyzer IIx	Y	Y
6086	Sr:3	CS77267	Admixed	58.90	11.20	GMI	SRR1945638	Genome Analyzer IIx	Y	Y
6087	Stu-2	CS78033	South Sweden	56.47	16.13	GMI	SRR1945639	Genome Analyzer IIx	Y	Y
6088	Stu1-1	CS77285	South Sweden	56.47	16.13	GMI	SRR1945640	Genome Analyzer IIx	Y	Y
6090	T1000	CS77288	South Sweden	55.65	13.22	GMI	SRR1945641	Genome Analyzer IIx	Y	Y
6091	T1010	CS78035	South Sweden	55.65	13.22	GMI	SRR1945642	HiSeq 2000	Y	Y
6092	T1020	CS77289	South Sweden	55.65	13.22	GMI	SRR1945643	Genome Analyzer IIx	N	N
6094	T1040	CS77290	South Sweden	55.65	13.21	GMI	SRR1945644	HiSeq 2000	N	N

6095	T1050	CS78039	South Sweden	55.65	13.22	GMI	SRR1945645	Genome Analyzer IIx	Y	Y
6096	T1060	CS78040	South Sweden	55.65	13.22	GMI	SRR1945646	Genome Analyzer IIx	Y	Y
6097	T1070	CS77291	South Sweden	55.65	13.23	GMI	SRR1945647	Genome Analyzer IIx	Y	Y
6098	T1080	CS77292	South Sweden	55.66	13.22	GMI	SRR1945648	Genome Analyzer IIx	Y	Y
6099	T1090	CS77293	South Sweden	55.66	13.24	GMI	SRR1945649	Genome Analyzer IIx	Y	Y
6100	T1110	CS77294	South Sweden	55.60	13.20	GMI	SRR1945650	Genome Analyzer IIx	Y	Y
6101	T1120	CS78045	South Sweden	55.60	13.20	GMI	SRR1945651	HiSeq 2000	Y	Y
6102	T1130	CS77295	South Sweden	55.60	13.20	GMI	SRR1945652	Genome Analyzer IIx	Y	Y
6104	T1160	CS77296	South Sweden	55.70	13.20	GMI	SRR1945653	Genome Analyzer IIx	Y	Y
6105	T450	CS77297	South Sweden	55.80	13.12	GMI	SRR1945654	HiSeq 2000	N	N
6106	T460	CS77298	South Sweden	55.79	13.12	GMI	SRR1945655	Genome Analyzer IIx	Y	Y
6107	T470	CS77299	South Sweden	55.79	13.12	GMI	SRR1945656	Genome Analyzer IIx	Y	Y
6108	T480	CS77300	Western Europe	55.80	13.12	GMI	SRR1945657	Genome Analyzer IIx	Y	Y
6109	T510	CS77301	South Sweden	55.79	13.12	GMI	SRR1945658	HiSeq 2000	Y	Y
6111	T530	CS77302	South Sweden	55.80	13.12	GMI	SRR1945659	Genome Analyzer IIx	Y	Y
6112	T540	CS77303	South Sweden	55.80	13.10	GMI	SRR1945660	Genome Analyzer IIx	Y	Y
6113	T550	CS77304	South Sweden	55.81	13.10	GMI	SRR1945661	Genome Analyzer IIx	Y	Y

6114	T570	CS77305	South Sweden	55.81	13.13	GMI	SRR1945662	Genome Analyzer IIx	Y	Y
6115	T580	CS77306	South Sweden	55.80	13.14	GMI	SRR1945663	HiSeq 2000	N	N
6118	T610	CS77307	South Sweden	55.70	13.20	GMI	SRR1945664	HiSeq 2000	Y	Y
6119	T620	CS78060	South Sweden	55.70	13.20	GMI	SRR1945665	HiSeq 2000	Y	Y
6122	T670	CS77308	South Sweden	55.84	13.31	GMI	SRR1945666	HiSeq 2000	N	N
6123	T680	CS78064	South Sweden	55.84	13.30	GMI	SRR1945667	HiSeq 2000	Y	Y
6124	T690	CS77309	South Sweden	55.84	13.31	GMI	SRR1945668	HiSeq 2000	Y	Y
6125	T710	CS77310	South Sweden	55.84	13.31	GMI	SRR1945669	Genome Analyzer IIx	Y	Y
6126	T720	CS77311	South Sweden	55.84	13.30	GMI	SRR1945670	Genome Analyzer IIx	N	N
6128	T740	CS77313	South Sweden	55.84	13.29	GMI	SRR1945671	Genome Analyzer IIx	Y	Y
6131	T780	CS77315	South Sweden	55.84	13.32	GMI	SRR1945672	Genome Analyzer IIx	Y	Y
6132	T790	CS77316	South Sweden	55.84	13.32	GMI	SRR1945673	Genome Analyzer IIx	Y	Y
6133	T800	CS77317	South Sweden	55.84	13.29	GMI	SRR1945674	Genome Analyzer IIx	Y	Y
6134	T810	CS77318	South Sweden	55.84	13.29	GMI	SRR1945675	Genome Analyzer IIx	Y	Y
6136	T840	CS77319	South Sweden	55.93	13.55	GMI	SRR1945676	Genome Analyzer IIx	Y	Y
6137	T850	CS77320	South Sweden	55.94	13.56	GMI	SRR1945677	Genome Analyzer IIx	Y	Y
6138	T860	CS77321	South Sweden	55.94	13.55	GMI	SRR1945678	Genome Analyzer IIx	Y	Y

6140	T880	CS77322	South Sweden	55.94	13.55	GMI	SRR1945679	Genome Analyzer IIx	Y	Y
6141	T890	CS78079	South Sweden	55.94	13.55	GMI	SRR1945680	Genome Analyzer IIx	Y	Y
6142	T900	CS77323	South Sweden	55.94	13.56	GMI	SRR1945681	Genome Analyzer IIx	Y	Y
6145	T930	CS77324	South Sweden	55.95	13.55	GMI	SRR1945682	Genome Analyzer IIx	Y	Y
6148	T960	CS77325	South Sweden	55.93	13.55	GMI	SRR1945683	Genome Analyzer IIx	Y	Y
6149	T970	CS77326	South Sweden	55.93	13.55	GMI	SRR1945684	HiSeq 2000	N	N
6150	T980	CS77327	South Sweden	55.93	13.53	GMI	SRR1945685	Genome Analyzer IIx	Y	Y
6151	T990	CS77328	South Sweden	55.65	13.22	GMI	SRR1945686	Genome Analyzer IIx	Y	Y
6153	TAA 03	CS77329	North Sweden	62.64	17.74	GMI	SRR1945687	HiSeq 2000	Y	Y
6154	TAA 04	CS77330	North Sweden	62.64	17.74	GMI	SRR1945688	Genome Analyzer IIx	Y	Y
6163	TAA 14	CS77331	North Sweden	62.64	17.74	GMI	SRR1945689	Genome Analyzer IIx	N	N
6166	TAA 17	CS77332	North Sweden	62.64	17.74	GMI	SRR1945690	Genome Analyzer IIx	Y	Y
6169	TÅD 01	CS77333	North Sweden	62.87	18.34	GMI	SRR1945691	Genome Analyzer IIx	Y	Y
6172	TÅD 04	CS77335	North Sweden	62.87	18.34	GMI	SRR1945692	Genome Analyzer IIx	Y	Y
6173	TÅD 05	CS77336	North Sweden	62.87	18.34	GMI	SRR1945693	Genome Analyzer IIx	Y	Y
6174	TÅD 06	CS77337	North Sweden	62.87	18.34	GMI	SRR1945694	Genome Analyzer IIx	Y	Y
6177	TÄL 03	CS77338	North Sweden	62.63	17.69	GMI	SRR1945695	Genome Analyzer IIx	Y	Y

6180	TÄL 07	CS77339	Germany	62.63	17.69	GMI	SRR1945696	Genome Analyzer IIx	Y	Y
6184	TBÖ 01	CS77343	North Sweden	62.89	18.45	GMI	SRR1945697	Genome Analyzer IIx	Y	Y
6188	TDr-1	CS77345	South Sweden	55.77	14.14	GMI	SRR1945698	Genome Analyzer IIx	Y	Y
6189	TDr-2	CS77351	South Sweden	55.77	14.14	GMI	SRR1945699	Genome Analyzer IIx	Y	Y
6191	TDr-4	CS77352	South Sweden	55.77	14.14	GMI	SRR1945700	HiSeq 2000	Y	Y
6192	TDr-5	CS77353	South Sweden	55.77	14.14	GMI	SRR1945701	HiSeq 2000	Y	Y
6193	TDr-7	CS77354	South Sweden	55.77	14.13	GMI	SRR1945702	Genome Analyzer IIx	Y	Y
6194	TDr-8	CS77355	South Sweden	55.77	14.13	GMI	SRR1945703	Genome Analyzer IIx	Y	Y
6195	TDr-9	CS77356	South Sweden	55.77	14.13	GMI	SRR1945704	Genome Analyzer IIx	Y	Y
6198	TDr-13	CS77347	South Sweden	55.77	14.13	GMI	SRR1945705	Genome Analyzer IIx	Y	Y
6201	TDr-16	CS77348	South Sweden	55.77	14.12	GMI	SRR1945706	Genome Analyzer IIx	Y	Y
6202	TDr-17	CS77349	South Sweden	55.77	14.12	GMI	SRR1945707	Genome Analyzer IIx	Y	Y
6203	TDr-18	CS77350	South Sweden	55.77	14.12	GMI	SRR1945708	HiSeq 2000	N	N
6209	TEDEN 02	CS77358	North Sweden	62.88	18.18	GMI	SRR1945709	Genome Analyzer IIx	Y	Y
6210	TEDEN 03	CS77359	North Sweden	62.88	18.18	GMI	SRR1945710	Genome Analyzer IIx	Y	Y
6214	TFÄ 04	CS78121	North Sweden	63.02	18.33	GMI	SRR1945711	HiSeq 2000	Y	Y
6216	TFÄ 06	CS77362	North Sweden	63.02	18.33	GMI	SRR1945712	HiSeq 2000	Y	Y

6217	TFÄ 07	CS77363	North Sweden	63.02	18.33	GMI	SRR1945713	Genome Analyzer IIx	Y	Y
6218	TFÄ 08	CS77364	North Sweden	63.02	18.33	GMI	SRR1945714	HiSeq 2000	Y	Y
6220	TGR 01	CS77365	North Sweden	62.81	18.19	GMI	SRR1945715	Genome Analyzer IIx	Y	Y
6221	TGR 02	CS77366	North Sweden	62.81	18.19	GMI	SRR1945716	HiSeq 2000	Y	Y
6231	TNY 04	CS77368	North Sweden	62.96	18.28	GMI	SRR1945717	Genome Analyzer IIx	Y	Y
6235	TOM 01	CS77372	North Sweden	62.96	18.36	GMI	SRR1945718	Genome Analyzer IIx	Y	Y
6237	TOM 03	CS77373	North Sweden	62.96	18.35	GMI	SRR1945719	HiSeq 2000	Y	Y
6238	TOM 04	CS77374	North Sweden	62.96	18.35	GMI	SRR1945720	Genome Analyzer IIx	Y	Y
6240	TOM 06	CS77375	North Sweden	62.96	18.35	GMI	SRR1945721	Genome Analyzer IIx	Y	Y
6241	TOM 07	CS77376	North Sweden	62.96	18.36	GMI	SRR1945722	Genome Analyzer IIx	Y	Y
6242	Tomegap-2	CS77377	South Sweden	55.70	13.20	GMI	SRR1945723	Genome Analyzer IIx	Y	Y
6243	Tottarp-2	CS77381	Central Europe	56.27	13.90	GMI	SRR1945724	Genome Analyzer IIx	Y	Y
6244	TRÄ 01	CS77384	North Sweden	62.92	18.47	GMI	SRR1945725	Genome Analyzer IIx	N	N
6252	TV-4	CS78771	Germany	55.58	14.33	GMI	SRR1945726	HiSeq 2000	Y	Y
6255	TV-7	CS78772	Germany	55.58	14.33	GMI	SRR1945727	Genome Analyzer IIx	Y	Y
6258	TV-10	CS78767	Admixed	55.58	14.33	GMI	SRR1945728	Genome Analyzer IIx	Y	Y
6268	TV-22	CS78768	Germany	55.58	14.33	GMI	SRR1945729	HiSeq 2000	Y	Y
6276	TV-30	CS78769	Germany	55.58	14.33	GMI	SRR1945730	HiSeq 2000	Y	Y

6284	TV-38	CS78770	South Sweden	55.58	14.33	GMI	SRR1945731	HiSeq 2000	Y	Y
6296	UduI 1-11	CS78774	Central Europe	49.28	16.63	Monsanto	SRR1945732	HiSeq 2000	Y	Y
6390	UduI 3-36	CS78775	Central Europe	49.28	16.63	Monsanto	SRR1945733	HiSeq 2000	Y	Y
6396	UduI 4-9	CS78776	Central Europe	49.28	16.63	Monsanto	SRR1945734	HiSeq 2000	Y	Y
6413	Ull3-4	CS78819	South Sweden	56.06	13.97	GMI	SRR1945735	HiSeq 2000	N	N
6424	ZdrI 1-23	CS78875	Central Europe	49.39	16.25	Monsanto	SRR1945736	HiSeq 2000	Y	Y
6434	ZdrI 2-9	CS78877	Admixed	49.39	16.25	Monsanto	SRR1945737	HiSeq 2000	N	N
6445	ZdrI 2-21	CS78876	Central Europe	49.39	16.25	Monsanto	SRR1945738	HiSeq 2000	Y	Y
6680	ANH-1	CS76437	Western Europe	51.85	6.43	Salk	SRR1945739	HiSeq 2000	Y	Y
6739	CSHL-15	CS79011	Germany	40.86	-73.47	MPI	SRR1945740	HiSeq 2000	N	N
6740	CSHL-17	CS79012	Germany	40.86	-73.47	MPI	SRR1945741	HiSeq 2000	N	N
6744	CSHL-5	CS76779	Germany	40.86	-73.47	Monsanto	SRR1945742	HiSeq 2000	Y	Y
6749	FM-10	CS79013	Germany	42.45	-76.51	MPI	SRR1945743	HiSeq 2000	N	N
6750	FM-11	CS79014	Germany	42.45	-76.51	MPI	SRR1945744	HiSeq 2000	N	N
6805	HS-12	CS79015	Germany	42.37	-71.06	MPI	SRR1945745	HiSeq 2000	N	N
6806	HS-17	CS79016	Germany	42.37	-71.06	MPI	SRR1945746	HiSeq 2000	N	N
6814	KNO-15	CS79017	Germany	41.28	-86.62	MPI	SRR1945747	HiSeq 2000	N	N
6830	Kz-13	CS76994	Admixed	49.50	73.10	MPI	SRR1945748	HiSeq 2000	Y	Y
6897	Ag-0	CS76430	Western Europe	45	1.30	Salk	SRR1945749	HiSeq 2000	Y	Y
6898	An-1	CS76435	Admixed	51.22	4.40	Salk	SRR1945750	HiSeq 2000	Y	Y
6900	Bil-5	CS76709	North Sweden	63.32	18.48	GMI	SRR1945751	Genome Analyzer IIx	Y	Y
6901	Bil-7	CS76710	North Sweden	63.32	18.48	GMI	SRR1945752	Genome Analyzer IIx	Y	Y

6903	Bor-4	CS76454	Central Europe	49.40	16.23	Salk	SRR1945753	HiSeq 2000	Y	Y
6904	Br-0	CS76455	Western Europe	49.20	16.62	Salk	SRR1945754	HiSeq 2000	Y	Y
6907	CIBC-17	CS76770	Admixed	51.41	-0.64	Salk	SRR1945755	HiSeq 2000	Y	Y
6908	CIBC-5	CS78894	Western Europe	51.41	-0.64	Salk	SRR1945756	HiSeq 2000	N	N
6909	Col-0	CS76778	Germany	38.30	-92.30	GMI	SRR1945757	HiSeq 2000	Y	Y
6911	Cvi-0	CS76789	Relict	15.11	-23.62	Salk	SRR1945758	HiSeq 2000	Y	Y
6913	Eden-2	CS76827	North Sweden	62.88	18.18	GMI	SRR1945759	Genome Analyzer IIx	Y	Y
6915	Ei-2	CS76478	Germany	50.30	6.30	Salk	SRR1945760	HiSeq 2000	Y	Y
6917	Fäb-2	CS76850	North Sweden	63.02	18.32	GMI	SRR1945761	Genome Analyzer IIx	N	N
6918	Fäb-4	CS76851	North Sweden	63.02	18.32	GMI	SRR1945762	Genome Analyzer IIx	Y	Y
6919	Ga-0	CS76490	Central Europe	50.30	8	Salk	SRR1945763	HiSeq 2000	Y	Y
6920	Got-22	CS76884	Admixed	51.53	9.94	Salk	SRR1945764	HiSeq 2000	Y	Y
6922	Gu-0	CS76498	Germany	50.30	8	Salk	SRR1945765	HiSeq 2000	Y	Y
6923	HR-10	CS76940	Western Europe	51.41	-0.64	Salk	SRR1945766	HiSeq 2000	Y	Y
6924	HR-5	CS76514	Western Europe	51.41	-0.64	Salk	SRR1945767	HiSeq 2000	N	N
6926	Kin-0	CS76527	Western Europe	44.46	-85.37	Salk	SRR1945768	HiSeq 2000	Y	Y
6927	KNO-10	CS76973	Germany	41.28	-86.62	Salk,MPI	SRR1945769	unspecified	N	N
6929	Kondara	CS76532	Asia	38.48	68.49	Salk	SRR1945770	HiSeq 2000	Y	Y
6931	Kz-9	CS76537	Asia	49.50	73.10	Salk	SRR1945771	HiSeq 2000	Y	Y
6932	Ler-1	CS77021	Admixed	47.98	10.87	MPI,GMI	SRR1945772	HiSeq 2000	Y	Y
6933	LL-0	CS77047	Spain	41.59	2.49	Salk	SRR1945773	HiSeq 2000	Y	Y
6938	Ms-0	CS76555	Asia	55.75	37.63	Salk	SRR1945774	HiSeq 2000	Y	Y
6940	Mz-0	CS76557	Germany	50.30	8.30	Salk	SRR1945775	HiSeq 2000	Y	Y

6943	NFA-10	CS77126	Western Europe	51.41	-0.64	Salk	SRR1945776	HiSeq 2000	Y	Y
6944	NFA-8	CS78913	Western Europe	51.41	-0.64	Salk	SRR1945777	HiSeq 2000	Y	Y
6945	Nok-3	CS76562	Germany	52.24	4.45	Salk	SRR1945778	HiSeq 2000	Y	Y
6951	Pu2-23	CS76579	Central Europe	49.42	16.36	Salk	SRR1945779	HiSeq 2000	Y	Y
6956	Pu2-7	CS76580	Central Europe	49.42	16.36	Salk	SRR1945780	HiSeq 2000	Y	Y
6957	Pu2-8	CS77192	Central Europe	49.42	16.36	Salk	SRR1945781	HiSeq 2000	N	N
6958	Ra-0	CS76582	Western Europe	46	3.30	Salk	SRR1945782	HiSeq 2000	Y	Y
6959	Rennes-1	CS77210	Western Europe	48.50	-1.41	Salk	SRR1945783	HiSeq 2000	Y	Y
6960	Rennes-11	CS77211	Western Europe	48.50	-1.41	Salk	SRR1945784	HiSeq 2000	Y	Y
6961	Se-0	CS76597	Spain	38.33	-3.53	Salk	SRR1945785	HiSeq 2000	Y	Y
6963	Sorbo	CS78917	Asia	38.35	68.48	Salk	SRR1945786	HiSeq 2000	Y	Y
6966	Sq-1	CS77266	Western Europe	51.41	-0.64	Salk	SRR1945787	HiSeq 2000	Y	Y
6967	Sq-8	CS76604	Western Europe	51.41	-0.64	Salk	SRR1945788	HiSeq 2000	Y	Y
6968	Tamm-2	CS76610	North Sweden	60	23.50	Salk,GMI	SRR1945789	Genome Analyzer IIx	N	N
6969	Tamm-27	CS77341	North Sweden	60	23.50	Salk	SRR1945790	HiSeq 2000	Y	Y
6970	Ts-1	CS76615	Spain	41.72	2.93	Salk	SRR1945791	HiSeq 2000	Y	Y
6971	Ts-5	CS77388	Spain	41.72	2.93	Salk	SRR1945792	HiSeq 2000	Y	Y
6973	Ull2-3	CS78817	Germany	56.06	13.97	GMI	SRR1945793	Genome Analyzer IIx	Y	Y
6974	Ull2-5	CS78818	South Sweden	56.06	13.97	GMI	SRR1945794	Genome Analyzer IIx	Y	Y

6975	Uod-1	CS76621	Central Europe	48.30	14.45	Salk	SRR1945795	HiSeq 2000	Y	Y
6976	Uod-7	CS78823	Central Europe	48.30	14.45	Salk	SRR1945796	HiSeq 2000	Y	Y
6979	Wei-0	CS76628	Central Europe	47.25	8.26	Salk	SRR1945797	HiSeq 2000	Y	Y
6981	Ws-2	CS78920	Admixed	52.30	30	MPI,Salk	SRR1945798	HiSeq 2000	Y	Y
6982	Wt-5	CS76632	Germany	52.30	9.30	Salk	SRR1945799	HiSeq 2000	Y	Y
6984	Zdr-1	CS76635	Central Europe	49.39	16.25	Salk	SRR1945800	HiSeq 2000	Y	Y
6986	Abd-0	CS76429	Western Europe	57.15	-2.22	Salk	SRR1945801	HiSeq 2000	Y	Y
6987	Ak-1	CS76431	Admixed	48.07	7.63	Salk	SRR1945802	HiSeq 2000	Y	Y
6989	Alst-1	CS76432	Western Europe	54.80	-2.43	Salk	SRR1945803	HiSeq 2000	Y	Y
6990	Amel-1	CS76434	Admixed	53.45	5.73	Salk	SRR1945804	HiSeq 2000	Y	Y
6992	Ang-0	CS76436	Admixed	50.30	5.30	Salk	SRR1945805	HiSeq 2000	Y	Y
6997	Appt-1	CS76440	Germany	51.83	5.58	Salk	SRR1945806	HiSeq 2000	Y	Y
7000	Aa-0	CS76428	Germany	50.92	9.57	Salk	SRR1945807	HiSeq 2000	Y	Y
7002	Baa-1	CS76442	Germany	51.33	6.10	Salk	SRR1945808	HiSeq 2000	Y	Y
7003	Bs-1	CS78888	Admixed	47.50	7.50	Salk	SRR1945809	HiSeq 2000	Y	Y
7008	Benk-1	CS76447	Germany	52	5.68	Salk	SRR1945810	HiSeq 2000	Y	Y
7013	Bd-0	CS76445	South Sweden	52.46	13.29	Salk	SRR1945811	HiSeq 2000	Y	Y
7014	Ba-1	CS76441	Germany	56.55	-4.80	Salk	SRR1945812	HiSeq 2000	Y	Y
7025	Bl-1	CS76450	Central Europe	44.50	11.34	Salk	SRR1945813	HiSeq 2000	Y	Y
7026	Boot-1	CS76452	Western Europe	54.40	-3.27	Salk	SRR1945814	HiSeq 2000	Y	Y
7028	Bch-1	CS76444	Admixed	49.52	9.32	Salk	SRR1945815	HiSeq 2000	Y	Y
7031	Bsch-0	CS76457	Germany	50.02	8.67	Salk	SRR1945816	HiSeq 2000	Y	Y
7033	Buckhorn Pass	CS76733	Germany	41.36	-122.76	Salk,MPI	SRR1945817	HiSeq 2000	N	N
7036	Bu-0	CS78889	Germany	50.50	9.50	MPI,Salk	SRR1945818	HiSeq 2000	Y	Y

7058	Bur-0	CS76734	Admixed	53.08	-9.08	Mott	SRR1945819	Genome Analyzer II	N	N
7061	Cal-0	CS76460	Admixed	53.27	-1.64	Salk	SRR1945820	HiSeq 2000	N	N
7062	Ca-0	CS76459	Germany	50.30	8.27	Salk	SRR1945821	HiSeq 2000	Y	Y
7063	Can-0	CS76740	Relict	29.21	-13.48	Mott	SRR1945822	Genome Analyzer II	N	N
7064	Cnt-1	CS76467	Western Europe	51.30	1.10	Salk	SRR1945823	HiSeq 2000	N	N
7067	Ct-1	CS76786	Central Europe	37.30	15	Mott	SRR1945824	Genome Analyzer II	N	N
7068	Cerv-1	CS76462	Italy Balkan Caucasus	42	12.10	Salk	SRR1945825	HiSeq 2000	Y	Y
7071	Chat-1	CS76463	Western Europe	48.07	1.34	Salk	SRR1945826	HiSeq 2000	Y	Y
7072	Chi-0	CS76464	Admixed	53.75	34.74	Salk	SRR1945827	HiSeq 2000	Y	Y
7077	Co-1	CS76468	Italy Balkan Caucasus	40.12	-8.25	Salk	SRR1945828	HiSeq 2000	Y	Y
7081	Co	CS78895	Spain	40.21	-8.43	Salk	SRR1945829	HiSeq 2000	Y	Y
7092	Com-1	CS76469	Western Europe	49.42	2.82	Salk	SRR1945830	HiSeq 2000	Y	Y
7094	Da-0	CS76791	Germany	49.87	8.65	Monsanto	SRR1945831	HiSeq 2000	Y	Y
7096	Di-G	CS76472	Admixed	47.32	5.04	Salk	SRR1945832	HiSeq 2000	N	N
7102	Do-0	CS76474	Germany	50.72	8.24	Salk	SRR1945833	HiSeq 2000	Y	Y
7103	Dra-0	CS76476	Central Europe	49.42	16.27	Salk	SRR1945834	HiSeq 2000	Y	Y
7106	Dr-0	CS78897	Central Europe	51.05	13.73	MPI,Salk	SRR1945835	HiSeq 2000	Y	Y
7107	Durh-1	CS76477	Western Europe	54.78	-1.57	Salk	SRR1945836	HiSeq 2000	N	N
7109	Ema-1	CS76480	Western Europe	51.30	0.50	Salk	SRR1945837	HiSeq 2000	N	N

7111	Edi-0	CS76831	Admixed	55.95	-3.16	Mott	SRR1945838	Genome Analyzer II	N	N
7117	El-0	CS76479	Germany	51.51	9.68	Salk	SRR1945839	HiSeq 2000	Y	Y
7119	En-2	CS76481	Germany	50	8.50	Salk	SRR1945840	HiSeq 2000	Y	Y
7120	En-D	CS76482	Central Europe	50	8.50	Salk	SRR1945841	HiSeq 2000	Y	Y
7125	Er-0	CS78898	Germany	49.60	11.01	MPI,Salk	SRR1945842	HiSeq 2000	Y	Y
7126	Es-0	CS76484	Admixed	60.20	24.57	Salk	SRR1945843	HiSeq 2000	Y	Y
7127	Est	CS76485	Admixed	58.67	24.99	Salk	SRR1945844	HiSeq 2000	Y	Y
7130	Et-0	CS76486	Western Europe	44.64	2.56	Salk	SRR1945845	HiSeq 2000	Y	Y
7133	Fr-2	CS76489	Germany	50.11	8.68	Salk	SRR1945846	HiSeq 2000	Y	Y
7138	Fi-0	CS76488	Admixed	50.50	8.02	Salk	SRR1945847	HiSeq 2000	N	N
7143	Gel-1	CS76492	Germany	51.02	5.87	Salk	SRR1945848	HiSeq 2000	Y	Y
7147	Gie-0	CS76493	Admixed	50.58	8.68	Salk	SRR1945849	HiSeq 2000	Y	Y
7158	Gr-5	CS76885	Central Europe	47	15.50	Monsanto	SRR1945850	HiSeq 2000	Y	Y
7160	Gre-0	CS76497	Germany	43.18	-85.25	Salk	SRR1945851	HiSeq 2000	N	N
7161	Gd-1	CS76491	Germany	53.50	10.50	Salk	SRR1945852	HiSeq 2000	N	N
7162	Hs-0	CS76515	Germany	52.24	9.44	Salk	SRR1945853	HiSeq 2000	Y	Y
7163	Ha-0	CS76500	Admixed	52.37	9.74	Salk	SRR1945854	HiSeq 2000	Y	Y
7164	Hau-0	CS76915	South Sweden	55.68	12.57	Salk	SRR1945855	HiSeq 2000	Y	Y
7165	Hn-0	CS76513	Germany	51.35	8.29	Salk	SRR1945856	HiSeq 2000	Y	Y
7169	Hh-0	CS76512	Admixed	54.42	9.89	Salk	SRR1945857	HiSeq 2000	Y	Y
7177	Jm-0	CS76520	Central Europe	49	15	Salk	SRR1945858	HiSeq 2000	Y	Y
7181	Je-0	CS76518	Admixed	50.93	11.59	Salk	SRR1945859	HiSeq 2000	Y	Y
7183	Kas-1	CS79018	Asia	35	77	Salk	SRR1945860	HiSeq 2000	Y	Y
7186	Kn-0	CS76969	Central Europe	54.90	23.89	Mott	SRR1945861	Genome Analyzer II	N	N
7192	Kil-0	CS76526	Germany	55.64	-5.66	Salk	SRR1945862	HiSeq 2000	N	N
7199	Kl-5	CS76528	Germany	50.95	6.97	Salk	SRR1945863	HiSeq 2000	N	N
7202	Kb-0	CS76524	Germany	50.18	8.51	Salk	SRR1945864	HiSeq 2000	Y	Y

7203	Krot-0	CS76534	Central Europe	49.63	11.57	Salk	SRR1945865	HiSeq 2000	Y	Y
7207	Kyoto	CS76535	Central Europe	35.01	135.75	Salk	SRR1945866	HiSeq 2000	Y	Y
7208	Lan-0	CS76539	Germany	55.67	-3.78	Salk	SRR1945867	HiSeq 2000	Y	Y
7209	La-0	CS76538	Admixed	52.73	15.23	Salk	SRR1945868	HiSeq 2000	Y	Y
7213	Ler-0	CS77020	Admixed	47.98	10.87	Mott	SRR1945869	Genome Analyzer II	N	N
7217	Lm-2	CS76545	Western Europe	48	0.50	Salk	SRR1945870	HiSeq 2000	Y	Y
7218	Le-0	CS76540	Admixed	52.16	4.49	Salk	SRR1945871	HiSeq 2000	Y	Y
7223	Li-2:1	CS76541	Central Europe	50.38	8.07	Salk	SRR1945872	HiSeq 2000	Y	Y
7231	Li-7	CS77035	Germany	50.38	8.07	Monsanto	SRR1945873	HiSeq 2000	Y	Y
7236	Litva	CS76543	Central Europe	NA	NA	Salk	SRR1945874	HiSeq 2000	Y	Y
7244	Mnz-0	CS76552	Germany	50	8.27	Salk	SRR1945875	HiSeq 2000	Y	Y
7248	Mv-0	CS76556	Germany	41.39	-70.67	Salk	SRR1945876	HiSeq 2000	N	N
7250	Me-0	CS76549	Germany	51.92	10.11	Salk	SRR1945877	HiSeq 2000	N	N
7255	Mh-0	CS76550	Germany	50.95	20.50	Salk	SRR1945878	HiSeq 2000	Y	Y
7258	Nw-0	CS76564	Germany	50.50	8.50	Salk	SRR1945879	HiSeq 2000	Y	Y
7268	Np-0	CS76563	Admixed	52.70	10.98	Salk	SRR1945880	HiSeq 2000	Y	Y
7273	No-0	CS77128	Central Europe	51.06	13.30	Mott	SRR1945881	Genome Analyzer II	N	N
7276	Ob-0	CS76566	Germany	50.20	8.58	Salk	SRR1945882	HiSeq 2000	Y	Y
7280	Old-1	CS76567	Germany	53.17	8.20	Salk	SRR1945883	HiSeq 2000	Y	Y
7282	Or-0	CS76568	Germany	50.38	8.01	Salk	SRR1945884	HiSeq 2000	Y	Y
7287	Ove-0	CS76569	Germany	53.34	8.42	Salk	SRR1945885	HiSeq 2000	Y	Y
7288	Oy-0	CS77156	Admixed	60.39	6.19	Mott	SRR1945886	Genome Analyzer II	N	N
7296	Petergof	CS77170	Central Europe	59	29	Monsanto	SRR1945887	HiSeq 2000	Y	Y
7298	Pi-0	CS76572	Central Europe	47.04	10.51	Salk	SRR1945888	HiSeq 2000	Y	Y

7305	Pt-0	CS78915	Admixed	53.48	10.61	Salk	SRR1945889	HiSeq 2000	Y	Y
7306	Pog-0	CS76576	Western Europe	49.27	-123.21	Salk	SRR1945890	HiSeq 2000	Y	Y
7307	Pn-0	CS77182	Western Europe	48.07	-2.97	Monsanto	SRR1945891	HiSeq 2000	Y	Y
7314	Ragl-1	CS76583	Admixed	54.35	-3.42	Salk	SRR1945892	HiSeq 2000	N	N
7316	Rhen-1	CS78916	Admixed	51.97	5.57	Salk	SRR1945893	HiSeq 2000	Y	Y
7319	Rome-1	CS76590	Admixed	42	12.10	Salk	SRR1945894	HiSeq 2000	Y	Y
7320	Rou-0	CS76591	Western Europe	49.44	1.10	Salk	SRR1945895	HiSeq 2000	Y	Y
7322	Rsch-4	CS77222	Germany	56.30	34	Mott	SRR1945896	Genome Analyzer II	N	N
7323	Rubezhnoe-1	CS76594	Asia	49	38.28	Salk	SRR1945897	HiSeq 2000	Y	Y
7327	Sf-1	CS77246	Spain	41.78	3.03	Salk	SRR1945898	HiSeq 2000	Y	Y
7328	Sf-2	CS77247	Spain	41.78	3.03	Mott	SRR1945899	Genome Analyzer II	N	N
7332	Seattle-0	CS76598	Western Europe	47	-122.20	Salk	SRR1945900	HiSeq 2000	N	N
7333	Sei-0	CS76599	Central Europe	46.54	11.56	Salk	SRR1945901	HiSeq 2000	Y	Y
7337	Si-0	CS76601	Germany	50.87	8.02	Salk	SRR1945902	HiSeq 2000	Y	Y
7342	Su-0	CS76606	Admixed	53.65	-3.01	Salk	SRR1945903	HiSeq 2000	Y	Y
7343	Sp-0	CS76603	South Sweden	52.53	13.18	Salk	SRR1945904	HiSeq 2000	Y	Y
7344	Sg-1	CS76600	Admixed	47.67	9.50	Salk	SRR1945905	HiSeq 2000	Y	Y
7346	Sten-0	CS77277	South Sweden	52.61	11.86	Monsanto	SRR1945906	HiSeq 2000	Y	Y
7347	Stw-0	CS76605	Central Europe	52	36	Salk	SRR1945907	HiSeq 2000	Y	Y
7349	Ta-0	CS76608	Central Europe	49.50	14.50	Salk	SRR1945908	HiSeq 2000	Y	Y
7350	Tac-0	CS76609	Central Europe	47.24	-122.46	Salk	SRR1945909	HiSeq 2000	N	N

7353	Tha-1	CS76611	Admixed	52.08	4.30	Salk	SRR1945910	HiSeq 2000	Y	Y
7354	Ting-1	CS76612	South Sweden	56.50	14.90	Salk	SRR1945911	HiSeq 2000	Y	Y
7356	Tol-0	CS76614	Germany	41.66	-83.56	Salk,MPI	SRR1945912	HiSeq 2000	Y	Y
7358	Tol-2	CS79019	Germany	41.66	-83.56	MPI	SRR1945913	HiSeq 2000	N	N
7359	Tol-3	CS79020	Germany	41.66	-83.56	MPI	SRR1945914	HiSeq 2000	N	N
7372	Tscha-1	CS76616	Central Europe	47.07	9.90	Salk	SRR1945915	HiSeq 2000	Y	Y
7373	Tsu-0	CS77389	Admixed	34.43	136.31	Mott	SRR1945916	Genome Analyzer II	N	N
7377	Tul-0	CS76618	Germany	43.27	-85.26	Salk	SRR1945917	HiSeq 2000	N	N
7378	Uk-1	CS76620	Admixed	48.03	7.77	Salk	SRR1945918	HiSeq 2000	Y	Y
7382	Utrecht	CS76622	Admixed	52.09	5.11	Salk	SRR1945919	HiSeq 2000	Y	Y
7383	Van-0	CS76623	Western Europe	49.27	-123.21	Salk	SRR1945920	HiSeq 2000	Y	Y
7384	Ven-1	CS76624	Admixed	52.03	5.55	Salk	SRR1945921	HiSeq 2000	Y	Y
7387	Vind-1	CS76625	Western Europe	54.99	-2.37	Salk	SRR1945922	HiSeq 2000	Y	Y
7394	Wa-1	CS76626	Admixed	52.30	21	Salk	SRR1945923	HiSeq 2000	Y	Y
7396	Ws-0.2	CS78857	Central Europe	52.30	30	Mott	SRR1945924	Genome Analyzer II	N	N
7404	Wc-1	CS76627	Admixed	52.60	10.07	Salk	SRR1945925	HiSeq 2000	Y	Y
7411	Wl-0	CS76630	Central Europe	47.93	10.81	Salk	SRR1945926	HiSeq 2000	Y	Y
7413	Wil-2	CS78856	Central Europe	54.68	25.32	Mott	SRR1945927	Genome Analyzer II	N	N
7415	Wu-0	CS78858	Germany	49.79	9.94	Mott	SRR1945928	Genome Analyzer II	N	N
7416	Yo-0	CS76633	Germany	37.45	-119.35	Salk	SRR1945929	HiSeq 2000	Y	Y
7417	Zu-0	CS78880	Western Europe	47.37	8.55	Mott	SRR1945930	Genome Analyzer II	N	N
7418	Zu-1	CS78881	Admixed	47.37	8.55	Monsanto	SRR1945931	HiSeq 2000	Y	Y
7419	Db-1	CS76471	Germany	50.31	8.32	Salk	SRR1945932	HiSeq 2000	Y	Y

7424	Jl-3	CS76519	Central Europe	49.20	16.62	Salk	SRR1945933	HiSeq 2000	Y	Y
7427	Ko-2	CS76531	Central Europe	NA	NA	Salk	SRR1945934	HiSeq 2000	Y	Y
7430	Nc-1	CS76559	Admixed	48.62	6.25	Salk	SRR1945935	HiSeq 2000	Y	Y
7460	Da(1)-12	CS76470	Central Europe	NA	NA	Salk	SRR1945936	HiSeq 2000	N	N
7461	H55	CS76897	Germany	49	15	Salk	SRR1945937	HiSeq 2000	N	N
7471	RLD-1	CS76588	Admixed	NA	NA	Salk	SRR1945938	HiSeq 2000	Y	Y
7475	KEN	CS79021	Germany	41.77	-72.68	MPI	SRR1945939	unspecified	N	N
7477	WAR	CS78853	Admixed	41.73	-71.28	Monsanto	SRR1945940	HiSeq 2000	Y	Y
7514	RRS-7	CS76593	Admixed	41.56	-86.43	Salk	SRR1945941	HiSeq 2000	Y	Y
7515	RRS-10	CS76592	Germany	41.56	-86.43	MPI,Salk	SRR1945942	HiSeq 2000	N	N
7516	Vår2-1	CS78830	Germany	55.58	14.33	GMI	SRR1945943	Genome Analyzer IIx	Y	Y
7517	Vår2-6	CS78831	Germany	55.58	14.33	GMI	SRR1945944	Genome Analyzer IIx	Y	Y
7520	Lp2-2	CS76546	Central Europe	49.38	16.81	Salk	SRR1945945	HiSeq 2000	Y	Y
7521	Lp2-6	CS77052	Central Europe	49.38	16.81	Salk	SRR1945946	HiSeq 2000	Y	Y
7523	Pna-17	CS76575	Germany	42.09	-86.33	Salk	SRR1945947	HiSeq 2000	Y	Y
7525	Rmx-A180	CS77218	Germany	42.04	-86.51	Salk	SRR1945948	HiSeq 2000	Y	Y
7529	627RMX-1MN4	CS79022	Germany	42.03	-86.51	MPI	SRR1945949	HiSeq 2000	N	N
7530	627RMX-1MN5	CS79023	Germany	42.03	-86.51	MPI	SRR1945950	HiSeq 2000	Y	Y
7566	627ME-13Y1	CS78367	Germany	42.09	-86.36	MPI	SRR1945951	HiSeq 2000	Y	Y
7568	627ME-1MI1	CS79024	Germany	42.09	-86.36	MPI	SRR1945952	HiSeq 2000	N	N
7717	KNO1.37	CS76972	Germany	41.27	-86.63	Monsanto	SRR1945953	HiSeq 2000	Y	Y
7757	KNO2.41	CS79025	Germany	41.27	-86.63	MPI	SRR1945954	HiSeq 2000	N	N
7767	KNO2.54	CS79026	Germany	41.27	-86.63	MPI	SRR1945955	HiSeq 2000	N	N
7917	PNA3.10	CS77183	Germany	42.09	-86.33	Monsanto	SRR1945956	HiSeq 2000	Y	Y

7947	PNA3.40	CS77184	Germany	42.09	-86.33	Monsanto	SRR1945957	HiSeq 2000	Y	Y
8037	PT1.52	CS79027	Germany	41.34	-86.74	MPI	SRR1945958	HiSeq 2000	N	N
8057	PT1.85	CS79028	Germany	41.34	-86.74	MPI	SRR1945959	HiSeq 2000	N	N
8077	PT2.21	CS77191	Germany	41.34	-86.74	Monsanto	SRR1945960	HiSeq 2000	Y	Y
8132	RMX3.22	CS77219	Germany	42.04	-86.51	Monsanto	SRR1945961	HiSeq 2000	Y	Y
8171	RMX4.118	CS79029	Germany	42.04	-86.51	MPI	SRR1945962	HiSeq 2000	Y	Y
8214	Gy-0	CS78901	Western Europe	49	2	Salk	SRR1945963	HiSeq 2000	Y	Y
8222	Lis-2	CS77043	South Sweden	56.03	14.78	GMI	SRR1945964	Genome Analyzer IIx	Y	Y
8227	THÖ 03	CS77367	North Sweden	62.80	17.91	GMI	SRR1945965	HiSeq 2000	Y	Y
8230	Algutsrum	CS76657	South Sweden	56.68	16.50	GMI	SRR1945966	Genome Analyzer IIx	Y	Y
8231	Brö1-6	CS76726	South Sweden	56.30	16	GMI	SRR1945967	Genome Analyzer IIx	N	N
8233	Dem-4	CS76794	Germany	41.19	-87.19	Salk	SRR1945968	HiSeq 2000	N	N
8234	Gul1-2	CS76896	South Sweden	56.46	15.81	GMI,Salk	SRR1945969	HiSeq 2000	Y	Y
8235	Hod	CS76924	Central Europe	48.80	17.10	Salk	SRR1945970	HiSeq 2000	Y	Y
8236	HSm	CS76941	Central Europe	49.33	15.76	Salk	SRR1945971	HiSeq 2000	N	N
8237	Kävlinge-1	CS76964	South Sweden	55.80	13.10	GMI	SRR1945972	Genome Analyzer IIx	Y	Y
8238	Kent	CS76967	Germany	51.15	0.40	Salk	SRR1945973	HiSeq 2000	Y	Y
8239	PHW-3	CS76976	Germany	51	7	Salk	SRR1945974	HiSeq 2000	N	N
8240	Kulturen-1	CS76987	South Sweden	55.71	13.20	GMI	SRR1945975	Genome Analyzer IIx	Y	Y
8241	Liarum	CS77038	South Sweden	55.95	13.82	GMI	SRR1945976	Genome Analyzer IIx	Y	Y
8242	Lillö-1	CS77039	South Sweden	56.15	15.79	GMI	SRR1945977	Genome Analyzer IIx	Y	Y

8243	PHW-2	CS77173	Western Europe	43.77	11.25	Salk	SRR1945978	HiSeq 2000	Y	Y
8244	PHW-34	CS77174	Western Europe	48.61	2.31	Salk	SRR1945979	HiSeq 2000	Y	Y
8246	NC-6	CS77124	Germany	35	-79.18	Salk	SRR1945980	HiSeq 2000	Y	Y
8247	San-2	CS77233	South Sweden	56.07	13.74	GMI	SRR1945981	Genome Analyzer IIx	Y	Y
8249	Vimmerby	CS78845	South Sweden	57.70	15.80	GMI	SRR1945982	Genome Analyzer IIx	Y	Y
8256	Bå1-2	CS76676	Admixed	56.40	12.90	GMI	SRR1945983	Genome Analyzer IIx	Y	Y
8258	Bå4-1	CS76677	South Sweden	56.40	12.90	GMI	SRR1945984	Genome Analyzer IIx	Y	Y
8259	Bå5-1	CS76678	South Sweden	56.40	12.90	GMI	SRR1945985	Genome Analyzer IIx	N	N
8264	Bla-1	CS76451	Spain	41.68	2.80	Salk	SRR1945986	HiSeq 2000	Y	Y
8283	Dra3-1	CS76811	South Sweden	55.76	14.12	GMI	SRR1945987	Genome Analyzer IIx	Y	Y
8284	DraII-1	CS76813	Central Europe	49.41	16.28	Salk	SRR1945988	HiSeq 2000	Y	Y
8285	DraIII-1	CS76815	Central Europe	49.41	16.28	Salk	SRR1945989	HiSeq 2000	Y	Y
8290	En-1	CS76841	Central Europe	50	8.50	Salk	SRR1945990	HiSeq 2000	N	N
8297	Ge-0	CS76875	Western Europe	46.50	6.08	Salk	SRR1945991	HiSeq 2000	Y	Y
8306	Hov4-1	CS76936	South Sweden	56.10	13.74	GMI	SRR1945992	Genome Analyzer IIx	Y	Y
8307	Hovdala-6	CS76938	South Sweden	56.10	13.74	GMI	SRR1945993	Genome Analyzer IIx	Y	Y
8311	In-0	CS78903	Central Europe	47.50	11.50	Salk	SRR1945994	HiSeq 2000	Y	Y
8312	Is-0	CS78904	Germany	50.50	7.50	MPI,Salk	SRR1945995	HiSeq 2000	Y	Y

8326	Lis-1	CS77042	South Sweden	56.03	14.78	GMI	SRR1945996	HiSeq 2000	Y	Y
8334	Lu-1	CS77056	Admixed	55.71	13.20	GMI	SRR1945997	Genome Analyzer IIx	Y	Y
8335	Lund	CS77060	South Sweden	55.71	13.20	GMI	SRR1945998	Genome Analyzer IIx	Y	Y
8337	Mir-0	CS76551	Western Europe	44	12.37	Salk	SRR1945999	HiSeq 2000	Y	Y
8343	Na-1	CS76558	Admixed	47.50	1.50	Salk	SRR1946000	HiSeq 2000	Y	Y
8351	Ost-0	CS77154	North Sweden	60.25	18.37	GMI	SRR1946001	Genome Analyzer IIx	Y	Y
8354	Per-1	CS76571	Asia	58	56.32	Salk	SRR1946002	HiSeq 2000	Y	Y
8357	Pla-0	CS76573	Spain	41.50	2.25	Salk	SRR1946003	HiSeq 2000	Y	Y
8365	Rak-2	CS77201	Central Europe	49	16	Salk	SRR1946004	HiSeq 2000	Y	Y
8366	Rd-0	CS76584	Admixed	50.50	8.50	Salk	SRR1946005	HiSeq 2000	Y	Y
8369	Rev-1	CS77214	South Sweden	55.69	13.45	GMI	SRR1946006	Genome Analyzer IIx	Y	Y
8376	Sanna-2	CS77234	North Sweden	62.69	18	GMI	SRR1946007	Genome Analyzer IIx	Y	Y
8386	Sr:5	CS77268	Central Europe	58.90	11.20	GMI	SRR1946008	Genome Analyzer IIx	Y	Y
8387	St-0	CS77270	Germany	59	18	GMI	SRR1946009	Genome Analyzer IIx	Y	Y
8419	Wil-1	CS78855	Central Europe	54.68	25.32	Salk	SRR1946010	HiSeq 2000	Y	Y
8420	Kelsterbach-4	CS76525	Germany	50.07	8.53	Salk	SRR1946011	HiSeq 2000	Y	Y
8422	Fjä1-1	CS76859	South Sweden	56.06	14.29	GMI	SRR1946012	Genome Analyzer IIx	Y	Y
8424	Kas-2	CS78905	Asia	35	77	Salk	SRR1946013	HiSeq 2000	N	N
8426	Ull1-1	CS78816	South Sweden	56.06	13.97	GMI	SRR1946014	Genome Analyzer IIx	Y	Y

8427	Ull2-13	CS78552	South Sweden	56.06	13.97	GMI	SRR1946015	HiSeq 2000	Y	Y
8464	LP3413.31	CS79030	Germany	41.69	-86.85	MPI	SRR1946016	HiSeq 2000	Y	Y
8483	LP3413.53	CS79031	Germany	41.69	-86.85	MPI	SRR1946017	HiSeq 2000	N	N
8699	328PNA062	CS79032	Germany	42.09	-86.33	MPI	SRR1946018	HiSeq 2000	N	N
8723	11PNA1.14	CS79033	Germany	42.09	-86.33	MPI	SRR1946019	HiSeq 2000	N	N
9027	RMX413.85	CS79034	Germany	42.04	-86.51	MPI	SRR1946020	HiSeq 2000	Y	Y
9057	Vinslöv	CS78847	South Sweden	56.10	13.92	GMI	SRR1946021	Genome Analyzer IIx	Y	Y
9058	Västervik	CS78834	Admixed	57.75	16.63	GMI	SRR1946022	Genome Analyzer IIx	Y	Y
9067	Xan-3	CS78860	Italy Balkan Caucasus	38.65	48.80	Monsanto	SRR1946023	HiSeq 2000	Y	Y
9069	Xan-5	CS78861	Italy Balkan Caucasus	38.65	48.80	Monsanto	SRR1946024	HiSeq 2000	Y	Y
9070	Xan-6	CS78862	Italy Balkan Caucasus	38.65	48.80	Monsanto	SRR1946025	HiSeq 2000	Y	Y
9075	Lerik1-4	CS77023	Italy Balkan Caucasus	38.74	48.61	Monsanto	SRR1946026	HiSeq 2000	Y	Y
9078	Lerik1-7	CS77024	Italy Balkan Caucasus	38.74	48.61	Monsanto	SRR1946027	HiSeq 2000	Y	Y
9079	Lerik2-1	CS77025	Italy Balkan Caucasus	38.78	48.55	Monsanto	SRR1946028	HiSeq 2000	Y	Y
9081	Lerik2-3	CS77026	Italy Balkan Caucasus	38.78	48.55	Monsanto	SRR1946029	HiSeq 2000	Y	Y
9084	Lerik2-6	CS77028	Italy Balkan Caucasus	38.78	48.55	Monsanto	SRR1946030	HiSeq 2000	N	N

9085	Lerik2-7	CS77029	Italy Balkan Caucasus	38.78	48.55	Monsanto	SRR1946031	HiSeq 2000	Y	Y
9089	Nar-3	CS77119	Italy Balkan Caucasus	38.95	48.93	Monsanto	SRR1946032	HiSeq 2000	Y	Y
9091	Nar-5	CS77121	Italy Balkan Caucasus	38.95	48.93	Monsanto	SRR1946033	HiSeq 2000	Y	Y
9095	Istisu-5	CS76950	Italy Balkan Caucasus	38.98	48.56	Monsanto	SRR1946034	HiSeq 2000	N	N
9099	Istisu-9	CS76953	Italy Balkan Caucasus	38.98	48.56	Monsanto	SRR1946035	HiSeq 2000	Y	Y
9100	Lag1-2	CS76998	Italy Balkan Caucasus	41.83	46.28	Monsanto	SRR1946036	HiSeq 2000	Y	Y
9102	Lag1-4	CS76999	Italy Balkan Caucasus	41.83	46.28	Monsanto	SRR1946037	HiSeq 2000	Y	Y
9103	Lag1-5	CS77000	Italy Balkan Caucasus	41.83	46.28	Monsanto	SRR1946038	HiSeq 2000	Y	Y
9104	Lag1-6	CS77001	Italy Balkan Caucasus	41.83	46.28	Monsanto	SRR1946039	HiSeq 2000	Y	Y
9105	Lag1-7	CS77002	Italy Balkan Caucasus	41.83	46.28	Monsanto	SRR1946040	HiSeq 2000	N	N
9106	Lag1-8	CS77003	Italy Balkan Caucasus	41.83	46.28	Monsanto	SRR1946041	HiSeq 2000	Y	Y

9111	Lag2-4	CS77005	Italy Balkan Caucasus	41.83	46.28	Monsanto	SRR1946042	HiSeq 2000	Y	Y
9113	Lag2-6	CS77006	Italy Balkan Caucasus	41.83	46.28	Monsanto	SRR1946043	HiSeq 2000	Y	Y
9114	Lag2-7	CS77007	Italy Balkan Caucasus	41.83	46.28	Monsanto	SRR1946044	HiSeq 2000	Y	Y
9115	Lag2-10	CS77004	Italy Balkan Caucasus	41.83	46.28	Monsanto	SRR1946045	HiSeq 2000	N	N
9121	Bak-5	CS76685	Italy Balkan Caucasus	41.79	43.48	Monsanto	SRR1946046	HiSeq 2000	Y	Y
9125	Geg-14	CS76876	Asia	40.14	44.82	Monsanto	SRR1946047	HiSeq 2000	Y	Y
9128	Yeg-2	CS78864	Asia	39.87	45.36	Monsanto	SRR1946048	HiSeq 2000	Y	Y
9130	Yeg-4	CS78865	Asia	39.87	45.36	Monsanto	SRR1946049	HiSeq 2000	N	N
9131	Yeg-5	CS78866	Asia	39.87	45.36	Monsanto	SRR1946050	HiSeq 2000	Y	Y
9133	Yeg-7	CS78867	Asia	39.87	45.36	Monsanto	SRR1946051	HiSeq 2000	Y	Y
9134	Yeg-8	CS78868	Asia	39.87	45.36	Monsanto	SRR1946052	HiSeq 2000	N	N
9298	Edi-1	CS76832	Western Europe	55.97	-3.22	Monsanto	SRR1946053	HiSeq 2000	Y	Y
9312	Ullapool-8	CS78821	Western Europe	57.90	-5.15	Monsanto	SRR1946054	HiSeq 2000	N	N
9314	Gol-2	CS76883	Western Europe	57.97	-3.97	Monsanto	SRR1946055	HiSeq 2000	N	N
9321	Ådal 1	CS76643	North Sweden	62.86	18.34	GMI	SRR1946056	Genome Analyzer IIx	Y	Y
9323	Ådal 3	CS76644	North Sweden	62.86	18.34	GMI	SRR1946057	Genome Analyzer IIx	Y	Y
9332	Bar 1	CS76688	North Sweden	62.87	18.38	GMI	SRR1946058	HiSeq 2000	N	N
9336	Bön 1	CS76715	Admixed	62.88	18.45	GMI	SRR1946059	HiSeq 2000	Y	Y

9339	Böt 1	CS76720	South Sweden	57.71	15.07	GMI	SRR1946060	HiSeq 2000	Y	Y
9343	Dju-1	CS78896	Admixed	57.31	18.15	GMI	SRR1946061	HiSeq 2000	Y	Y
9352	Död 2	CS76797	South Sweden	57.26	16.37	GMI	SRR1946062	Genome Analyzer IIx	Y	Y
9353	Död 3	CS76798	South Sweden	57.26	16.37	GMI	SRR1946063	HiSeq 2000	Y	Y
9363	EdJ 2	CS76833	North Sweden	62.91	18.40	GMI	SRR1946064	HiSeq 2000	N	N
9369	EkS 2	CS76837	South Sweden	57.68	15	GMI	SRR1946065	HiSeq 2000	Y	Y
9370	EkS 3	CS79035	South Sweden	57.68	15	GMI	SRR1946066	HiSeq 2000	Y	Y
9371	FäL 1	CS76852	North Sweden	63.02	18.32	GMI	SRR1946067	Genome Analyzer IIx	Y	Y
9380	FlyA 3	CS76865	South Sweden	55.75	13.37	GMI	SRR1946068	HiSeq 2000	Y	Y
9381	Fri 1	CS76868	Admixed	55.81	14.21	GMI	SRR1946069	HiSeq 2000	Y	Y
9382	Fri 2	CS76869	Admixed	55.81	14.21	GMI	SRR1946070	Genome Analyzer IIx	Y	Y
9383	Fri 3	CS76870	Admixed	55.81	14.21	GMI	SRR1946071	HiSeq 2000	N	N
9386	Grön 12	CS76891	North Sweden	62.81	18.19	GMI	SRR1946072	Genome Analyzer IIx	Y	Y
9388	Grön 14	CS76892	North Sweden	62.81	18.19	GMI	SRR1946073	Genome Analyzer IIx	Y	Y
9390	Hadd-1	CS78659	South Sweden	57.33	15.90	GMI	SRR1946074	Genome Analyzer IIx	Y	Y
9391	Hadd-2	CS76905	South Sweden	57.33	15.90	GMI	SRR1946075	HiSeq 2000	Y	Y
9392	Hadd-3	CS76906	South Sweden	57.33	15.90	GMI	SRR1946076	Genome Analyzer IIx	Y	Y
9394	Hag-2	CS76907	Admixed	56.58	16.41	GMI	SRR1946077	Genome Analyzer IIx	Y	Y

9395	Hal-1	CS76908	South Sweden	57.51	15.01	GMI	SRR1946078	HiSeq 2000	Y	Y
9399	Hamm-1	CS76910	South Sweden	55.42	13.99	GMI	SRR1946079	Genome Analyzer IIx	Y	Y
9402	Hel-3	CS76918	South Sweden	57.88	14.85	GMI	SRR1946080	Genome Analyzer IIx	Y	Y
9404	HolA-1 1	CS76926	South Sweden	55.75	13.40	GMI	SRR1946081	HiSeq 2000	Y	Y
9405	HolA-1 2	CS76927	South Sweden	55.75	13.40	GMI	SRR1946082	Genome Analyzer IIx	Y	Y
9407	HolA-2 2	CS76928	South Sweden	55.75	13.40	GMI	SRR1946083	Genome Analyzer IIx	Y	Y
9408	Kal 1	CS76959	South Sweden	56.05	13.95	GMI	SRR1946084	Genome Analyzer IIx	Y	Y
9409	Kia 1	CS76968	South Sweden	56.06	14.30	GMI	SRR1946085	Genome Analyzer IIx	Y	Y
9412	Kor 3	CS76981	South Sweden	57.27	16.15	GMI	SRR1946086	Genome Analyzer IIx	Y	Y
9413	Kor 4	CS76982	South Sweden	57.27	16.15	GMI	SRR1946087	Genome Analyzer IIx	Y	Y
9416	Kru-3	CS76986	South Sweden	57.72	18.38	GMI	SRR1946088	HiSeq 2000	Y	Y
9421	Lan 1	CS77009	South Sweden	55.97	14.40	GMI	SRR1946089	Genome Analyzer IIx	Y	Y
9427	Näs 2	CS77122	North Sweden	62.88	18.41	GMI	SRR1946090	Genome Analyzer IIx	Y	Y
9433	Nyl 13	CS77135	North Sweden	62.95	18.28	GMI	SRR1946091	Genome Analyzer IIx	Y	Y
9436	Puk-1	CS77194	South Sweden	56.16	14.68	GMI	SRR1946092	Genome Analyzer IIx	Y	Y
9437	Puk-2	CS77195	South Sweden	56.16	14.68	GMI	SRR1946093	Genome Analyzer IIx	Y	Y
9442	Sim-1	CS77250	Germany	55.57	14.34	GMI	SRR1946094	HiSeq 2000	Y	Y

9450	Spro 1	CS77263	South Sweden	57.25	18.21	GMI	SRR1946095	Genome Analyzer IIx	Y	Y
9451	Spro 2	CS77264	South Sweden	57.25	18.21	GMI	SRR1946096	Genome Analyzer IIx	Y	Y
9452	Spro 3	CS77265	South Sweden	57.25	18.21	GMI	SRR1946097	Genome Analyzer IIx	Y	Y
9453	Stenk-2	CS77274	South Sweden	57.80	18.52	GMI	SRR1946098	HiSeq 2000	Y	Y
9454	Stenk-3	CS77275	South Sweden	57.80	18.52	GMI	SRR1946099	Genome Analyzer IIx	Y	Y
9455	Stenk-4	CS77276	South Sweden	57.80	18.52	GMI	SRR1946100	Genome Analyzer IIx	Y	Y
9470	Tur-4	CS77399	South Sweden	57.65	14.80	GMI	SRR1946101	Genome Analyzer IIx	Y	Y
9471	Ull-A-1	CS78820	South Sweden	56.06	13.97	GMI	SRR1946102	Genome Analyzer IIx	Y	Y
9476	VårA 1	CS78832	Germany	55.58	14.33	GMI	SRR1946103	Genome Analyzer IIx	Y	Y
9481	Yst-1	CS78869	South Sweden	55.42	13.85	GMI	SRR1946104	Genome Analyzer IIx	Y	Y
9503	11C1	CS76640	Western Europe	55.89	-3.21	Monsanto	SRR1946105	HiSeq 2000	Y	Y
9506	IP-Alo-0	CS76662	Admixed	40.11	-7.47	Monsanto	SRR1946106	HiSeq 2000	Y	Y
9507	IP-Coa-0	CS76775	Spain	38.45	-7.50	Monsanto	SRR1946107	HiSeq 2000	Y	Y
9508	IP-Mos-1	CS77108	Admixed	40.04	-7.11	Monsanto	SRR1946108	HiSeq 2000	Y	Y
9509	IP-Reg-0	CS77207	Spain	39.29	-7.40	Monsanto	SRR1946109	HiSeq 2000	Y	Y
9510	IP-Rei-0	CS77208	Spain	38.75	-7.59	Monsanto	SRR1946110	HiSeq 2000	Y	Y
9511	IP-Vav-0	CS78835	Spain	38.53	-8.02	Monsanto	SRR1946111	HiSeq 2000	Y	Y
9512	IP-Vid-1	CS78842	Spain	38.22	-7.84	Monsanto	SRR1946112	HiSeq 2000	Y	Y
9513	IP-Adc-5	CS76646	Admixed	38.77	-4.07	Monsanto	SRR1946113	HiSeq 2000	Y	Y
9514	IP-Adm-0	CS76647	Spain	39.15	-4.54	Monsanto	SRR1946114	HiSeq 2000	Y	Y
9515	IP-Ala-0	CS76650	Spain	39.72	-6.89	Monsanto	SRR1946115	HiSeq 2000	Y	Y
9517	IP-All-0	CS76659	Western Europe	42.19	-7.80	Monsanto	SRR1946116	HiSeq 2000	Y	Y

9518	IP-Alm-0	CS76660	Spain	39.88	-0.36	Monsanto	SRR1946117	HiSeq 2000	Y	Y
9519	IP-Ang-0	CS78886	Spain	41.94	2.64	Monsanto	SRR1946118	HiSeq 2000	Y	Y
9520	IP-Ara-4	CS76670	Spain	41.70	-3.68	Monsanto	SRR1946119	HiSeq 2000	Y	Y
9521	IP-Bar-1	CS76689	Spain	41.43	2.13	Monsanto	SRR1946120	HiSeq 2000	Y	Y
9522	IP-Bea-0	CS76695	Spain	36.52	-5.27	Monsanto	SRR1946121	HiSeq 2000	Y	Y
9523	IP-Ben-0	CS76700	Admixed	38.37	-2.66	Monsanto	SRR1946122	HiSeq 2000	Y	Y
9524	IP-Ber-0	CS78887	Spain	42.52	-0.56	Monsanto	SRR1946123	HiSeq 2000	Y	Y
9525	IP-Bis-0	CS76711	Spain	42.49	0.54	Monsanto	SRR1946124	HiSeq 2000	Y	Y
9526	IP-Cab-3	CS76738	Spain	41.54	2.39	Monsanto	SRR1946125	HiSeq 2000	Y	Y
9527	IP-Cad-0	CS76739	Admixed	40.37	-5.74	Monsanto	SRR1946126	HiSeq 2000	Y	Y
9528	IP-Cal-0	CS78890	Spain	40.94	-1.37	Monsanto	SRR1946127	HiSeq 2000	Y	Y
9529	IP-Cap-1	CS76741	Admixed	36.97	-3.36	Monsanto	SRR1946128	HiSeq 2000	Y	Y
9530	IP-Car-1	CS76742	Admixed	38.25	-4.32	Monsanto	SRR1946129	HiSeq 2000	Y	Y
9531	IP-Cdc-3	CS76761	Spain	41.21	-4.54	Monsanto	SRR1946130	HiSeq 2000	Y	Y
9532	IP-Cdo-0	CS76762	Spain	42.23	-4.64	Monsanto	SRR1946131	HiSeq 2000	Y	Y
9533	IP-Cem-0	CS76763	Relict	41.15	-4.32	Monsanto	SRR1946132	HiSeq 2000	Y	Y
9534	IP-Cmo-3	CS76774	Spain	40.05	-4.65	Monsanto	SRR1946133	HiSeq 2000	Y	Y
9535	IP-Coc-1	CS76776	Spain	42.31	3.19	Monsanto	SRR1946134	HiSeq 2000	Y	Y
9536	IP-Cor-0	CS76782	Admixed	40.83	-2	Monsanto	SRR1946135	HiSeq 2000	Y	Y
9537	IP-Cum-1	CS76787	Spain	38.07	-6.66	Monsanto	SRR1946136	HiSeq 2000	Y	Y
9539	IP-Deh-1	CS76793	Spain	40.29	-6.67	Monsanto	SRR1946137	HiSeq 2000	Y	Y
9540	IP-Elb-0	CS76838	Spain	41.81	2.34	Monsanto	SRR1946138	HiSeq 2000	Y	Y
9541	IP-Fue-2	CS76871	Spain	38.26	-5.42	Monsanto	SRR1946139	HiSeq 2000	Y	Y
9542	IP-Fun-0	CS76872	Relict	40.79	-4.05	Monsanto	SRR1946140	HiSeq 2000	Y	Y
9543	IP-Gra-0	CS76886	Relict	36.77	-5.39	Monsanto	SRR1946141	HiSeq 2000	Y	Y
9544	IP-Gua-1	CS76894	Spain	39.40	-5.33	Monsanto	SRR1946142	HiSeq 2000	Y	Y
9545	IP-Her-12	CS76920	Relict	39.40	-5.78	Monsanto	SRR1946143	HiSeq 2000	Y	Y
9546	IP-Hom-4	CS76929	Spain	40.82	-1.68	Monsanto	SRR1946144	HiSeq 2000	Y	Y
9547	IP-Hor-0	CS76930	Spain	41.67	2.62	Monsanto	SRR1946145	HiSeq 2000	Y	Y
9548	IP-Hoy-0	CS76939	Admixed	40.40	-5	Monsanto	SRR1946146	HiSeq 2000	Y	Y
9549	IP-Hum-2	CS76943	Relict	42.23	-3.69	Monsanto	SRR1946147	HiSeq 2000	Y	Y
9550	IP-Iso-4	CS76946	Relict	43.05	-5.37	Monsanto	SRR1946148	HiSeq 2000	Y	Y
9551	IP-Jim-1	CS76955	Admixed	42.28	-5.92	Monsanto	SRR1946149	HiSeq 2000	Y	Y

9552	IP-Lab-7	CS76995	Admixed	40.87	-4.50	Monsanto	SRR1946150	HiSeq 2000	Y	Y
9553	IP-Ldd-0	CS77012	Spain	41.58	-4.71	Monsanto	SRR1946151	HiSeq 2000	Y	Y
9554	IP-Lso-0	CS77055	Relict	38.86	-3.16	Monsanto	SRR1946152	HiSeq 2000	Y	Y
9555	IP-Mar-1	CS77068	Relict	39.58	-3.93	Monsanto	SRR1946153	HiSeq 2000	Y	Y
9556	IP-Men-2	CS77081	Spain	39.66	-4.34	Monsanto	SRR1946154	HiSeq 2000	Y	Y
9557	IP-Moa-0	CS77102	Spain	42.46	0.70	Monsanto	SRR1946155	HiSeq 2000	Y	Y
9558	IP-Moc-11	CS77103	Admixed	41.57	-5.64	Monsanto	SRR1946156	HiSeq 2000	Y	Y
9559	IP-Mon-5	CS77107	Admixed	38.06	-4.38	Monsanto	SRR1946157	HiSeq 2000	Y	Y
9560	IP-Mot-0	CS77109	Spain	38.19	-6.24	Monsanto	SRR1946158	HiSeq 2000	Y	Y
9561	IP-Mun-0	CS77114	Admixed	40.71	-5.04	Monsanto	SRR1946159	HiSeq 2000	Y	Y
9562	IP-Mur-0	CS77115	Spain	41.67	2	Monsanto	SRR1946160	HiSeq 2000	Y	Y
9564	IP-Nog-17	CS77129	Spain	40.45	-1.60	Monsanto	SRR1946161	HiSeq 2000	Y	Y
9565	IP-Orb-10	CS77152	Admixed	42.97	-1.23	Monsanto	SRR1946162	HiSeq 2000	Y	Y
9567	IP-Pal-0	CS77159	Spain	42.34	1.30	Monsanto	SRR1946163	HiSeq 2000	Y	Y
9568	IP-Pan-0	CS77160	Spain	42.76	-0.23	Monsanto	SRR1946164	HiSeq 2000	Y	Y
9569	IP-Pds-1	CS77166	Western Europe	42.87	-6.45	Monsanto	SRR1946165	HiSeq 2000	Y	Y
9571	IP-Pro-0	CS78914	Western Europe	43.28	-6.01	Monsanto	SRR1946166	HiSeq 2000	Y	Y
9573	IP-Rds-0	CS77206	Spain	41.86	2.99	Monsanto	SRR1946167	HiSeq 2000	Y	Y
9574	IP-Rel-0	CS77209	Relict	38.60	-2.70	Monsanto	SRR1946168	HiSeq 2000	Y	Y
9576	IP-Rev-0	CS77213	Admixed	40.86	-4.11	Monsanto	SRR1946169	HiSeq 2000	Y	Y
9577	IP-Ria-0	CS77216	Spain	42.34	2.17	Monsanto	SRR1946170	HiSeq 2000	Y	Y
9578	IP-Sac-0	CS77229	Western Europe	42.13	-6.70	Monsanto	SRR1946171	HiSeq 2000	Y	Y
9579	IP-San-10	CS77232	Admixed	38.33	-3.51	Monsanto	SRR1946172	HiSeq 2000	Y	Y
9581	IP-Sdv-3	CS77242	Admixed	42.84	-5.12	Monsanto	SRR1946173	HiSeq 2000	Y	Y
9582	IP-Ses-0	CS77244	Spain	41.48	-1.63	Monsanto	SRR1946174	HiSeq 2000	Y	Y
9583	IP-Sne-0	CS77258	Relict	37.09	-3.38	Monsanto	SRR1946175	HiSeq 2000	Y	Y
9584	IP-Stp-0	CS77283	Spain	41.19	-3.58	Monsanto	SRR1946176	HiSeq 2000	Y	Y
9585	IP-Svi-0	CS77287	Western Europe	43.40	-7.39	Monsanto	SRR1946177	HiSeq 2000	Y	Y
9586	IP-Tam-0	CS77340	Spain	41.03	-3.27	Monsanto	SRR1946178	HiSeq 2000	Y	Y
9587	IP-Tdc-0	CS77344	Spain	41.50	-1.88	Monsanto	SRR1946179	HiSeq 2000	Y	Y

9588	IP-Tol-7	CS77371	Spain	42.11	0.60	Monsanto	SRR1946180	HiSeq 2000	Y	Y
9589	IP-Tor-1	CS77378	Spain	41.60	-2.83	Monsanto	SRR1946181	HiSeq 2000	Y	Y
9590	IP-Trs-0	CS77387	Western Europe	43.37	-5.49	Monsanto	SRR1946182	HiSeq 2000	Y	Y
9591	IP-Vad-0	CS78826	Admixed	42.86	-3.59	Monsanto	SRR1946183	HiSeq 2000	Y	Y
9592	IP-Vae-2	CS78827	Admixed	42.10	-5.44	Monsanto	SRR1946184	HiSeq 2000	Y	Y
9593	IP-Vaz-0	CS78836	Spain	42.26	-2.99	Monsanto	SRR1946185	HiSeq 2000	Y	Y
9594	IP-Vdm-0	CS78837	Spain	42.04	1.01	Monsanto	SRR1946186	HiSeq 2000	Y	Y
9595	IP-Vdt-0	CS78838	Admixed	40.89	-5.50	Monsanto	SRR1946187	HiSeq 2000	Y	Y
9596	IP-Ver-5	CS78841	Admixed	41.95	-7.45	Monsanto	SRR1946188	HiSeq 2000	Y	Y
9597	IP-Vig-1	CS78843	Spain	42.31	-2.53	Monsanto	SRR1946189	HiSeq 2000	Y	Y
9598	IP-Vim-0	CS78844	Relict	41.88	-6.51	Monsanto	SRR1946190	HiSeq 2000	Y	Y
9599	IP-Vin-0	CS78846	Western Europe	42.80	-5.77	Monsanto	SRR1946191	HiSeq 2000	Y	Y
9600	IP-Vis-0	CS78848	Relict	39.85	-6.04	Monsanto	SRR1946192	HiSeq 2000	Y	Y
9601	IP-Voz-0	CS78849	Spain	41.85	-1.88	Monsanto	SRR1946193	HiSeq 2000	Y	Y
9602	IP-Vpa-1	CS78850	Spain	40.50	-3.96	Monsanto	SRR1946194	HiSeq 2000	Y	Y
9606	Aitba-1	CS76649	Relict	31.48	-7.45	Monsanto	SRR1946195	HiSeq 2000	Y	Y
9607	Panik-1	CS77161	Asia	53.05	52.15	Monsanto	SRR1946196	HiSeq 2000	Y	Y
9608	Karag-2	CS76961	Asia	51.37	59.44	Monsanto	SRR1946197	HiSeq 2000	Y	Y
9609	Adam-1	CS76645	Asia	51.41	59.98	Monsanto	SRR1946198	HiSeq 2000	Y	Y
9610	Lesno-4	CS77034	Asia	53.04	51.96	Monsanto	SRR1946199	HiSeq 2000	Y	Y
9611	Lesno-1	CS77032	Asia	53.04	51.90	Monsanto	SRR1946200	HiSeq 2000	Y	Y
9612	Lesno-2	CS77033	Asia	53.04	51.94	Monsanto	SRR1946201	HiSeq 2000	Y	Y
9613	Balan-1	CS76687	Italy Balkan Caucasus	55.36	61.41	Monsanto	SRR1946202	HiSeq 2000	Y	Y
9615	Parti-1	CS77163	Asia	52.99	52.16	Monsanto	SRR1946203	HiSeq 2000	Y	Y
9616	Krazo-1	CS76984	Asia	53.06	51.96	Monsanto	SRR1946204	HiSeq 2000	Y	Y
9617	Karag-1	CS76960	Asia	51.37	59.44	Monsanto	SRR1946205	HiSeq 2000	Y	Y
9619	Basta-1	CS76691	Asia	51.84	79.48	Monsanto	SRR1946206	HiSeq 2000	Y	Y
9620	Basta-2	CS76692	Asia	51.82	79.48	Monsanto	SRR1946207	HiSeq 2000	Y	Y
9621	Basta-3	CS76693	Asia	51.84	79.46	Monsanto	SRR1946208	HiSeq 2000	Y	Y
9622	Bijisk-4	CS76707	Admixed	52.52	85.27	Monsanto	SRR1946209	HiSeq 2000	Y	Y

9624	Chaba-2	CS76767	Asia	53.60	79.37	Monsanto	SRR1946210	HiSeq 2000	Y	Y
9625	Kolyv-2	CS76977	Asia	51.31	82.59	Monsanto	SRR1946211	HiSeq 2000	Y	Y
9626	Kolyv-3	CS76978	Asia	51.36	82.59	Monsanto	SRR1946212	HiSeq 2000	Y	Y
9627	Kolyv-5	CS76979	Asia	51.32	82.55	Monsanto	SRR1946213	HiSeq 2000	Y	Y
9628	Kolyv-6	CS76980	Asia	51.33	82.54	Monsanto	SRR1946214	HiSeq 2000	Y	Y
9629	K-oze-1	CS76957	Asia	51.35	82.18	Monsanto	SRR1946215	HiSeq 2000	Y	Y
9630	K-oze-3	CS76958	Asia	51.34	82.16	Monsanto	SRR1946216	HiSeq 2000	Y	Y
9631	Lebja-1	CS77015	Asia	51.65	80.79	Monsanto	SRR1946217	HiSeq 2000	Y	Y
9632	Lebja-2	CS77016	Asia	51.67	80.82	Monsanto	SRR1946218	HiSeq 2000	Y	Y
9633	Lebja-4	CS77017	Asia	51.63	80.83	Monsanto	SRR1946219	HiSeq 2000	Y	Y
9634	Masl-1	CS77073	Asia	54.13	81.31	Monsanto	SRR1946220	HiSeq 2000	Y	Y
9635	Nosov-1	CS77130	Asia	51.87	80.60	Monsanto	SRR1946221	HiSeq 2000	Y	Y
9636	Noveg-1	CS77131	Asia	51.75	80.82	Monsanto	SRR1946222	HiSeq 2000	Y	Y
9637	Noveg-2	CS77132	Asia	51.77	80.85	Monsanto	SRR1946223	HiSeq 2000	Y	Y
9638	Noveg-3	CS77133	Asia	51.73	80.86	Monsanto	SRR1946224	HiSeq 2000	Y	Y
9639	Panke-1	CS77162	Asia	53.82	80.31	Monsanto	SRR1946225	HiSeq 2000	Y	Y
9640	Rakit-1	CS77202	Asia	51.87	80.06	Monsanto	SRR1946226	HiSeq 2000	Y	Y
9641	Rakit-2	CS77203	Asia	51.90	80.06	Monsanto	SRR1946227	HiSeq 2000	Y	Y
9642	Rakit-3	CS77204	Asia	51.84	80.06	Monsanto	SRR1946228	HiSeq 2000	Y	Y
9643	Sever-1	CS77245	Asia	52.10	79.31	Monsanto	SRR1946229	HiSeq 2000	Y	Y
9644	Zupan-1	CS78882	Central Europe	45.07	18.72	Monsanto	SRR1946230	HiSeq 2000	Y	Y
9645	Gradi-1	CS76887	Central Europe	45.17	18.70	Monsanto	SRR1946231	HiSeq 2000	Y	Y
9646	Aiell-1	CS76648	Italy Balkan Caucasus	39.13	16.17	Monsanto	SRR1946232	HiSeq 2000	Y	Y
9647	Basen-1	CS76690	Italy Balkan Caucasus	40.37	16.77	Monsanto	SRR1946233	HiSeq 2000	Y	Y
9648	Bisig-1	CS76712	Italy Balkan Caucasus	39.48	16.28	Monsanto	SRR1946234	HiSeq 2000	Y	Y

9649	Bivio-1	CS76713	Italy Balkan Caucasus	39.13	16.17	Monsanto	SRR1946235	HiSeq 2000	Y	Y
9651	Filet-1	CS76858	Italy Balkan Caucasus	40.68	14.87	Monsanto	SRR1946236	HiSeq 2000	Y	Y
9653	Giffo-1	CS76878	Italy Balkan Caucasus	38.44	16.13	Monsanto	SRR1946237	HiSeq 2000	Y	Y
9655	Marce-1	CS77071	Italy Balkan Caucasus	38.92	16.47	Monsanto	SRR1946238	HiSeq 2000	Y	Y
9656	Marti-1	CS77072	Italy Balkan Caucasus	40.64	17.31	Monsanto	SRR1946239	HiSeq 2000	Y	Y
9657	Melic-1	CS77078	Italy Balkan Caucasus	38.45	16.04	Monsanto	SRR1946240	HiSeq 2000	Y	Y
9658	Nicas-1	CS77127	Italy Balkan Caucasus	38.97	16.34	Monsanto	SRR1946241	HiSeq 2000	Y	Y
9659	Pigna-1	CS77177	Italy Balkan Caucasus	41.18	14.18	Monsanto	SRR1946242	HiSeq 2000	Y	Y
9660	Sarno-1	CS77236	Italy Balkan Caucasus	40.84	14.57	Monsanto	SRR1946243	HiSeq 2000	Y	Y
9661	Cimin-1	CS76771	Italy Balkan Caucasus	39.58	16.21	Monsanto	SRR1946244	HiSeq 2000	Y	Y
9663	Teano-1	CS77357	Admixed	41.33	14.09	Monsanto	SRR1946245	HiSeq 2000	Y	Y
9664	Mitterberg-1-179	CS78907	Central Europe	46.37	11.28	Monsanto	SRR1946246	HiSeq 2000	Y	Y
9665	Mitterberg-1-180	CS78908	Central Europe	46.37	11.28	Monsanto	SRR1946247	HiSeq 2000	Y	Y

9666	Mitterberg-1-182	CS78909	Central Europe	46.37	11.28	Monsanto	SRR1946248	HiSeq 2000	Y	Y
9667	Mitterberg-1-183	CS78910	Central Europe	46.37	11.28	Monsanto	SRR1946249	HiSeq 2000	N	N
9668	Mitterberg-2-184	CS77085	Central Europe	46.37	11.28	Monsanto	SRR1946250	HiSeq 2000	Y	Y
9669	Mitterberg-2-185	CS77086	Central Europe	46.37	11.28	Monsanto	SRR1946251	HiSeq 2000	Y	Y
9670	Mitterberg-2-186	CS77087	Central Europe	46.37	11.28	Monsanto	SRR1946252	HiSeq 2000	Y	Y
9671	Mitterberg-3-187	CS77088	Central Europe	46.37	11.28	Monsanto	SRR1946253	HiSeq 2000	Y	Y
9672	Mitterberg-3-188	CS77089	Central Europe	46.37	11.28	Monsanto	SRR1946254	HiSeq 2000	Y	Y
9673	Mitterberg-3-189	CS77090	Central Europe	46.37	11.28	Monsanto	SRR1946255	HiSeq 2000	N	N
9676	Mitterberg-4-192	CS77093	Central Europe	46.37	11.29	Monsanto	SRR1946256	HiSeq 2000	N	N
9677	Mitterberg-4-193	CS77094	Central Europe	46.37	11.29	Monsanto	SRR1946257	HiSeq 2000	Y	Y
9678	Mitterberg-4-194	CS77095	Central Europe	46.37	11.29	Monsanto	SRR1946258	HiSeq 2000	Y	Y
9679	Castelfed-1-195	CS76744	Central Europe	46.34	11.29	Monsanto	SRR1946259	HiSeq 2000	N	N
9680	Castelfed-1-196	CS76745	Central Europe	46.34	11.29	Monsanto	SRR1946260	HiSeq 2000	N	N
9681	Castelfed-1-197	CS76746	Central Europe	46.34	11.29	Monsanto	SRR1946261	HiSeq 2000	N	N
9682	Castelfed-1-198	CS76747	Central Europe	46.34	11.29	Monsanto	SRR1946262	HiSeq 2000	N	N
9683	Castelfed-1-199	CS76748	Central Europe	46.34	11.29	Monsanto	SRR1946263	HiSeq 2000	Y	Y
9684	Castelfed-2-200	CS76749	Central Europe	46.34	11.29	Monsanto	SRR1946264	HiSeq 2000	N	N

9685	Castelfed-2-201	CS76750	Central Europe	46.34	11.29	Monsanto	SRR1946265	HiSeq 2000	N	N
9686	Castelfed-2-202	CS76751	Central Europe	46.34	11.29	Monsanto	SRR1946266	HiSeq 2000	Y	Y
9687	Castelfed-2-203	CS76752	Central Europe	46.34	11.29	Monsanto	SRR1946267	HiSeq 2000	Y	Y
9689	Castelfed-3-205	CS76754	Central Europe	46.34	11.29	Monsanto	SRR1946268	HiSeq 2000	N	N
9690	Castelfed-3-206	CS76755	Central Europe	46.34	11.29	Monsanto	SRR1946269	HiSeq 2000	Y	Y
9691	Castelfed-3-207	CS76756	Admixed	46.34	11.29	Monsanto	SRR1946270	HiSeq 2000	Y	Y
9692	Castelfed-3-208	CS76757	Central Europe	46.34	11.29	Monsanto	SRR1946271	HiSeq 2000	N	N
9693	Castelfed-3-209	CS76758	Central Europe	46.34	11.29	Monsanto	SRR1946272	HiSeq 2000	Y	Y
9694	Castelfed-4-210	CS78891	Central Europe	46.34	11.29	Monsanto	SRR1946273	HiSeq 2000	Y	Y
9695	Castelfed-4-211	CS78892	Central Europe	46.34	11.29	Monsanto	SRR1946274	HiSeq 2000	N	N
9696	Castelfed-4-214	CS78893	Central Europe	46.34	11.29	Monsanto	SRR1946275	HiSeq 2000	Y	Y
9697	Dolen-1	CS76802	Italy Balkan Caucasus	41.62	23.94	Monsanto	SRR1946276	HiSeq 2000	Y	Y
9698	Goced-1	CS76882	Italy Balkan Caucasus	41.57	23.85	Monsanto	SRR1946277	HiSeq 2000	Y	Y
9699	Kolar-1	CS76974	Italy Balkan Caucasus	41.37	23.14	Monsanto	SRR1946278	HiSeq 2000	Y	Y
9700	Dolna-1-10	CS76803	Italy Balkan Caucasus	42.32	23.10	Monsanto	SRR1946279	HiSeq 2000	Y	Y

9701	Ivano-1	CS76954	Italy Balkan Caucasus	43.70	25.91	Monsanto	SRR1946280	HiSeq 2000	Y	Y
9703	Melni-1	CS77079	Italy Balkan Caucasus	41.53	23.39	Monsanto	SRR1946281	HiSeq 2000	Y	Y
9704	Melni-2	CS77080	Italy Balkan Caucasus	41.53	23.39	Monsanto	SRR1946282	HiSeq 2000	Y	Y
9705	Choto-1	CS76769	Italy Balkan Caucasus	41.50	23.33	Monsanto	SRR1946283	HiSeq 2000	Y	Y
9706	Dospa-1	CS76807	Italy Balkan Caucasus	41.64	24.18	Monsanto	SRR1946284	HiSeq 2000	Y	Y
9707	Podvi-1	CS77187	Italy Balkan Caucasus	41.57	24.84	Monsanto	SRR1946285	HiSeq 2000	Y	Y
9708	Kardz-1	CS76962	Italy Balkan Caucasus	41.62	25.35	Monsanto	SRR1946286	HiSeq 2000	Y	Y
9709	Zerev-1-34	CS78878	Italy Balkan Caucasus	41.85	23.13	Monsanto	SRR1946287	HiSeq 2000	Y	Y
9710	Zerev-1-35	CS78879	Italy Balkan Caucasus	41.85	23.13	Monsanto	SRR1946288	HiSeq 2000	Y	Y
9711	Dolna-1-39	CS76804	Italy Balkan Caucasus	42.32	23.10	Monsanto	SRR1946289	HiSeq 2000	Y	Y
9712	Dolna-1-40	CS76805	Italy Balkan Caucasus	42.32	23.10	Monsanto	SRR1946290	HiSeq 2000	N	N

9713	Stara-1	CS77271	Italy Balkan Caucasus	42.49	25.61	Monsanto	SRR1946291	HiSeq 2000	Y	Y
9714	Grivo-1	CS76888	Italy Balkan Caucasus	41.84	25.75	Monsanto	SRR1946292	HiSeq 2000	Y	Y
9716	Leska-1-44	CS77030	Italy Balkan Caucasus	41.54	24.98	Monsanto	SRR1946293	HiSeq 2000	Y	Y
9717	Kardz-2	CS76963	Italy Balkan Caucasus	41.66	25.47	Monsanto	SRR1946294	HiSeq 2000	Y	Y
9718	Smolj-1	CS77256	Italy Balkan Caucasus	41.55	24.75	Monsanto	SRR1946295	HiSeq 2000	Y	Y
9719	Koren-1	CS76983	Italy Balkan Caucasus	41.83	25.69	Monsanto	SRR1946296	HiSeq 2000	Y	Y
9720	Malak-1	CS77064	Italy Balkan Caucasus	41.77	25.68	Monsanto	SRR1946297	HiSeq 2000	Y	Y
9721	Schip-1	CS77239	Italy Balkan Caucasus	42.72	25.33	Monsanto	SRR1946298	HiSeq 2000	N	N
9722	Groch-1	CS76890	Italy Balkan Caucasus	41.71	24.41	Monsanto	SRR1946299	HiSeq 2000	Y	Y
9723	Slavi-2	CS77252	Italy Balkan Caucasus	41.42	23.67	Monsanto	SRR1946300	HiSeq 2000	Y	Y
9725	Epidauros-1	CS76844	Italy Balkan Caucasus	37.60	23.08	Monsanto	SRR1946301	HiSeq 2000	Y	Y

9726	Faneronemi-3	CS76853	Italy Balkan Caucasus	37.07	22.04	Monsanto	SRR1946302	HiSeq 2000	Y	Y
9727	Olympia-2	CS77144	Central Europe	37.63	21.62	Monsanto	SRR1946303	HiSeq 2000	Y	Y
9728	Stiav-1	CS77279	Central Europe	48.46	18.90	Monsanto	SRR1946304	HiSeq 2000	Y	Y
9729	Stiav-2	CS77280	Central Europe	48.46	18.90	Monsanto	SRR1946305	HiSeq 2000	Y	Y
9730	Bela-1	CS76696	Central Europe	48.47	18.94	Monsanto	SRR1946306	HiSeq 2000	Y	Y
9731	Stiav-3	CS77281	Central Europe	48.46	18.90	Monsanto	SRR1946307	HiSeq 2000	Y	Y
9732	Halca-1	CS76909	Central Europe	48.47	18.96	Monsanto	SRR1946308	HiSeq 2000	Y	Y
9733	Bela-2	CS76697	Central Europe	48.47	18.94	Monsanto	SRR1946309	HiSeq 2000	Y	Y
9735	Bela-4	CS76699	Central Europe	48.47	18.94	Monsanto	SRR1946310	HiSeq 2000	Y	Y
9736	Teiu-2	CS77361	Admixed	44.69	25.17	Monsanto	SRR1946311	HiSeq 2000	Y	Y
9737	Ulies-1	CS78815	Asia	45.95	22.62	Monsanto	SRR1946312	HiSeq 2000	Y	Y
9738	Bran-1	CS76722	Admixed	45.57	25.42	Monsanto	SRR1946313	HiSeq 2000	Y	Y
9739	Toc-1	CS77370	Central Europe	46.01	22.33	Monsanto	SRR1946314	HiSeq 2000	Y	Y
9741	Orast-1	CS77151	Central Europe	45.84	23.16	Monsanto	SRR1946315	HiSeq 2000	Y	Y
9743	Furni-1	CS76873	Admixed	45.14	25	Monsanto	SRR1946316	HiSeq 2000	Y	Y
9744	Iasi-1	CS76944	Admixed	47.16	27.59	Monsanto	SRR1946317	HiSeq 2000	Y	Y
9745	Sij 1/96	CS77249	Asia	41.45	70.05	Monsanto	SRR1946318	HiSeq 2000	Y	Y
9747	Zabar-1	CS78870	Central Europe	44.38	21.22	Monsanto	SRR1946319	HiSeq 2000	Y	Y
9748	Zagub-1	CS78871	Admixed	44.23	21.71	Monsanto	SRR1946320	HiSeq 2000	Y	Y

9749	Knjas-1	CS76971	Italy Balkan Caucasus	43.54	22.29	Monsanto	SRR1946321	HiSeq 2000	Y	Y
9754	Sredn-1	CS77269	Admixed	44.66	21.37	Monsanto	SRR1946322	HiSeq 2000	Y	Y
9755	Vajug-1	CS78828	Italy Balkan Caucasus	44.56	22.56	Monsanto	SRR1946323	HiSeq 2000	Y	Y
9756	Staro-2	CS77273	Central Europe	44.30	21.08	Monsanto	SRR1946324	HiSeq 2000	Y	Y
9757	Staro-1	CS77272	Italy Balkan Caucasus	44.30	21.08	Monsanto	SRR1946325	HiSeq 2000	Y	Y
9758	Altai-5	CS76433	Asia	47.75	88.40	Salk	SRR1946326	HiSeq 2000	Y	Y
9759	Anz-0	CS76439	Italy Balkan Caucasus	37.47	49.47	Salk	SRR1946327	HiSeq 2000	Y	Y
9761	Bik-1	CS76449	Central Europe	33.92	35.70	Salk	SRR1946328	HiSeq 2000	Y	Y
9762	Etna-2	CS76487	Admixed	37.69	14.98	Salk	SRR1946329	HiSeq 2000	Y	Y
9764	Qar-8a	CS76581	Admixed	34.10	35.84	Salk	SRR1946330	HiSeq 2000	Y	Y
9766	Westkar-4	CS76629	Asia	42.26	74.16	Salk	SRR1946331	HiSeq 2000	Y	Y
9768	Ru4-16	CS77225	Central Europe	48.57	9.16	Monsanto	SRR1946332	HiSeq 2000	Y	Y
9769	HE-1	CS76916	Central Europe	48.55	8.99	Monsanto	SRR1946333	HiSeq 2000	Y	Y
9770	KBG2-13	CS76966	Central Europe	48.53	9.01	Monsanto	SRR1946334	HiSeq 2000	Y	Y
9771	Pfn-N2.2-6	CS77172	Central Europe	48.56	9.11	Monsanto	SRR1946335	HiSeq 2000	Y	Y
9772	Hof-1	CS76925	Central Europe	48.41	8.85	Monsanto	SRR1946336	HiSeq 2000	Y	Y
9774	Alt-1	CS76663	Central Europe	48.59	9.22	Monsanto	SRR1946337	HiSeq 2000	Y	Y

9775	Berg-1	CS76701	Central Europe	48.41	8.79	Monsanto	SRR1946338	HiSeq 2000	Y	Y
9776	Fell3-7	CS76857	Central Europe	48.43	8.79	Monsanto	SRR1946339	HiSeq 2000	Y	Y
9777	Gn-1	CS76880	Central Europe	48.57	9.17	Monsanto	SRR1946340	HiSeq 2000	Y	Y
9778	Bach-7	CS76679	Central Europe	48.41	8.84	Monsanto	SRR1946341	HiSeq 2000	Y	Y
9779	Bai-10	CS76682	Central Europe	48.50	8.78	Monsanto	SRR1946342	HiSeq 2000	Y	Y
9780	Fell2-4	CS76856	Central Europe	48.43	8.79	Monsanto	SRR1946343	HiSeq 2000	Y	Y
9781	Kus2-2	CS76990	Central Europe	48.52	9.11	Monsanto	SRR1946344	HiSeq 2000	Y	Y
9782	Lu3-30	CS77057	Central Europe	48.53	9.09	Monsanto	SRR1946345	HiSeq 2000	Y	Y
9783	Tu-PK-7	CS77396	Admixed	48.52	9.05	Monsanto	SRR1946346	HiSeq 2000	Y	Y
9784	Erg2-6	CS76845	Central Europe	48.50	8.80	Monsanto	SRR1946347	HiSeq 2000	Y	Y
9785	Ha-HBT1-2	CS76898	Central Europe	48.54	9.02	Monsanto	SRR1946348	HiSeq 2000	Y	Y
9786	Ha-P-13	CS76901	Central Europe	48.54	9.01	Monsanto	SRR1946349	HiSeq 2000	Y	Y
9787	HI-4	CS76922	Central Europe	48.50	9	Monsanto	SRR1946350	HiSeq 2000	Y	Y
9788	KBG1-14	CS76965	Central Europe	48.53	9.01	Monsanto	SRR1946351	HiSeq 2000	Y	Y
9789	Obh-13	CS77140	Central Europe	48.39	8.96	Monsanto	SRR1946352	HiSeq 2000	Y	Y
9790	Gn2-3	CS76881	Central Europe	48.58	9.18	Monsanto	SRR1946353	HiSeq 2000	Y	Y
9791	Haes-1	CS76914	Central Europe	48.60	9.20	Monsanto	SRR1946354	HiSeq 2000	Y	Y

9792	Lu4-2	CS77058	Central Europe	48.54	9.09	Monsanto	SRR1946355	HiSeq 2000	Y	Y
9793	Ru-N2	CS77224	Central Europe	48.57	9.16	Monsanto	SRR1946356	HiSeq 2000	Y	Y
9794	Tu-B1-2	CS77391	Central Europe	48.52	9.08	Monsanto	SRR1946357	HiSeq 2000	Y	Y
9795	Wank-2	CS78852	Central Europe	48.50	9.11	Monsanto	SRR1946358	HiSeq 2000	Y	Y
9796	Bach2-1	CS76680	Central Europe	48.41	8.84	Monsanto	SRR1946359	HiSeq 2000	Y	Y
9797	Ha-HBT2-10	CS76899	Central Europe	48.54	9.02	Monsanto	SRR1946360	HiSeq 2000	Y	Y
9798	Ha-P2-1	CS76902	Central Europe	48.54	9.01	Monsanto	SRR1946361	HiSeq 2000	Y	Y
9799	Hart-2	CS76913	Central Europe	48.39	8.85	Monsanto	SRR1946362	HiSeq 2000	Y	Y
9800	Ha-S-B	CS76903	Central Europe	48.54	9.01	Monsanto	SRR1946363	HiSeq 2000	Y	Y
9801	Ha-SP-2	CS76904	Central Europe	48.54	9.01	Monsanto	SRR1946364	HiSeq 2000	Y	Y
9802	Kus3-1	CS76991	Central Europe	48.51	9.11	Monsanto	SRR1946365	HiSeq 2000	Y	Y
9803	Muh-2	CS77113	Central Europe	48.42	8.76	Monsanto	SRR1946366	HiSeq 2000	Y	Y
9804	Obe1-15	CS77139	Central Europe	48.45	8.87	Monsanto	SRR1946367	HiSeq 2000	Y	Y
9805	Pfn-10	CS77171	Central Europe	48.54	9.09	Monsanto	SRR1946368	HiSeq 2000	Y	Y
9806	Ru-2	CS77223	Central Europe	48.56	9.16	Monsanto	SRR1946369	HiSeq 2000	Y	Y
9807	Schl-7	CS77240	Central Europe	48.60	9.22	Monsanto	SRR1946370	HiSeq 2000	Y	Y
9808	Tu-B2-3	CS77392	Central Europe	48.52	9.08	Monsanto	SRR1946371	HiSeq 2000	Y	Y

9809	Tu-KB-6	CS77393	Western Europe	48.52	9.05	Monsanto	SRR1946372	HiSeq 2000	Y	Y
9810	Tu-KS-7	CS77394	Central Europe	48.53	9.07	Monsanto	SRR1946373	HiSeq 2000	Y	Y
9811	Tu-NK-12	CS77395	Central Europe	48.52	9.05	Monsanto	SRR1946374	HiSeq 2000	Y	Y
9812	Tu-W1	CS77397	Central Europe	48.52	9.03	Monsanto	SRR1946375	HiSeq 2000	Y	Y
9813	BI-4	CS76706	Central Europe	48.40	8.77	Monsanto	SRR1946376	HiSeq 2000	Y	Y
9814	Fell1-10	CS76855	Central Europe	48.42	8.79	Monsanto	SRR1946377	HiSeq 2000	Y	Y
9815	Ha-HBT3-11	CS76900	Central Europe	48.54	9.02	Monsanto	SRR1946378	HiSeq 2000	Y	Y
9816	Tu-WH	CS77398	Central Europe	48.55	9.06	Monsanto	SRR1946379	HiSeq 2000	Y	Y
9817	IP-Ace-0	CS76642	Spain	39.84	-6.60	Monsanto	SRR1946380	HiSeq 2000	Y	Y
9819	IP-Amu-0	CS76664	Spain	42.35	-3.03	Monsanto	SRR1946381	HiSeq 2000	Y	Y
9820	IP-Are-0	CS76671	Spain	41	-4.71	Monsanto	SRR1946382	HiSeq 2000	Y	Y
9821	IP-Aru-0	CS76674	Spain	41.81	2.49	Monsanto	SRR1946383	HiSeq 2000	Y	Y
9822	IP-Aul-0	CS76675	Spain	40.52	-4.02	Monsanto	SRR1946384	HiSeq 2000	Y	Y
9823	IP-Bae-0	CS76681	Western Europe	43.34	-5.84	Monsanto	SRR1946385	HiSeq 2000	Y	Y
9824	IP-Bes-5	CS76702	Admixed	42.91	-4.91	Monsanto	SRR1946386	HiSeq 2000	Y	Y
9825	IP-Boa-0	CS76714	Spain	40.40	-3.88	Monsanto	SRR1946387	HiSeq 2000	Y	Y
9826	IP-Bor-0	CS76717	Western Europe	42.49	-6.71	Monsanto	SRR1946388	HiSeq 2000	Y	Y
9827	IP-Bos-0	CS76719	Western Europe	42.78	0.69	Monsanto	SRR1946389	HiSeq 2000	Y	Y
9828	IP-Bra-0	CS76721	Western Europe	42.50	-6.15	Monsanto	SRR1946390	HiSeq 2000	Y	Y
9830	IP-Bus-0	CS76736	Admixed	36.97	-3.28	Monsanto	SRR1946391	HiSeq 2000	Y	Y
9831	IP-Cas-0	CS76743	Admixed	38.54	-3.39	Monsanto	SRR1946392	HiSeq 2000	Y	Y
9832	IP-Cat-0	CS76759	Relict	40.54	-3.69	Monsanto	SRR1946393	HiSeq 2000	Y	Y

9833	IP-Cha-0	CS76764	Spain	40.38	-4.21	Monsanto	SRR1946394	HiSeq 2000	Y	Y
9834	IP-Cho-0	CS76768	Spain	40.51	-3.90	Monsanto	SRR1946395	HiSeq 2000	Y	Y
9835	IP-Cir-0	CS76772	Admixed	40.61	-6.57	Monsanto	SRR1946396	HiSeq 2000	Y	Y
9836	IP-Cod-0	CS76777	Spain	41.25	-1.32	Monsanto	SRR1946397	HiSeq 2000	Y	Y
9837	IP-Con-0	CS76780	Relict	37.94	-5.60	Monsanto	SRR1946398	HiSeq 2000	Y	Y
9838	IP-Cot-0	CS76784	Admixed	41.83	-5.38	Monsanto	SRR1946399	HiSeq 2000	Y	Y
9839	IP-Coy-0	CS76785	Admixed	40.44	-4.27	Monsanto	SRR1946400	HiSeq 2000	Y	Y
9840	IP-Dar-0	CS76792	Spain	41.13	-1.43	Monsanto	SRR1946401	HiSeq 2000	Y	Y
9841	IP-Ees-0	CS76836	Spain	40.59	-4.15	Monsanto	SRR1946402	HiSeq 2000	Y	Y
9843	IP-Elp-0	CS76840	Spain	40.53	-3.92	Monsanto	SRR1946403	HiSeq 2000	Y	Y
9844	IP-Esn-2	CS76846	Spain	42.27	0.19	Monsanto	SRR1946404	HiSeq 2000	Y	Y
9845	IP-Evs-0	CS76848	Spain	40.48	-3.96	Monsanto	SRR1946405	HiSeq 2000	Y	Y
9846	IP-Ezc-2	CS76849	Spain	42.31	-3.02	Monsanto	SRR1946406	HiSeq 2000	Y	Y
9847	IP-Fel-2	CS76854	Western Europe	43.31	-5.70	Monsanto	SRR1946407	HiSeq 2000	Y	Y
9848	IP-Glo-1	CS76879	Spain	40.11	-5.77	Monsanto	SRR1946408	HiSeq 2000	Y	Y
9849	IP-Gud-3	CS76895	Admixed	40.65	-4.11	Monsanto	SRR1946409	HiSeq 2000	Y	Y
9850	IP-Hec-0	CS76917	Spain	42.86	-0.70	Monsanto	SRR1946410	HiSeq 2000	Y	Y
9851	IP-Hue-3	CS76942	Western Europe	42.96	-6.10	Monsanto	SRR1946411	HiSeq 2000	Y	Y
9852	IP-Ini-0	CS76945	Spain	40.46	-3.75	Monsanto	SRR1946412	HiSeq 2000	Y	Y
9853	IP-Lac-0	CS76996	Western Europe	43.33	-5.91	Monsanto	SRR1946413	HiSeq 2000	Y	Y
9854	IP-Laf-1	CS76997	Western Europe	43.36	-5.88	Monsanto	SRR1946414	HiSeq 2000	Y	Y
9855	IP-Lam-0	CS77008	Spain	40.57	-3.89	Monsanto	SRR1946415	HiSeq 2000	Y	Y
9856	IP-Lch-0	CS77010	Spain	40.51	-4	Monsanto	SRR1946416	HiSeq 2000	Y	Y
9857	IP-Leg-0	CS77019	Spain	40.33	-3.80	Monsanto	SRR1946417	HiSeq 2000	Y	Y
9858	IP-Loz-0	CS77051	Admixed	40.98	-3.80	Monsanto	SRR1946418	HiSeq 2000	Y	Y
9859	IP-Lro-0	CS77054	Spain	40.50	-3.88	Monsanto	SRR1946419	HiSeq 2000	Y	Y
9860	IP-Lum-0	CS77059	Spain	42.24	-2.62	Monsanto	SRR1946420	HiSeq 2000	Y	Y
9861	IP-Mac-0	CS77061	Spain	40.72	-3.21	Monsanto	SRR1946421	HiSeq 2000	Y	Y
9862	IP-Mad-0	CS77062	Western Europe	40.45	-3.67	Monsanto	SRR1946422	HiSeq 2000	Y	Y

9864	IP-Mat-0	CS77074	Spain	41.76	2.69	Monsanto	SRR1946423	HiSeq 2000	Y	Y
9866	IP-Mdd-0	CS77076	Spain	41.89	-2.79	Monsanto	SRR1946424	HiSeq 2000	Y	Y
9867	IP-Mie-1	CS77083	Spain	40.94	-3.22	Monsanto	SRR1946425	HiSeq 2000	Y	Y
9868	IP-Moe-0	CS77104	Spain	41.78	2.37	Monsanto	SRR1946426	HiSeq 2000	Y	Y
9869	IP-Moj-0	CS77105	Relict	36.76	-5.28	Monsanto	SRR1946427	HiSeq 2000	Y	Y
9870	IP-Moz-0	CS77111	Spain	41.91	0.17	Monsanto	SRR1946428	HiSeq 2000	Y	Y
9871	IP-Nac-0	CS77117	Relict	40.75	-3.99	Monsanto	SRR1946429	HiSeq 2000	Y	Y
9873	IP-Ndc-0	CS77125	Spain	37.94	-5.45	Monsanto	SRR1946430	HiSeq 2000	Y	Y
9874	IP-Oja-0	CS77143	Spain	42.34	-3	Monsanto	SRR1946431	HiSeq 2000	Y	Y
9875	IP-Ovi-1	CS77155	Western Europe	43.38	-5.87	Monsanto	SRR1946432	HiSeq 2000	Y	Y
9876	IP-Pad-0	CS77158	Spain	41.34	0.99	Monsanto	SRR1946433	HiSeq 2000	Y	Y
9877	IP-Pdl-0	CS77165	Admixed	43.02	-5.60	Monsanto	SRR1946434	HiSeq 2000	Y	Y
9878	IP-Pee-0	CS77167	Spain	40.78	-3.62	Monsanto	SRR1946435	HiSeq 2000	Y	Y
9879	IP-Per-0	CS77169	Relict	37.60	-1.12	Monsanto	SRR1946436	HiSeq 2000	Y	Y
9880	IP-Pib-1	CS77175	Spain	42.72	-3.44	Monsanto	SRR1946437	HiSeq 2000	Y	Y
9881	IP-Pie-0	CS77176	Admixed	40.46	-5.32	Monsanto	SRR1946438	HiSeq 2000	Y	Y
9882	IP-Pil-0	CS77178	Spain	40.46	-4.26	Monsanto	SRR1946439	HiSeq 2000	Y	Y
9883	IP-Piq-0	CS77179	Spain	42.10	-2.56	Monsanto	SRR1946440	HiSeq 2000	Y	Y
9885	IP-Prd-0	CS77189	Spain	41.14	-3.68	Monsanto	SRR1946441	HiSeq 2000	Y	Y
9886	IP-Pru-0	CS77190	Spain	42.38	1.73	Monsanto	SRR1946442	HiSeq 2000	Y	Y
9887	IP-Pun-0	CS77196	Relict	40.40	-4.77	Monsanto	SRR1946443	HiSeq 2000	Y	Y
9888	IP-Pva-1	CS77197	Spain	40.93	-3.31	Monsanto	SRR1946444	HiSeq 2000	Y	Y
9890	IP-Rib-1	CS77217	Admixed	43.16	-5.07	Monsanto	SRR1946445	HiSeq 2000	Y	Y
9891	IP-Sal-0	CS77230	Spain	41.93	2.92	Monsanto	SRR1946446	HiSeq 2000	Y	Y
9892	IP-Sam-0	CS77231	Admixed	42.68	-6.96	Monsanto	SRR1946447	HiSeq 2000	Y	Y
9894	IP-Sen-0	CS77243	Admixed	42.59	0.76	Monsanto	SRR1946448	HiSeq 2000	Y	Y
9895	IP-Sfb-6	CS77248	Spain	41.78	2.57	Monsanto	SRR1946449	HiSeq 2000	Y	Y
9897	IP-Smt-1	CS77257	Admixed	40.95	-5.63	Monsanto	SRR1946450	HiSeq 2000	Y	Y
9898	IP-Som-0	CS77259	Spain	41.14	-3.58	Monsanto	SRR1946451	HiSeq 2000	Y	Y
9899	IP-Tau-0	CS77342	Spain	42.54	0.84	Monsanto	SRR1946452	HiSeq 2000	Y	Y
9900	IP-Tri-0	CS77386	Spain	37.38	-6.01	Monsanto	SRR1946453	HiSeq 2000	Y	Y
9901	IP-Urd-1	CS78824	Spain	42.27	-2.98	Monsanto	SRR1946454	HiSeq 2000	Y	Y
9902	IP-Usa-0	CS78825	Spain	40.71	-3.24	Monsanto	SRR1946455	HiSeq 2000	Y	Y

9903	IP-Val-0	CS78829	Spain	42.31	-3.10	Monsanto	SRR1946456	HiSeq 2000	Y	Y
9904	IP-Vas-0	CS78833	Spain	40.95	-3.31	Monsanto	SRR1946457	HiSeq 2000	Y	Y
9905	IP-Ven-0	CS78840	Relict	40.76	-4.01	Monsanto	SRR1946458	HiSeq 2000	Y	Y
9906	IP-Mah-6	CS77063	Admixed	40	4.25	Monsanto	SRR1946459	HiSeq 2000	Y	Y
9908	ESP-1-11	CS76847	Western Europe	50.72	3.47	Monsanto	SRR1946460	HiSeq 2000	N	N
9909	GEN-8	CS76877	Western Europe	50.59	3.30	Monsanto	SRR1946461	HiSeq 2000	N	N
9910	BRI-2	CS76725	Western Europe	50.68	3.52	Monsanto	SRR1946462	HiSeq 2000	N	N
9911	ARGE-1-15	CS76672	Western Europe	47.16	4.28	Monsanto	SRR1946463	HiSeq 2000	Y	Y
9912	CIRY-13	CS76773	Western Europe	46.67	4.55	Monsanto	SRR1946464	HiSeq 2000	N	N
9914	IST-29	CS76948	Central Europe	47.58	5.33	Monsanto	SRR1946465	HiSeq 2000	N	N
9915	Mar-4-16	CS77069	Central Europe	47.45	3.94	Monsanto	SRR1946466	HiSeq 2000	Y	Y
9917	RAD-21	CS77200	Western Europe	46.69	4.34	Monsanto	SRR1946467	HiSeq 2000	Y	Y
9918	SAUL-24	CS77237	Western Europe	47.43	5.21	Monsanto	SRR1946468	HiSeq 2000	Y	Y
9920	DIR-9	CS76796	Germany	48.54	4.32	Monsanto	SRR1946469	HiSeq 2000	N	N
9921	FOR-23	CS76867	Western Europe	48.57	4.41	Monsanto	SRR1946470	HiSeq 2000	Y	Y
9924	PLY-20	CS77181	Admixed	48.59	4.24	Monsanto	SRR1946471	HiSeq 2000	Y	Y
9925	RUM-20	CS77226	Western Europe	48.91	4.52	Monsanto	SRR1946472	HiSeq 2000	N	N
9926	TRE-1	CS77385	Western Europe	48.86	4.10	Monsanto	SRR1946473	HiSeq 2000	N	N
9927	ARR-17	CS76673	Western Europe	44.05	3.69	Monsanto	SRR1946474	HiSeq 2000	N	N
9928	BEZ-9	CS76703	Western Europe	44.12	3.77	Monsanto	SRR1946475	HiSeq 2000	N	N

9929	ISS-20	CS76947	Western Europe	43.92	3.71	Monsanto	SRR1946476	HiSeq 2000	N	N
9930	LEC-25	CS77018	Central Europe	43.91	4.14	Monsanto	SRR1946477	HiSeq 2000	N	N
9932	NOZ-6	CS77134	Admixed	44.12	4.33	Monsanto	SRR1946478	HiSeq 2000	Y	Y
9933	VED-10	CS78839	Admixed	43.74	3.89	Monsanto	SRR1946479	HiSeq 2000	Y	Y
9935	BAU-15	CS76694	Western Europe	50.60	2.93	Monsanto	SRR1946480	HiSeq 2000	Y	Y
9937	CATS-6	CS76760	Western Europe	50.79	2.69	Monsanto	SRR1946481	HiSeq 2000	Y	Y
9938	WAV-8	CS78854	Western Europe	50.65	2.99	Monsanto	SRR1946482	HiSeq 2000	N	N
9939	Aitba-2	CS76347	Relict	31.48	-7.45	MPI	SRR1946483	Genome Analyzer II	N	N
9941	Fei-0	CS76412	Western Europe	40.92	-8.54	MPI	SRR1946484	Genome Analyzer II	N	N
9942	Agu-1	CS76409	Spain	41.32	-1.34	MPI	SRR1946485	Genome Analyzer II	N	N
9943	Cdm-0	CS76410	Spain	39.73	-5.74	MPI	SRR1946486	Genome Analyzer II	N	N
9944	Don-0	CS76411	Relict	36.83	-6.36	MPI	SRR1946487	Genome Analyzer II	N	N
9945	Leo-1	CS76413	Admixed	41.80	-3.11	MPI	SRR1946488	Genome Analyzer II	N	N
9946	Mer-6	CS76414	Spain	38.92	-6.34	MPI	SRR1946489	Genome Analyzer II	N	N
9947	Ped-0	CS76415	Relict	40.74	-3.90	MPI	SRR1946490	Genome Analyzer II	N	N
9948	Pra-6	CS76416	Spain	41.05	-3.54	MPI	SRR1946491	Genome Analyzer II	N	N
9949	Qui-0	CS76417	Western Europe	42.69	-6.93	MPI	SRR1946492	Genome Analyzer II	Y	Y
9950	Vie-0	CS76418	Spain	42.63	0.76	MPI	SRR1946493	Genome Analyzer II	N	N

9951	Kly-1	CS76385	Asia	51.33	82.57	MPI	SRR1946494	Genome Analyzer II	N	N
9952	Kly-4	CS76384	Asia	51.32	82.55	MPI	SRR1946495	Genome Analyzer II	N	N
9953	Koz-2	CS76383	Asia	51.33	82.19	MPI	SRR1946496	Genome Analyzer II	N	N
9955	Stepn-2	CS76377	Asia	54.09	60.46	MPI	SRR1946497	Genome Analyzer II	N	N
9956	Stepn-1	CS76378	Asia	54.06	60.48	MPI	SRR1946498	Genome Analyzer II	N	N
9957	Borsk-2	CS76421	Asia	53.04	51.75	MPI	SRR1946499	Genome Analyzer II	N	N
9958	Shigu-1	CS76375	Asia	53.33	49.48	MPI	SRR1946500	Genome Analyzer II	N	N
9959	Shigu-2	CS76374	Asia	53.33	49.48	MPI	SRR1946501	Genome Analyzer II	N	N
9960	Kidr-1	CS76376	Asia	51.31	57.56	MPI	SRR1946502	Genome Analyzer II	N	N
9962	Galdo-1	CS76423	Italy Balkan Caucasus	40.57	15.32	MPI	SRR1946503	Genome Analyzer II	N	N
9963	Lago-1	CS76367	Italy Balkan Caucasus	39.18	16.26	MPI	SRR1946504	Genome Analyzer II	N	N
9964	Mammo-1	CS76365	Italy Balkan Caucasus	38.36	16.23	MPI	SRR1946505	Genome Analyzer II	N	N
9965	Mammo-2	CS76364	Italy Balkan Caucasus	38.38	16.22	MPI	SRR1946506	Genome Analyzer II	N	N
9966	Monte-1	CS76361	Italy Balkan Caucasus	40.28	15.65	MPI	SRR1946507	Genome Analyzer II	N	N

9968	Timpo-1	CS76424	Italy Balkan Caucasus	39.27	16.27	MPI	SRR1946508	Genome Analyzer II	N	N
9969	Valsi-1	CS76425	Italy Balkan Caucasus	40.18	16.45	MPI	SRR1946509	Genome Analyzer II	N	N
9970	Altenb-2	CS76353	Central Europe	46.37	11.24	MPI	SRR1946510	Genome Analyzer II	N	N
9971	Bozen-1.1	CS76357	Central Europe	46.51	11.33	MPI	SRR1946511	Genome Analyzer II	N	N
9972	Bozen-1.2	CS76358	Central Europe	46.51	11.33	MPI	SRR1946512	Genome Analyzer II	N	N
9973	Mitterberg-1-181	CS76354	Central Europe	46.37	11.28	MPI	SRR1946513	Genome Analyzer II	N	N
9974	Castelfed-4-212	CS76355	Central Europe	46.34	11.29	MPI	SRR1946514	Genome Analyzer II	N	N
9975	Castelfed-4-213	CS76356	Central Europe	46.34	11.29	MPI	SRR1946515	Genome Analyzer II	N	N
9976	Rovero-1	CS76351	Central Europe	46.25	11.17	MPI	SRR1946516	Genome Analyzer II	N	N
9978	Vezzano-2.2	CS76350	Central Europe	46.63	10.82	MPI	SRR1946517	Genome Analyzer II	N	N
9979	Voeran-1	CS76352	Central Europe	46.36	11.23	MPI	SRR1946518	Genome Analyzer II	N	N
9980	Angel-1	CS76362	Italy Balkan Caucasus	38.62	16.17	MPI	SRR1946519	Genome Analyzer II	N	N
9981	Angit-1	CS76366	Italy Balkan Caucasus	38.76	16.24	MPI	SRR1946520	Genome Analyzer II	N	N
9982	Apost-1	CS76368	Italy Balkan Caucasus	39.01	16.47	MPI	SRR1946521	Genome Analyzer II	N	N
9983	Ciste-1	CS76359	Admixed	41.62	12.87	MPI	SRR1946522	Genome Analyzer II	N	N

9984	Ciste-2	CS76360	Admixed	41.62	12.87	MPI	SRR1946523	Genome Analyzer II	N	N
9985	Slavi-1	CS76419	Italy Balkan Caucasus	41.43	23.65	MPI	SRR1946524	Genome Analyzer II	N	N
9986	Jablo-1	CS76372	Italy Balkan Caucasus	41.59	25.20	MPI	SRR1946525	Genome Analyzer II	N	N
9987	Lecho-1	CS76371	Italy Balkan Caucasus	41.43	23.50	MPI	SRR1946526	Genome Analyzer II	N	N
9988	Bak-2	CS76392	Italy Balkan Caucasus	41.79	43.48	MPI	SRR1946527	Genome Analyzer II	N	N
9990	Lag2-2	CS76390	Italy Balkan Caucasus	41.83	46.28	MPI	SRR1946528	Genome Analyzer II	N	N
9991	Vash-1	CS76391	Italy Balkan Caucasus	41.24	46.37	MPI	SRR1946529	Genome Analyzer II	N	N
9993	Nemrut-1	CS76398	Admixed	38.64	42.24	MPI	SRR1946530	Genome Analyzer II	N	N
9995	HKT2.4	CS76404	Central Europe	48.14	9.40	MPI	SRR1946531	Genome Analyzer II	N	N
9996	Nie1-2	CS76402	Central Europe	48.52	8.80	MPI	SRR1946532	Genome Analyzer II	N	N
9997	Rue3-1-31	CS76406	Central Europe	48.56	9.16	MPI	SRR1946533	Genome Analyzer II	N	N
9998	Star-8	CS76400	Admixed	48.43	8.82	MPI	SRR1946534	Genome Analyzer II	N	N
9999	TueSB30-3	CS76403	Central Europe	48.53	9.06	MPI	SRR1946535	Genome Analyzer II	N	N
10001	TueV-13	CS76407	Western Europe	48.52	9.05	MPI	SRR1946536	Genome Analyzer II	N	N

10002	TueWa1-2	CS76405	Western Europe	48.53	9.04	MPI	SRR1946537	Genome Analyzer II	N	N
10004	Bolin-1	CS76373	Italy Balkan Caucasus	44.46	25.74	MPI	SRR1946538	Genome Analyzer II	N	N
10005	Copac-1	CS76420	Central Europe	46.11	21.95	MPI	SRR1946539	Genome Analyzer II	N	N
10006	Kastel-1	CS76395	Italy Balkan Caucasus	44.64	34.38	MPI	SRR1946540	Genome Analyzer II	N	N
10008	Sij-1	CS76379	Asia	41.45	70.05	MPI	SRR1946541	Genome Analyzer II	N	N
10009	Sij-2	CS76380	Asia	41.45	70.05	MPI	SRR1946542	Genome Analyzer II	N	N
10010	Sij-4	CS76381	Asia	41.45	70.05	MPI	SRR1946543	Genome Analyzer II	N	N
10011	Yeg-1	CS76394	Asia	39.87	45.36	MPI	SRR1946544	Genome Analyzer II	N	N
10012	Istisu-1	CS76389	Italy Balkan Caucasus	38.98	48.56	MPI	SRR1946545	Genome Analyzer II	N	N
10013	Lerik1-3	CS76388	Italy Balkan Caucasus	38.74	48.61	MPI	SRR1946546	Genome Analyzer II	N	N
10014	Xan-1	CS76387	Italy Balkan Caucasus	38.65	48.80	MPI	SRR1946547	Genome Analyzer II	N	N
10015	Ara-1	CS76382	Asia	37.29	71.30	MPI	SRR1946548	Genome Analyzer II	N	N
10017	Petro-1	CS76370	Central Europe	44.34	21.46	MPI	SRR1946549	Genome Analyzer II	N	N
10018	Dobra-1	CS76369	Central Europe	44.84	20.16	MPI	SRR1946550	Genome Analyzer II	N	N
10020	Jl-2	CS76956	Central Europe	49.17	16.50	MPI	SRR1946551	Genome Analyzer II	Y	Y

10022	Uk-3	CS78777	Admixed	48.03	7.77	MPI	SRR1946552	Genome Analyzer II	Y	Y
10023	Strand-1	CS77284	Admixed	68.80	15.45	MPI	SRR1946553	unspecified	Y	Y
10027	Uk-6	CS78938	Central Europe	48.03	7.77	MPI	SRR1946554	unspecified	Y	Y
14312	Kos-1	CS78923	Asia	62.02	34.12	GMI	SRR1946555	HiSeq 2000	Y	Y
14313	Kos-2	CS78924	Asia	62.02	34.12	GMI	SRR1946556	HiSeq 2000	Y	Y
14314	Radk-1	CS78927	Asia	61.59	35.11	GMI	SRR1946557	HiSeq 2000	Y	Y
14315	Radk-2	CS78928	Asia	61.59	35.11	GMI	SRR1946558	HiSeq 2000	Y	Y
14318	Shu-1	CS78930	Asia	61.94	34.24	GMI	SRR1946559	HiSeq 2000	Y	Y
14319	Shu-2	CS78931	Asia	61.94	34.24	GMI	SRR1946560	HiSeq 2000	Y	Y
15560	Valm	CS78932	Asia	61.37	61.37	GMI	SRR1946561	HiSeq 2000	Y	Y
15591	OOE1-1	CS78939	Central Europe	48.33	14.73	GMI	SRR1946562	HiSeq 2000	Y	Y
15592	OOE3-1	CS78940	Central Europe	48.33	14.72	GMI	SRR1946563	HiSeq 2000	Y	Y
15593	OOE3-2	CS78941	Central Europe	48.33	14.72	GMI	SRR1946564	HiSeq 2000	Y	Y
18694	Pien	CS78926	Asia	60.40	32.09	GMI	SRR1946565	HiSeq 2000	Y	Y
18696	Samm	CS78929	Asia	61.57	30.63	GMI	SRR1946566	HiSeq 2000	Y	Y
19949	OOE2-1	CS79036	Central Europe	48.33	14.72	GMI	SRR1946567	HiSeq 2000	N	N
19950	OOE2-2	CS79037	Central Europe	48.33	14.72	GMI	SRR1946568	HiSeq 2000	N	N
19951	OOE23	CS79038	Central Europe	48.33	14.72	GMI	SRR1946569	HiSeq 2000	N	N
22006	Agl-0	NA	Africa	32.97	-5.45	Durvasula*	ERR2026784	HiSeq 2500	Y	N
35619	Agl-1	NA	Africa	32.97	-5.45	Durvasula*	ERR2026779	HiSeq 2500	Y	N
35623	Agl-2	NA	Africa	32.97	-5.45	Durvasula*	ERR2026780	HiSeq 2500	Y	N
35615	Agl-3	NA	Africa	32.97	-5.45	Durvasula*	ERR2026781	HiSeq 2500	Y	N
35607	Agl-5	NA	Africa	32.97	-5.45	Durvasula*	ERR2026782	HiSeq 2500	Y	N
35605	Agl-9	NA	Africa	32.97	-5.45	Durvasula*	ERR2026783	HiSeq 2500	Y	N
22010	Ait-14	NA	Africa	31.24	-7.81	Durvasula*	ERR2026741	HiSeq 2500	Y	N
22003	Ait-9	NA	Africa	31.24	-7.81	Durvasula*	ERR2026742	HiSeq 2500	Y	N

21135	Aitba	NA	Africa	31.48	-7.45	Durvasula*	ERR2026739	HiSeq 2500	N	N
18513	Arb-0	NA	Africa	31.42	-7.53	Durvasula*	ERR2026744	HiSeq 2500	Y	N
35604	Arb-2	NA	Africa	31.42	-7.53	Durvasula*	ERR2026743	HiSeq 2500	Y	N
18514	Azr-0	NA	Africa	33.42	-5.18	Durvasula*	ERR2026791	HiSeq 2500	Y	N
35599	Azr-11	NA	Africa	33.42	-5.18	Durvasula*	ERR2026785	HiSeq 2500	Y	N
35622	Azr-13	NA	Africa	33.42	-5.18	Durvasula*	ERR2026786	HiSeq 2500	Y	N
37457	Azr-16	NA	Africa	33.42	-5.18	Durvasula*	ERR2026788	HiSeq 2500	Y	N
35625	Azr-16	NA	Africa	33.42	-5.18	Durvasula*	ERR2026787	HiSeq 2500	Y	N
35611	Azr-5	NA	Africa	33.42	-5.18	Durvasula*	ERR2026789	HiSeq 2500	Y	N
35594	Azr-7	NA	Africa	33.42	-5.18	Durvasula*	ERR2026790	HiSeq 2500	Y	N
22008	Bab-0	NA	Africa	35.04	-5.02	Durvasula*	ERR2026772	HiSeq 2500	Y	N
35617	Bab-3	NA	Africa	35.04	-5.02	Durvasula*	ERR2026771	HiSeq 2500	Y	N
22001	Bba-0	NA	Africa	35.04	-5.02	Durvasula*	ERR2026759	HiSeq 2500	Y	N
35521	Bba-1	NA	Africa	34.02	-4.08	Durvasula*	ERR2026757	HiSeq 2500	Y	N
35522	Bba-2	NA	Africa	34.02	-4.08	Durvasula*	ERR2026758	HiSeq 2500	Y	N
22007	Bbe-0	NA	Africa	35	-4.83	Durvasula*	ERR2026773	HiSeq 2500	Y	N
35523	Elh-10	NA	Africa	31.47	-7.41	Durvasula*	ERR2026745	HiSeq 2500	Y	N
35598	Elh-15	NA	Africa	31.47	-7.41	Durvasula*	ERR2026746	HiSeq 2500	Y	N
35616	Elh-2	NA	Africa	31.47	-7.41	Durvasula*	ERR2026748	HiSeq 2500	Y	N
18511	Elh-20	NA	Africa	31.47	-7.41	Durvasula*	ERR2026753	HiSeq 2500	Y	N
35606	Elh-23	NA	Africa	31.47	-7.41	Durvasula*	ERR2026747	HiSeq 2500	Y	N
18516	Elh-27	NA	Africa	31.47	-7.41	Durvasula*	ERR2026754	HiSeq 2500	Y	N
35596	Elh-33	NA	Africa	31.47	-7.41	Durvasula*	ERR2026749	HiSeq 2500	Y	N
35601	Elh-39	NA	Africa	31.47	-7.41	Durvasula*	ERR2026750	HiSeq 2500	Y	N
35595	Elh-46	NA	Africa	31.47	-7.41	Durvasula*	ERR2026751	HiSeq 2500	Y	N
35613	Elh-52	NA	Africa	31.47	-7.41	Durvasula*	ERR2026752	HiSeq 2500	Y	N
18512	Elk-1	NA	Africa	32.54	-6.01	Durvasula*	ERR2026796	HiSeq 2500	Y	N
37469	Elk-20	NA	Africa	32.54	-6.01	Durvasula*	ERR2026792	HiSeq 2500	Y	N
35621	Elk-28	NA	Africa	32.54	-6.01	Durvasula*	ERR2026793	HiSeq 2500	Y	N
37470	Elk-3	NA	Africa	32.54	-6.01	Durvasula*	ERR2026794	HiSeq 2500	Y	N
37468	Elk-5	NA	Africa	32.54	-6.01	Durvasula*	ERR2026795	HiSeq 2500	Y	N
22002	Ifr-0	NA	Africa	33.55	-5.17	Durvasula*	ERR2026797	HiSeq 2500	Y	N
35600	Ifr-3	NA	Africa	33.55	-5.17	Durvasula*	ERR2026804	HiSeq 2500	Y	N

35610	Ifr-4	NA	Africa	33.55	-5.17	Durvasula*	ERR2026798	HiSeq 2500	Y	N
35618	Ifr-6	NA	Africa	33.55	-5.17	Durvasula*	ERR2026799	HiSeq 2500	Y	N
21137	Ita-0	NA	Africa	34.08	-4.20	Durvasula*	ERR2026740	HiSeq 2500	Y	N
35512	Ket-10.1	NA	Africa	34.96	-4.67	Durvasula*	ERR2026774	HiSeq 2500	Y	N
21999	Ket-10.2	NA	Africa	34.96	-4.67	Durvasula*	ERR2026776	HiSeq 2500	Y	N
37471	Ket-12	NA	Africa	34.96	-4.67	Durvasula*	ERR2026775	HiSeq 2500	Y	N
22004	Khe-0	NA	Africa	32.93	-5.51	Durvasula*	ERR2026801	HiSeq 2500	Y	N
35608	Khe-32	NA	Africa	32.93	-5.51	Durvasula*	ERR2026800	HiSeq 2500	Y	N
22000	Meh-0	NA	Africa	33.96	-4.05	Durvasula*	ERR2026762	HiSeq 2500	Y	N
37472	Meh-4	NA	Africa	33.96	-4.05	Durvasula*	ERR2026760	HiSeq 2500	Y	N
35603	Meh-7	NA	Africa	33.96	-4.05	Durvasula*	ERR2026761	HiSeq 2500	Y	N
35513	Oua-0	NA	Africa	32.08	-6.28	Durvasula*	ERR2026802	HiSeq 2500	Y	N
22009	Set-0	NA	Africa	31.23	-7.67	Durvasula*	ERR2026756	HiSeq 2500	Y	N
35602	Set-6	NA	Africa	31.23	-7.67	Durvasula*	ERR2026755	HiSeq 2500	Y	N
18509	Tah-0	NA	Africa	34.05	-4.22	Durvasula*	ERR2026764	HiSeq 2500	Y	N
35612	Tah-4	NA	Africa	34.05	-4.22	Durvasula*	ERR2026763	HiSeq 2500	Y	N
22005	Taz-0	NA	Africa	34.09	-4.10	Durvasula*	ERR2026768	HiSeq 2500	Y	N
35620	Taz-11	NA	Africa	34.09	-4.10	Durvasula*	ERR2026765	HiSeq 2500	Y	N
35609	Taz-16	NA	Africa	34.09	-4.10	Durvasula*	ERR2026766	HiSeq 2500	Y	N
35593	Taz-18	NA	Africa	34.09	-4.10	Durvasula*	ERR2026767	HiSeq 2500	Y	N
18510	Til-2	NA	Africa	32.04	-6.23	Durvasula*	ERR2026803	HiSeq 2500	Y	N
22011	Tiz-0	NA	Africa	33.87	-4.03	Durvasula*	ERR2026770	HiSeq 2500	Y	N
35624	Tiz-7	NA	Africa	33.87	-4.03	Durvasula*	ERR2026769	HiSeq 2500	Y	N
35614	Zin-4	NA	Africa	35.45	-5.43	Durvasula*	ERR2026777	HiSeq 2500	Y	N
18515	Zin-9	NA	Africa	35.45	-5.43	Durvasula*	ERR2026778	HiSeq 2500	Y	N
1-32	1-32	NA	China	30.68	118.97	Zou*	SRR2189709	HiSeq 2000	Y	N
1-8	1-8	NA	China	30.68	118.97	Zou*	SRR2183387	HiSeq 2000	Y	N
10-1	10-1	NA	China	31.55	118.49	Zou*	SRR2189719	HiSeq 2000	Y	N
10-3	10-3	NA	China	31.55	118.49	Zou*	SRR2189720	HiSeq 2000	Y	N
10-5	10-5	NA	China	31.55	118.49	Zou*	SRR2204160	HiSeq 2000	Y	N
11-4	11-4	NA	China	26.75	114.30	Zou*	SRR2204161	HiSeq 2000	Y	N
12-8	12-8	NA	China	29.59	115.91	Zou*	SRR2204162	HiSeq 2000	Y	N
13-13	13-13	NA	China	26.99	116.24	Zou*	SRR2204163	HiSeq 2000	Y	N

13-5	13-5	NA	China	26.59	116.15	Zou*	SRR6414604	HiSeq X Ten	Y	N
14-10	14-10	NA	China	28.74	115.74	Zou*	SRR2204164	HiSeq 2000	Y	N
14-62	14-62	NA	China	28.74	115.74	Zou*	SRR2204165	HiSeq 2000	Y	N
15-11	15-11	NA	China	29.80	118.85	Zou*	SRR2204166	HiSeq 2000	Y	N
17-2	17-2	NA	China	29.32	119.30	Zou*	SRR6414611	HiSeq X Ten	Y	N
17-5	17-5	NA	China	29.54	119.49	Zou*	SRR2204167	HiSeq 2000	Y	N
18-4	18-4	NA	China	29.11	118.38	Zou*	SRR2204168	HiSeq 2000	Y	N
18-7	18-7	NA	China	29.11	118.38	Zou*	SRR2204169	HiSeq 2000	Y	N
19-33	19-33	NA	China	30.05	119.91	Zou*	SRR2204170	HiSeq 2000	Y	N
2-5	2-5	NA	China	30.75	117.62	Zou*	SRR2189710	HiSeq 2000	Y	N
20-2	20-2	NA	China	29.69	119.67	Zou*	SRR2204171	HiSeq 2000	Y	N
20-36	20-36	NA	China	29.69	119.67	Zou*	SRR2204172	HiSeq 2000	Y	N
23-19	23-19	NA	China	32.03	118.50	Zou*	SRR6414610	HiSeq X Ten	Y	N
23-34	23-34	NA	China	32.05	118.83	Zou*	SRR2204173	HiSeq 2000	Y	N
24-10	24-10	NA	China	30.52	114.47	Zou*	SRR2204174	HiSeq 2000	Y	N
25-16	25-16	NA	China	29.79	106.48	Zou*	SRR2204175	HiSeq 2000	Y	N
26-5	26-5	NA	China	29.82	106.06	Zou*	SRR2204176	HiSeq 2000	Y	N
27-8	27-8	NA	China	32.72	105.12	Zou*	SRR2204177	HiSeq 2000	Y	N
27-9	27-9	NA	China	32.72	105.12	Zou*	SRR2204178	HiSeq 2000	N	N
28-6	28-6	NA	China	33.15	106.75	Zou*	SRR2204179	HiSeq 2000	Y	N
29-8	29-8	NA	China	32.93	107.21	Zou*	SRR2204626	HiSeq 2000	Y	N
3-2	3-2	NA	China	30.62	117.76	Zou*	SRR2189712	HiSeq 2000	Y	N
3-4	3-4	NA	China	30.62	117.76	Zou*	SRR2189711	HiSeq 2000	Y	N
30-1	30-1	NA	China	31.17	114.62	Zou*	SRR6414609	HiSeq X Ten	Y	N
30-6	30-6	NA	China	31.28	115.02	Zou*	SRR2204180	HiSeq 2000	Y	N
31-26	31-26	NA	China	30.78	112.11	Zou*	SRR2204189	HiSeq 2000	Y	N
32-28	32-28	NA	China	30.46	114.09	Zou*	SRR2204238	HiSeq 2000	Y	N
33-4	33-4	NA	China	29.41	110.44	Zou*	SRR2204239	HiSeq 2000	Y	N
33-46	33-46	NA	China	29.41	110.44	Zou*	SRR2204264	HiSeq 2000	Y	N
34-16	34-16	NA	China	28.52	110.72	Zou*	SRR2204313	HiSeq 2000	Y	N

35-1	35-1	NA	China	27.94	108.61	Zou*	SRR2204314	HiSeq 2000	Y	N
35-10	35-10	NA	China	27.94	108.61	Zou*	SRR2204315	HiSeq 2000	Y	N
36-17	36-17	NA	China	28.02	98.63	Zou*	SRR2204316	HiSeq 2000	Y	N
36-31	36-31	NA	China	28.02	98.63	Zou*	SRR2204703	HiSeq 2000	Y	N
37-10	37-10	NA	China	32.05	113.98	Zou*	SRR2204317	HiSeq 2000	Y	N
38-2	38-2	NA	China	31.10	110.95	Zou*	SRR2204318	HiSeq 2000	Y	N
38-4	38-4	NA	China	31.10	110.95	Zou*	SRR2204319	HiSeq 2000	Y	N
39-16	39-16	NA	China	46.75	90.27	Zou*	SRR2204320	HiSeq 2000	Y	N
4-15	4-15	NA	China	29.51	118.23	Zou*	SRR6414607	HiSeq X Ten	Y	N
40-2	40-2	NA	China	47.22	89.84	Zou*	SRR2204321	HiSeq 2000	Y	N
41-10	41-10	NA	China	47.59	88.77	Zou*	SRR2204322	HiSeq 2000	Y	N
41-11	41-11	NA	China	47.59	88.77	Zou*	SRR2204323	HiSeq 2000	Y	N
42-3	42-3	NA	China	46.83	84.18	Zou*	SRR2204324	HiSeq 2000	Y	N
42-8	42-8	NA	China	46.83	84.18	Zou*	SRR2204325	HiSeq 2000	Y	N
43-12	43-12	NA	China	46.74	90.34	Zou*	SRR2204704	HiSeq 2000	Y	N
43-7	43-7	NA	China	46.74	90.34	Zou*	SRR2204326	HiSeq 2000	Y	N
45-20	45-20	NA	China	46.75	90.34	Zou*	SRR2204327	HiSeq 2000	Y	N
45-23	45-23	NA	China	46.75	90.34	Zou*	SRR2204328	HiSeq 2000	Y	N
46-28	46-28	NA	China	46.74	90.34	Zou*	SRR2204329	HiSeq 2000	Y	N
46-31	46-31	NA	China	46.74	90.34	Zou*	SRR2204330	HiSeq 2000	Y	N
48-1	48-1	NA	China	47.21	89.81	Zou*	SRR2204331	HiSeq 2000	Y	N
5-15	5-15	NA	China	30.28	117.18	Zou*	SRR6414606	HiSeq X Ten	Y	N
50-3	50-3	NA	China	47.36	89.65	Zou*	SRR2204332	HiSeq 2000	Y	N
50-5	50-5	NA	China	47.36	89.65	Zou*	SRR2204333	HiSeq 2000	Y	N
51-1	51-1	NA	China	47.77	88.38	Zou*	SRR2204334	HiSeq 2000	Y	N
51-4	51-4	NA	China	47.77	88.38	Zou*	SRR2204335	HiSeq 2000	Y	N
51-8	51-8	NA	China	47.77	88.38	Zou*	SRR2204336	HiSeq 2000	Y	N
52-10	52-10	NA	China	47.77	88.38	Zou*	SRR6414608	HiSeq X Ten	Y	N
52-13	52-13	NA	China	47.77	88.38	Zou*	SRR2204337	HiSeq 2000	Y	N
52-22	52-22	NA	China	47.77	88.38	Zou*	SRR2204345	HiSeq 2000	Y	N
53-18	53-18	NA	China	47.77	88.38	Zou*	SRR2204338	HiSeq 2000	Y	N

53-19	53-19	NA	China	47.77	88.38	Zou*	SRR2204339	HiSeq 2000	Y	N
54-5	54-5	NA	China	47.73	88.22	Zou*	SRR2204341	HiSeq 2000	Y	N
54-6	54-6	NA	China	47.73	88.22	Zou*	SRR2204340	HiSeq 2000	Y	N
55-12	55-12	NA	China	47.73	88.22	Zou*	SRR2204342	HiSeq 2000	Y	N
55-13	55-13	NA	China	47.73	88.22	Zou*	SRR2204343	HiSeq 2000	Y	N
57-1	57-1	NA	China	28.23	116.59	Zou*	SRR2204346	HiSeq 2000	Y	N
58-7	58-7	NA	China	28.28	116.61	Zou*	SRR2204347	HiSeq 2000	Y	N
59-12	59-12	NA	China	28.75	115.82	Zou*	SRR2204348	HiSeq 2000	Y	N
6-28	6-28	NA	China	31.39	118.38	Zou*	SRR2189713	HiSeq 2000	Y	N
6-9	6-9	NA	China	31.23	118.23	Zou*	SRR6414605	HiSeq X Ten	Y	N
60-1	60-1	NA	China	28.78	115.84	Zou*	SRR2204349	HiSeq 2000	Y	N
61-1	61-1	NA	China	29.86	116.52	Zou*	SRR2204578	HiSeq 2000	Y	N
62-1	62-1	NA	China	29.92	116.57	Zou*	SRR6414603	HiSeq X Ten	Y	N
63-1	63-1	NA	China	29.88	116.52	Zou*	SRR2204577	HiSeq 2000	Y	N
64-5	64-5	NA	China	29.87	116.53	Zou*	SRR2204350	HiSeq 2000	Y	N
65-1	65-1	NA	China	29.57	117.58	Zou*	SRR2204579	HiSeq 2000	Y	N
66-3	66-3	NA	China	29.34	117.34	Zou*	SRR2204581	HiSeq 2000	Y	N
67-1	67-1	NA	China	29.33	117.32	Zou*	SRR2204582	HiSeq 2000	Y	N
68-1	68-1	NA	China	29.32	117.31	Zou*	SRR2204583	HiSeq 2000	Y	N
69-7	69-7	NA	China	28.97	114.85	Zou*	SRR2204584	HiSeq 2000	Y	N
7-2	7-2	NA	China	29.80	118.18	Zou*	SRR2189714	HiSeq 2000	Y	N
70-1	70-1	NA	China	28.99	114.86	Zou*	SRR2204585	HiSeq 2000	Y	N
71-5	71-5	NA	China	29	114.87	Zou*	SRR2204586	HiSeq 2000	Y	N
72-2	72-2	NA	China	29.24	115.10	Zou*	SRR2204587	HiSeq 2000	Y	N
73-5	73-5	NA	China	29.29	115.98	Zou*	SRR2204588	HiSeq 2000	Y	N
74-14	74-14	NA	China	29.61	115.93	Zou*	SRR2204589	HiSeq 2000	Y	N
75-6	75-6	NA	China	29.60	115.93	Zou*	SRR2204590	HiSeq 2000	Y	N
76-3	76-3	NA	China	28.23	112.55	Zou*	SRR6414602	HiSeq X Ten	Y	N
76-4	76-4	NA	China	28.23	112.55	Zou*	SRR6414615	HiSeq X Ten	Y	N

76-5	76-5	NA	China	28.23	112.55	Zou*	SRR6414614	HiSeq X Ten	Y	N
77-2	77-2	NA	China	28.23	112.55	Zou*	SRR6414617	HiSeq X Ten	Y	N
77-3	77-3	NA	China	28.23	112.55	Zou*	SRR6414616	HiSeq X Ten	Y	N
78-4	78-4	NA	China	28.50	112.14	Zou*	SRR6414619	HiSeq X Ten	Y	N
78-5	78-5	NA	China	28.50	112.14	Zou*	SRR6414618	HiSeq X Ten	Y	N
79-2	79-2	NA	China	28.03	110.21	Zou*	SRR6414621	HiSeq X Ten	Y	N
79-4	79-4	NA	China	28.03	110.21	Zou*	SRR6414620	HiSeq X Ten	Y	N
8-17	8-17	NA	China	29.96	117.96	Zou*	SRR2189717	HiSeq 2000	Y	N
8-6	8-6	NA	China	29.96	117.96	Zou*	SRR2189716	HiSeq 2000	Y	N
82-1	82-1	NA	China	31.82	115.39	Zou*	SRR6414613	HiSeq X Ten	Y	N
82-3	82-3	NA	China	31.82	115.39	Zou*	SRR6414612	HiSeq X Ten	Y	N
83-2	83-2	NA	China	32.17	115.66	Zou*	SRR6414598	HiSeq X Ten	Y	N
83-5	83-5	NA	China	32.17	115.66	Zou*	SRR6414599	HiSeq X Ten	Y	N
84-3	84-3	NA	China	32.14	115.06	Zou*	SRR6414600	HiSeq X Ten	Y	N
84-4	84-4	NA	China	32.14	115.06	Zou*	SRR6414601	HiSeq X Ten	Y	N
85-3	85-3	NA	China	32.14	115.06	Zou*	SRR6414595	HiSeq X Ten	Y	N
85-5	85-5	NA	China	32.14	115.06	Zou*	SRR6414596	HiSeq X Ten	Y	N
86	86	NA	China	29.71	106.63	Zou*	SRR6414597	HiSeq X Ten	Y	N

87	87	NA	China	29.64	91.18	Zou*	SRR2204592	HiSeq 2000	N	N
9-5	9-5	NA	China	30.71	116.26	Zou*	SRR2189718	HiSeq 2000	Y	N

Seq. by. = Sequencing center for samples sequenced as part of the 1001 Genomes Project. For all other samples, Durvasula* refers to samples sequenced as part of Durvasula et al. PNAS. 2017 and Zou* refers to samples sequenced as part of Zou et al. Genome Biol. 2017.

Table 1.S2 Repeat library

ID	Length	Class	Subclass	Family	Cent	Pericent	Source	In meta-GWA
18S_At3	1808	SR	rDNA	NA	N	Y	Rabanal et al. *G3*. 2017	N
25S_At3	3387	SR	rDNA	NA	Y	N	Rabanal et al. *G3*. 2017	N
45S_At3	9378	SR	rDNA	NA	Y	Y	Rabanal et al. *G3*. 2017	N
5.8S_At3	164	SR	rDNA	NA	N	N	Rabanal et al. *G3*. 2017	N
AAAAAAAAAAAA	12	SR	mono	NA	N	N	NA	Y
AAAAACAAAAAC	12	SR	hexa	NA	N	N	NA	Y
AAAAAGAAAAAG	12	SR	hexa	NA	N	N	NA	Y
AAAAATAAAAAT	12	SR	hexa	NA	N	N	NA	Y
AAAACAAAACAA	12	SR	penta	NA	N	N	NA	Y
AAAACCAAAACC	12	SR	hexa	NA	N	N	NA	Y
AAAAGAAAAGAA	12	SR	penta	NA	N	N	NA	Y
AAAAGCAAAAGC	12	SR	hexa	NA	N	N	NA	Y
AAAAGGAAAAGG	12	SR	hexa	NA	N	N	NA	Y
AAAATAAAATAA	12	SR	penta	NA	N	N	NA	Y
AAAATCAAAATC	12	SR	hexa	NA	N	N	NA	Y
AAAATGAAAATG	12	SR	hexa	NA	N	N	NA	Y
AAAATTAAAATT	12	SR	hexa	NA	N	N	NA	Y
AAACCAAACCAA	12	SR	penta	NA	N	N	NA	Y
AAACCCAAACCC	12	SR	hexa	NA	N	N	NA	N
AAAGCAAAGCAA	12	SR	penta	NA	N	N	NA	Y
AAAGCCAAAGCC	12	SR	hexa	NA	N	N	NA	N
AAAGGAAAGGAA	12	SR	penta	NA	N	N	NA	Y
AAAGGCAAAGGC	12	SR	hexa	NA	N	N	NA	N
AAAGGGAAAGGG	12	SR	hexa	NA	N	N	NA	N
AAATCAAATCAA	12	SR	penta	NA	N	N	NA	Y
AAATCCAAATCC	12	SR	hexa	NA	N	N	NA	Y
AAATGAAATGAA	12	SR	penta	NA	N	N	NA	Y
AAATGCAAATGC	12	SR	hexa	NA	N	N	NA	Y

AAATGGAAATGG	12	SR	hexa	NA	N	N	NA	Y
AAATTAAATTAA	12	SR	penta	NA	N	N	NA	Y
AAATTCAAATTC	12	SR	hexa	NA	N	N	NA	Y
AAATTGAAATTG	12	SR	hexa	NA	N	N	NA	Y
AAATTTAAATTT	12	SR	hexa	NA	N	N	NA	Y
AACCCAACCCAA	12	SR	penta	NA	N	N	NA	Y
AACCCCAACCCC	12	SR	hexa	NA	N	N	NA	N
AAGCCAAGCCAA	12	SR	penta	NA	N	N	NA	Y
AAGCCCAAGCCC	12	SR	hexa	NA	N	N	NA	Y
AAGGCAAGGCAA	12	SR	penta	NA	N	N	NA	Y
AAGGCCAAGGCC	12	SR	hexa	NA	N	N	NA	Y
AAGGGAAGGGAA	12	SR	penta	NA	N	N	NA	Y
AAGGGCAAGGGC	12	SR	hexa	NA	N	N	NA	Y
AAGGGGAAGGGG	12	SR	hexa	NA	N	N	NA	Y
AATCCAATCCAA	12	SR	penta	NA	N	N	NA	Y
AATCCCAATCCC	12	SR	hexa	NA	N	N	NA	N
AATGCAATGCAA	12	SR	penta	NA	N	N	NA	N
AATGCCAATGCC	12	8216	hexa	NA	N	N	NA	Y
AATGGAATGGAA	12	SR	penta	NA	N	N	NA	N
AATGGCAATGGC	12	SR	hexa	NA	N	N	NA	Y
AATGGGAATGGG	12	SR	hexa	NA	N	N	NA	Y
AATTCAATTCAA	12	SR	penta	NA	N	N	NA	Y
AATTCCAATTCC	12	SR	hexa	NA	N	N	NA	N
AATTGAATTGAA	12	SR	penta	NA	N	N	NA	Y
AATTGCAATTGC	12	SR	hexa	NA	N	N	NA	N
AATTGGAATTGG	12	SR	hexa	NA	N	N	NA	Y
AATTTAATTTAA	12	SR	penta	NA	N	N	NA	Y
AATTTCAATTTC	12	SR	hexa	NA	N	N	NA	Y
AATTTGAATTTG	12	SR	hexa	NA	N	N	NA	Y
ACACACACACAC	12	SR	di	NA	N	N	NA	Y
ACCCCACCCCAC	12	SR	penta	NA	N	N	NA	Y
ACCCCCACCCCC	12	SR	hexa	NA	N	N	NA	Y
ACGACGACGACG	12	SR	tri	NA	N	N	NA	N

ACGTACGTACGT	12	SR	tetra	NA	N	N	NA	Y
ACTACTACTACT	12	SR	tri	NA	N	N	NA	Y
ACTGACTGACTG	12	SR	tetra	NA	N	N	NA	Y
AGAGAGAGAGAG	12	SR	di	NA	N	N	NA	Y
AGCAGCAGCAGC	12	SR	tri	NA	N	N	NA	N
AGCCCAGCCCAG	12	SR	penta	NA	N	N	NA	Y
AGCCCCAGCCCC	12	SR	hexa	NA	N	N	NA	Y
AGCTAGCTAGCT	12	SR	tetra	NA	N	N	NA	Y
AGGCCAGGCCAG	12	SR	penta	NA	N	N	NA	Y
AGGCCCAGGCCC	12	SR	hexa	NA	N	N	NA	Y
AGGGCAGGGCAG	12	SR	penta	NA	N	N	NA	Y
AGGGCCAGGGCC	12	SR	hexa	NA	N	N	NA	Y
AGGGGAGGGGAG	12	SR	penta	NA	N	N	NA	Y
AGGGGCAGGGGC	12	SR	hexa	NA	N	N	NA	Y
AGGGGGAGGGGG	12	SR	hexa	NA	N	N	NA	Y
AGTCAGTCAGTC	12	SR	tetra	NA	N	N	NA	Y
AR12	179	SR	Other	NA	Y	Y	Repbase	N
AR3	322	SR	Other	NA	Y	N	Repbase	N
ARNOLD1	15815	DNA	Other DNA	MuDR	Y	Y	Repbase	N
ARNOLD2	15490	DNA	Other DNA	MuDR	Y	Y	Repbase	Y
ARNOLD3	14724	DNA	Other DNA	MuDR	Y	Y	Repbase	N
ARNOLD4	8459	DNA	Other DNA	MuDR	Y	Y	Repbase	N
ARNOLDY1	1936	DNA	Other DNA	MuDR	Y	Y	Repbase	N
ARNOLDY2	1179	DNA	Other DNA	MuDR	Y	Y	Repbase	Y
AT10MU1	3770	DNA	Other DNA	MuDR	Y	Y	Repbase	Y
AT9MU1	2102	DNA	Other DNA	MuDR	N	Y	Repbase	Y
AT9NMU1	926	DNA	Other DNA	MuDR	Y	Y	Repbase	Y
AT9TSD1	2216	DNA	Other DNA	MuDR	Y	Y	Repbase	N
ATATATATATAT	12	SR	di	NA	N	N	NA	N
ATCATCATCATC	12	SR	tri	NA	N	N	NA	N
ATCCCATCCCAT	12	SR	penta	NA	N	N	NA	N
ATCCCCATCCCC	12	SR	hexa	NA	N	N	NA	Y
ATCGATCGATCG	12	SR	tetra	NA	N	N	NA	Y

ATCLUST1	188	SR	Other	NA	N	N	Repbase	N
ATCOPI1_I	4345	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPI1_LTR	394	RT	LTR RT	Copia	N	N	Repbase	N
ATCOPIA10_I	4220	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA10_LTR	483	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA11I	4654	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA11LTR	204	RT	LTR RT	Copia	Y	Y	Repbase	Y
ATCOPIA12I	4775	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA12LTR	168	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA13I	4598	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA13LTR	157	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA14I	4690	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA14LTR	139	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA15I	4478	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA15LTR	180	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA16I	4790	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA16LTR	172	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA17I	5034	RT	LTR RT	Copia	N	N	Repbase	N
ATCOPIA17LTR	205	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA18A_I	5050	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA18ALTR	103	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA18I	2144	RT	LTR RT	Copia	N	N	Repbase	N
ATCOPIA18LTR	120	RT	LTR RT	Copia	N	N	Repbase	Y
ATCOPIA19I	4226	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA19LTR	362	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA1I	4709	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA1LTR	215	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA20I	4559	RT	LTR RT	Copia	Y	Y	Repbase	Y
ATCOPIA20LTR	503	RT	LTR RT	Copia	Y	Y	Repbase	Y
ATCOPIA21I	4502	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA21LTR	120	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA22I	4510	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA22LTR	181	RT	LTR RT	Copia	N	Y	Repbase	Y

ATCOPIA23_I	4093	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA23_LTR	237	RT	LTR RT	Copia	N	N	Repbase	Y
ATCOPIA24I	4707	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA24LTR	196	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA25I	4228	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA25LTR	373	RT	LTR RT	Copia	N	N	Repbase	Y
ATCOPIA26I	4605	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA26LTR	135	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA27_I	5658	RT	LTR RT	Copia	Y	Y	Repbase	Y
ATCOPIA27_LTR	337	RT	LTR RT	Copia	Y	Y	Repbase	Y
ATCOPIA28_I	4706	RT	LTR RT	Copia	Y	Y	Repbase	Y
ATCOPIA28_LTR	182	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA29_I	3399	RT	LTR RT	Copia	Y	Y	Repbase	Y
ATCOPIA29_LTR	184	RT	LTR RT	Copia	Y	Y	Repbase	Y
ATCOPIA2I	4496	RT	LTR RT	Copia	Y	Y	Repbase	Y
ATCOPIA2LTR	166	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA30_I	3869	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA30_LTR	184	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA31_I	4084	RT	LTR RT	Copia	Y	Y	Repbase	Y
ATCOPIA31_LTR	271	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA31A_I	4088	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA31A_LTR	288	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA32_I	4245	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA32_LTR	771	RT	LTR RT	Copia	Y	N	Repbase	N
ATCOPIA32B_I	4239	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA32B_LTR	766	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA33_I	4261	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA33_LTR	393	RT	LTR RT	Copia	Y	N	Repbase	N
ATCOPIA34_I	4260	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA34_LTR	246	RT	LTR RT	Copia	Y	Y	Repbase	Y
ATCOPIA35_I	4148	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA35_LTR	281	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA36_I	4180	RT	LTR RT	Copia	N	Y	Repbase	Y

ATCOPIA36_LTR	273	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA37_I	5156	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA37_LTR	436	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA38_I	4490	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA38_LTR	171	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA38A_I	4206	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA38ALTR	162	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA38B_I	4479	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA38B_LTR	162	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA39_I	3282	RT	LTR RT	Copia	N	N	Repbase	N
ATCOPIA39_LTR	365	RT	LTR RT	Copia	Y	N	Repbase	N
ATCOPIA3I	4393	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA3LTR	120	RT	LTR RT	Copia	N	N	Repbase	Y
ATCOPIA40_I	4131	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA40_LTR	289	RT	LTR RT	Copia	Y	Y	Repbase	Y
ATCOPIA41I	5262	RT	LTR RT	Copia	Y	Y	Repbase	Y
ATCOPIA41LTR	608	RT	LTR RT	Copia	Y	Y	Repbase	Y
ATCOPIA42I	5072	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA42LTR	1326	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA43I	7963	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA43LTR	570	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA44_I	4190	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA44LTR	502	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA45_I	4211	RT	LTR RT	Copia	Y	Y	Repbase	Y
ATCOPIA45LTR	303	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA46_I	4260	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA46LTR	373	RT	LTR RT	Copia	N	N	Repbase	N
ATCOPIA47_I	4299	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA47LTR	382	RT	LTR RT	Copia	N	N	Repbase	N
ATCOPIA48_I	4420	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA48LTR	415	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA49_I	4216	RT	LTR RT	Copia	Y	Y	Repbase	Y
ATCOPIA49LTR	502	RT	LTR RT	Copia	Y	Y	Repbase	Y

ATCOPIA4I	4493	RT	LTR RT	Copia	Y	Y	Repbase	Y
ATCOPIA4LTR	130	RT	LTR RT	Copia	N	N	Repbase	Y
ATCOPIA50_I	4278	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA50LTR	687	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA51_I	4214	RT	LTR RT	Copia	Y	Y	Repbase	Y
ATCOPIA51LTR	379	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA52_I	4231	RT	LTR RT	Copia	Y	Y	Repbase	Y
ATCOPIA52LTR	353	RT	LTR RT	Copia	N	N	Repbase	Y
ATCOPIA53_I	4863	RT	LTR RT	Copia	Y	N	Repbase	N
ATCOPIA53LTR	150	RT	LTR RT	Copia	Y	N	Repbase	N
ATCOPIA54_I	4117	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA54LTR	288	RT	LTR RT	Copia	Y	Y	Repbase	Y
ATCOPIA55_I	4424	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA55LTR	427	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA56_I	4210	RT	LTR RT	Copia	Y	Y	Repbase	Y
ATCOPIA56LTR	633	RT	LTR RT	Copia	Y	Y	Repbase	Y
ATCOPIA57_I	1468	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA57LTR	297	RT	LTR RT	Copia	Y	Y	Repbase	Y
ATCOPIA58_I	4801	RT	LTR RT	Copia	Y	Y	Repbase	Y
ATCOPIA58LTR	551	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA59_I	4271	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA59LTR	228	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA5I	4464	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA5LTR	111	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA60_I	2213	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA60LTR	539	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA61_I	4653	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA61LTR	183	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA62_I	4639	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA62LTR	161	RT	LTR RT	Copia	Y	Y	Repbase	Y
ATCOPIA63_I	4071	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA63LTR	374	RT	LTR RT	Copia	Y	Y	Repbase	Y
ATCOPIA64_I	4145	RT	LTR RT	Copia	Y	Y	Repbase	N

ATCOPIA64LTR	275	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA65_I	4165	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA65A_I	311	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA65ALTR	305	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA65LTR	290	RT	LTR RT	Copia	Y	Y	Repbase	Y
ATCOPIA66_I	4231	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA66LTR	509	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA67_I	3668	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA67LTR	152	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA68_I	4165	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA68LTR	408	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA69_I	4270	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA69A_I	4308	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA69A_LTR	424	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA69LTR	445	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA6I	4480	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA6LTR	119	RT	LTR RT	Copia	N	N	Repbase	Y
ATCOPIA70_I	4541	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA70LTR	250	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA71_I	5188	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA71LTR	170	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA72_I	4483	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA72LTR	174	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA73_I	4502	RT	LTR RT	Copia	Y	N	Repbase	N
ATCOPIA73LTR	184	RT	LTR RT	Copia	N	N	Repbase	N
ATCOPIA74_I	2817	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA74LTR	522	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA75_I	4609	RT	LTR RT	Copia	Y	Y	Repbase	Y
ATCOPIA75LTR	129	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA76_I	4272	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA76LTR	724	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA77_I	4520	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA77LTR	190	RT	LTR RT	Copia	N	Y	Repbase	N

ATCOPIA78_I	4077	RT	LTR RT	Copia	Y	Y	Repbase	Y
ATCOPIA78LTR	440	RT	LTR RT	Copia	Y	Y	Repbase	Y
ATCOPIA79_I	4342	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA79LTR	500	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA7I	4337	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA7LTR	373	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA80_I	3998	RT	LTR RT	Copia	Y	N	Repbase	N
ATCOPIA80LTR	141	RT	LTR RT	Copia	Y	N	Repbase	N
ATCOPIA81_I	4502	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA81LTR	232	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA82_I	4279	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA82LTR	508	RT	LTR RT	Copia	N	N	Repbase	N
ATCOPIA83_I	4643	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA83LTR	140	RT	LTR RT	Copia	N	N	Repbase	Y
ATCOPIA84_I	4570	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA84LTR	156	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA85_I	3622	RT	LTR RT	Copia	Y	N	Repbase	N
ATCOPIA85LTR	128	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA86_I	4287	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA86LTR	469	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA87_I	4087	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA87LTR	567	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA88_I	4909	RT	LTR RT	Copia	Y	N	Repbase	N
ATCOPIA88LTR	227	RT	LTR RT	Copia	Y	N	Repbase	N
ATCOPIA89_I	4576	RT	LTR RT	Copia	N	N	Repbase	N
ATCOPIA89LTR	214	RT	LTR RT	Copia	N	N	Repbase	Y
ATCOPIA8AI	4487	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA8ALTR	389	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA8BI	4285	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA8BLTR	400	RT	LTR RT	Copia	N	N	Repbase	N
ATCOPIA90_I	4887	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA90LTR	130	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA91_I	4988	RT	LTR RT	Copia	N	Y	Repbase	N

ATCOPIA91LTR	141	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA92_I	4537	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA92LTR	133	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA93_I	4550	RT	LTR RT	Copia	N	Y	Repbase	N
ATCOPIA93LTR	399	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA94_I	4638	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA94LTR	150	RT	LTR RT	Copia	N	N	Repbase	N
ATCOPIA95_I	5139	RT	LTR RT	Copia	Y	Y	Repbase	Y
ATCOPIA95LTR	841	RT	LTR RT	Copia	Y	Y	Repbase	Y
ATCOPIA96_I	4506	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA96LTR	195	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA97I	3134	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA97LTR	304	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIA9I	4300	RT	LTR RT	Copia	Y	Y	Repbase	N
ATCOPIA9LTR	383	RT	LTR RT	Copia	N	Y	Repbase	Y
ATCOPIN_I	112	RT	LTR RT	Other	Y	Y	Repbase	Y
ATCOPIN_LTR	357	RT	LTR RT	Copia	Y	Y	Repbase	N
ATDNA12T3A	2372	DNA	Other DNA	Other	Y	Y	Repbase	N
ATDNA1T9A	3552	DNA	Other DNA	MuDR	Y	Y	Repbase	N
ATDNA2T9A	1596	DNA	Other DNA	MuDR	Y	Y	Repbase	Y
ATDNA2T9B	1472	DNA	Other DNA	MuDR	Y	Y	Repbase	Y
ATDNA2T9C	1477	DNA	Other DNA	MuDR	Y	Y	Repbase	Y
ATDNAI26T9	2432	DNA	Other DNA	MuDR	Y	Y	Repbase	Y
ATDNAI27T9A	1357	DNA	Other DNA	MuDR	Y	Y	Repbase	Y
ATDNAI27T9B	2090	DNA	Other DNA	MuDR	Y	Y	Repbase	Y
ATDNAI27T9C	1933	DNA	Other DNA	MuDR	Y	Y	Repbase	Y
ATDNATA1	241	DNA	Other DNA	mariner/Tc1	Y	Y	Repbase	Y
ATENSAT1	1949	SR	Knob	NA	Y	Y	Repbase	N
ATENSAT2	974	SR	Other	NA	Y	Y	Repbase	N
ATENSPM1	4548	DNA	Other DNA	En/Spm	Y	Y	Repbase	Y
ATENSPM10	8272	DNA	Other DNA	En/Spm	Y	Y	Repbase	N
ATENSPM11	8144	DNA	Other DNA	En/Spm	Y	Y	Repbase	N
ATENSPM12	9337	DNA	Other DNA	En/Spm	Y	Y	Repbase	N

ATENSPM1A	4279	DNA	Other DNA	En/Spm	Y	Y	Repbase	Y
ATENSPM2	8253	DNA	Other DNA	En/Spm	Y	Y	Repbase	Y
ATENSPM3	8456	DNA	Other DNA	En/Spm	Y	Y	Repbase	N
ATENSPM4	4855	DNA	Other DNA	En/Spm	Y	Y	Repbase	N
ATENSPM5	8717	DNA	Other DNA	En/Spm	Y	Y	Repbase	Y
ATENSPM6	8825	DNA	Other DNA	En/Spm	Y	Y	Repbase	N
ATENSPM7	8535	DNA	Other DNA	En/Spm	Y	Y	Repbase	N
ATENSPM8	2375	DNA	Other DNA	En/Spm	Y	Y	Repbase	N
ATENSPM9	9233	DNA	Other DNA	En/Spm	Y	Y	Repbase	N
ATGATGATGATG	12	SR	tri	NA	N	N	NA	N
ATGCATGCATGC	12	SR	tetra	NA	N	N	NA	Y
ATGCCATGCCAT	12	SR	penta	NA	N	N	NA	Y
ATGCCCATGCCC	12	SR	hexa	NA	N	N	NA	Y
ATGGCCATGGCC	12	SR	hexa	NA	N	N	NA	Y
ATGGGCATGGGC	12	SR	hexa	NA	N	N	NA	Y
ATGGGGATGGGG	12	SR	hexa	NA	N	N	NA	Y
ATGP10_I	6217	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATGP10LTR	706	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATGP11_I	2519	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATGP11_LTR	813	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATGP1I	5977	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATGP1LTR	1160	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATGP2I	5049	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATGP2LTR	1287	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATGP2N_I	1167	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATGP2NLTR	2033	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATGP3A_I	4563	RT	LTR RT	Gypsy	Y	Y	Repbase	N
ATGP3A_LTR	335	RT	LTR RT	Gypsy	Y	Y	Repbase	N
ATGP3B_I	4570	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATGP3B_LTR	384	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATGP3I	4589	RT	LTR RT	Gypsy	Y	Y	Repbase	N
ATGP3LTR	327	RT	LTR RT	Gypsy	Y	Y	Repbase	N
ATGP4_I	4900	RT	LTR RT	Gypsy	Y	Y	Repbase	Y

ATGP4_LTR	407	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATGP5A_I	4586	RT	LTR RT	Gypsy	Y	Y	Repbase	N
ATGP5A_LTR	1258	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATGP5I	4801	RT	LTR RT	Gypsy	Y	Y	Repbase	N
ATGP5LTR	779	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATGP6I	3973	RT	LTR RT	Gypsy	Y	Y	Repbase	N
ATGP6LTR	861	RT	LTR RT	Gypsy	Y	Y	Repbase	N
ATGP7I	4561	RT	LTR RT	Gypsy	Y	Y	Repbase	N
ATGP7LTR	822	RT	LTR RT	Gypsy	Y	Y	Repbase	N
ATGP8I	5093	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATGP8LTR	1795	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATGP9BI	2380	RT	LTR RT	Gypsy	N	Y	Repbase	N
ATGP9BLTR	478	RT	LTR RT	Gypsy	Y	Y	Repbase	N
ATGP9LTR	508	RT	LTR RT	Gypsy	N	N	Repbase	Y
ATHAT1	4060	DNA	Other DNA	hAT	Y	Y	Repbase	N
ATHAT10	3243	DNA	Other DNA	hAT	Y	Y	Repbase	N
ATHAT2	3573	DNA	Other DNA	hAT	Y	Y	Repbase	N
ATHAT3	4184	DNA	Other DNA	hAT	Y	Y	Repbase	N
ATHAT7	3500	DNA	Other DNA	hAT	Y	Y	Repbase	N
ATHAT8	3849	DNA	Other DNA	hAT	Y	Y	Repbase	N
ATHAT9	3126	DNA	Other DNA	hAT	Y	Y	Repbase	N
ATHATN1	498	DNA	Other DNA	hAT	Y	Y	Repbase	Y
ATHATN10	832	DNA	Other DNA	hAT	Y	Y	Repbase	Y
ATHATN2	649	DNA	Other DNA	hAT	Y	Y	Repbase	Y
ATHATN3	554	DNA	Other DNA	hAT	Y	Y	Repbase	Y
ATHATN3A	589	DNA	Other DNA	hAT	N	Y	Repbase	Y
ATHATN4	437	DNA	Other DNA	hAT	Y	Y	Repbase	Y
ATHATN5	541	DNA	Other DNA	hAT	Y	Y	Repbase	Y
ATHATN6	594	DNA	Other DNA	hAT	Y	Y	Repbase	Y
ATHATN7	598	DNA	Other DNA	hAT	N	Y	Repbase	Y
ATHATN8	249	DNA	Other DNA	hAT	Y	Y	Repbase	Y
ATHATN9	246	DNA	Other DNA	hAT	Y	Y	Repbase	Y
ATHILA_I	7414	RT	LTR RT	Gypsy	Y	Y	Repbase	N

ATHILA_LTR	1598	RT	LTR RT	Gypsy	Y	Y	Repbase	N
ATHILA0_I	10046	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATHILA2_I	7435	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATHILA2_LTR	1744	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATHILA3_I	7410	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATHILA3_LTR	1610	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATHILA4_I	3022	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATHILA4_LTR	1207	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATHILA4A_I	2636	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATHILA4A_LTR	1178	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATHILA4B_LTR	1209	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATHILA4C_I	8639	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATHILA4C_LTR	1158	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATHILA4D_I	4824	RT	LTR RT	Gypsy	Y	Y	Repbase	N
ATHILA4D_LTR	1165	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATHILA5_I	7505	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATHILA5_LTR	1623	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATHILA6A_I	7835	RT	LTR RT	Gypsy	Y	Y	Repbase	N
ATHILA6A_LTR	1888	RT	LTR RT	Gypsy	Y	Y	Repbase	N
ATHILA6B_I	7963	RT	LTR RT	Gypsy	Y	Y	Repbase	N
ATHILA6C_I	10531	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATHILA6C_LTR	1769	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATHILA7_I	9924	RT	LTR RT	Gypsy	Y	Y	Repbase	N
ATHILA7A_I	4754	RT	LTR RT	Gypsy	Y	Y	Repbase	N
ATHILA7LTR	1427	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATHILA8A_I	5635	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATHILA8ALTR	1617	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATHILA8B_I	5021	RT	LTR RT	Gypsy	Y	Y	Repbase	N
ATHILA8BLTR	1660	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATHPOGO	2114	DNA	Other DNA	pogo	Y	Y	Repbase	N
ATHPOGON1	538	DNA	Other DNA	pogo	Y	Y	Repbase	Y
ATHPOGON2	691	DNA	Other DNA	pogo	Y	Y	Repbase	Y
ATHPOGON3	712	DNA	Other DNA	pogo	Y	Y	Repbase	Y

ATIS112A	5099	DNA	Other DNA	Harbinger	Y	Y	Repbase	N
ATLANTYS1_I	10633	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATLANTYS1_LTR	517	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATLANTYS2_I	9311	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATLANTYS2_LTR	804	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATLANTYS3I	9668	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATLANTYS3LTR	494	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
ATLINE1_1	5851	RT	Non-LTR RT	L1	Y	Y	Repbase	N
ATLINE1_10	5643	RT	Non-LTR RT	L1	Y	Y	Repbase	N
ATLINE1_10A	5670	RT	Non-LTR RT	L1	Y	Y	Repbase	N
ATLINE1_11	5524	RT	Non-LTR RT	L1	Y	Y	Repbase	N
ATLINE1_12	4570	RT	Non-LTR RT	L1	Y	Y	Repbase	Y
ATLINE1_2	5814	RT	Non-LTR RT	L1	Y	Y	Repbase	N
ATLINE1_3A	330	RT	Non-LTR RT	L1	Y	Y	Repbase	N
ATLINE1_4	6700	RT	Non-LTR RT	L1	Y	Y	Repbase	N
ATLINE1_5	6835	RT	Non-LTR RT	L1	Y	Y	Repbase	N
ATLINE1_6	5525	RT	Non-LTR RT	L1	Y	Y	Repbase	N
ATLINE1_7	5559	RT	Non-LTR RT	L1	Y	Y	Repbase	N
ATLINE1_8	5591	RT	Non-LTR RT	L1	Y	Y	Repbase	N
ATLINE1_9	4053	RT	Non-LTR RT	L1	Y	Y	Repbase	N
ATLINE1A	2254	RT	Non-LTR RT	L1	Y	Y	Repbase	Y
ATLINE2	5318	RT	Non-LTR RT	L1	Y	Y	Repbase	N
ATLINEIII	5408	RT	Non-LTR RT	L1	Y	Y	Repbase	N
ATMSAT1	97	SR	Other	NA	Y	Y	Repbase	N
ATMU1	4929	DNA	Other DNA	MuDR	Y	Y	Repbase	N
ATMU10	4703	DNA	Other DNA	MuDR	Y	Y	Repbase	N
ATMU11	3831	DNA	Other DNA	MuDR	Y	Y	Repbase	N
ATMU12	4347	DNA	Other DNA	MuDR	Y	Y	Repbase	N
ATMU13	3652	DNA	Other DNA	MuDR	N	Y	Repbase	N
ATMU2	4444	DNA	Other DNA	MuDR	Y	Y	Repbase	N
ATMU3	4853	DNA	Other DNA	MuDR	Y	Y	Repbase	N
ATMU3N1	446	DNA	Other DNA	MuDR	Y	Y	Repbase	Y
ATMU4	4496	DNA	Other DNA	MuDR	Y	Y	Repbase	N

ATMU5	4895	DNA	Other DNA	MuDR	Y	Y	Repbase	N
ATMU6	4172	DNA	Other DNA	MuDR	Y	Y	Repbase	N
ATMU6N1	1012	DNA	Other DNA	MuDR	N	Y	Repbase	Y
ATMU7	3134	DNA	Other DNA	MuDR	Y	Y	Repbase	N
ATMU8	4433	DNA	Other DNA	MuDR	N	Y	Repbase	N
ATMU9	4693	DNA	Other DNA	MuDR	Y	Y	Repbase	N
ATMUN1	1000	DNA	Other DNA	MuDR	Y	Y	Repbase	Y
ATMUN2	1017	DNA	Other DNA	MuDR	Y	Y	Repbase	Y
ATMUNX1	377	DNA	Other DNA	MuDR	Y	Y	Repbase	Y
ATN9_1	678	DNA	Other DNA	MuDR	Y	Y	Repbase	Y
ATRAN	360	RT	LTR RT	Other	Y	Y	Repbase	Y
ATRE1_I	4490	RT	LTR RT	Copia	Y	Y	Repbase	Y
ATRE1_LTR	167	RT	LTR RT	Copia	N	Y	Repbase	Y
ATREP1	888	DNA	Helitron	Helitron	Y	Y	Repbase	N
ATREP10	899	DNA	Helitron	Helitron	Y	Y	Repbase	Y
ATREP10A	1380	DNA	Helitron	Helitron	Y	Y	Repbase	N
ATREP10B	1821	DNA	Helitron	Helitron	Y	Y	Repbase	N
ATREP10C	653	DNA	Helitron	Helitron	Y	Y	Repbase	Y
ATREP10D	777	DNA	Helitron	Helitron	Y	Y	Repbase	Y
ATREP11	1053	DNA	Helitron	Helitron	Y	Y	Repbase	Y
ATREP11A	1003	DNA	Helitron	Helitron	Y	Y	Repbase	Y
ATREP12	1342	DNA	Helitron	Helitron	Y	Y	Repbase	Y
ATREP13	648	DNA	Helitron	Helitron	Y	Y	Repbase	Y
ATREP14	737	DNA	Helitron	Helitron	Y	Y	Repbase	Y
ATREP15	1769	DNA	Helitron	Helitron	Y	Y	Repbase	Y
ATREP16	1391	DNA	Other DNA	MuDR	Y	Y	Repbase	Y
ATREP17	1268	DNA	Other DNA	MuDR	Y	Y	Repbase	Y
ATREP18	1791	SR	Telomere	NA	Y	Y	Repbase	N
ATREP19	587	Other	NA	NA	Y	Y	Repbase	N
ATREP2	564	DNA	Helitron	Helitron	Y	Y	Repbase	Y
ATREP20	2144	DNA	Helitron	Helitron	Y	Y	Repbase	N
ATREP21	484	DNA	Helitron	Helitron	Y	Y	Repbase	Y
ATREP2A	603	DNA	Helitron	Helitron	Y	Y	Repbase	N

ATREP3	2097	DNA	Helitron	Helitron	Y	Y	Repbase	Y
ATREP4	2240	DNA	Helitron	Helitron	Y	Y	Repbase	Y
ATREP5	2386	DNA	Helitron	Helitron	Y	Y	Repbase	Y
ATREP6	1189	DNA	Helitron	Helitron	Y	Y	Repbase	Y
ATREP7	940	DNA	Helitron	Helitron	Y	Y	Repbase	Y
ATREP8	1077	DNA	Helitron	Helitron	Y	Y	Repbase	Y
ATREP9	899	DNA	Helitron	Helitron	Y	Y	Repbase	Y
ATREPX1	2434	DNA	Helitron	Helitron	Y	Y	Repbase	Y
ATSAA5	648	SR	Other	NA	Y	Y	Repbase	N
ATSAB5	448	SR	Other	NA	Y	Y	Repbase	N
ATSAT5	2196	SR	Knob	NA	Y	Y	Repbase	N
AtSB2	171	RT	Non-LTR RT	Other	Y	Y	Repbase	Y
AtSB3	303	RT	Non-LTR RT	Other	Y	Y	Repbase	Y
AtSB4	159	RT	Non-LTR RT	Other	Y	Y	Repbase	Y
AtSB5	217	RT	Non-LTR RT	Other	N	N	Repbase	Y
AtSB6	333	RT	Non-LTR RT	Other	Y	Y	Repbase	Y
ATSINE2A	1396	RT	Non-LTR RT	Other	N	Y	Repbase	N
ATTCCCATTCCC	12	SR	hexa	NA	N	N	NA	Y
ATTGCCATTGCC	12	SR	hexa	NA	N	N	NA	Y
ATTGGCATTGGC	12	SR	hexa	NA	N	N	NA	Y
ATTGGGATTGGG	12	SR	hexa	NA	N	N	NA	N
ATTIR16T3A	501	DNA	Other DNA	Other	Y	Y	Repbase	Y
ATTIRTA1	265	DNA	Other DNA	mariner/Tc1	Y	Y	Repbase	Y
ATTIRX1A	382	DNA	Other DNA	Other	Y	Y	Repbase	Y
ATTIRX1B	373	DNA	Other DNA	Other	Y	Y	Repbase	Y
ATTIRX1C	406	DNA	Other DNA	Other	Y	Y	Repbase	Y
ATTIRX1D	349	DNA	Other DNA	Other	Y	Y	Repbase	Y
ATTTCCATTTCC	12	SR	hexa	NA	N	N	NA	N
ATTTGCATTTGC	12	SR	hexa	NA	N	N	NA	Y
ATTTGGATTTGG	12	SR	hexa	NA	N	N	NA	Y
ATTTTCATTTTC	12	SR	hexa	NA	N	N	NA	Y
ATTTTGATTTTG	12	SR	hexa	NA	N	N	NA	N
BOMZH1	1088	DNA	Other DNA	MuDR	Y	Y	Repbase	Y

BOMZH2	1044	DNA	Other DNA	MuDR	Y	Y	Repbase	Y
BRODYAGA1	1184	DNA	Other DNA	MuDR	Y	Y	Repbase	Y
BRODYAGA1A	1067	DNA	Other DNA	MuDR	Y	Y	Repbase	N
BRODYAGA2	1250	DNA	Other DNA	MuDR	Y	Y	Repbase	Y
CACACACACACA	12	SR	di	NA	N	N	NA	N
CAGCAGCAGCAG	12	SR	tri	NA	N	N	NA	Y
Cassandra_AT-I	112	RT	LTR RT	Cassandra	Y	Y	Repbase	Y
Cassandra_AT-LTR	356	RT	LTR RT	Cassandra	Y	Y	Repbase	Y
CASTOR_I	4461	RT	LTR RT	Copia	Y	Y	Repbase	Y
CASTOR_LTR	131	RT	LTR RT	Copia	N	Y	Repbase	Y
CATGCATGCATG	12	SR	tetra	NA	N	N	NA	Y
CCCCCCCCCCCC	12	SR	mono	NA	N	N	NA	Y
CEN_Cluster1_cons	182	SR	Other	NA	Y	Y	Maheshwari et al. *Genome Res.* 2017	N
CEN_Cluster2_cons	209	SR	Other	NA	Y	Y	Maheshwari et al. *Genome Res.* 2017	N
CEN_Cluster3_cons	186	SR	Other	NA	Y	Y	Maheshwari et al. *Genome Res.* 2017	N
CEN_Cluster4_cons	181	SR	Other	NA	Y	Y	Maheshwari et al. *Genome Res.* 2017	N
CEN_Cluster5_cons	181	SR	Other	NA	Y	Y	Maheshwari et al. *Genome Res.* 2017	N
CEN_Cluster6_cons	187	SR	Other	NA	Y	Y	Maheshwari et al. *Genome Res.* 2017	N
CGACGACGACGA	12	SR	tri	NA	N	N	NA	Y
CGCGCGCGCGCG	12	SR	di	NA	N	N	NA	Y
CGTACGTACGTA	12	SR	tetra	NA	N	N	NA	Y
Chester-1		DNA	Other DNA	En/Spm	Y	Y	Repbase	N
COLAR12	178	SR	Other	NA	Y	Y	Repbase	N
Copia-1_AT-I	4521	RT	LTR RT	Copia	N	Y	Repbase	N
Copia-1_AT-LTR	230	RT	LTR RT	Copia	N	Y	Repbase	N
Copia-2_AT-I	4153	RT	LTR RT	Copia	N	Y	Repbase	Y
Copia-2_AT-LTR	296	RT	LTR RT	Copia	N	Y	Repbase	Y
Copia-3_AT-I	4378	RT	LTR RT	Copia	Y	Y	Repbase	N

Copia-3_AT-LTR	388	RT	LTR RT	Copia	N	Y	Repbase	N
Copia-35_AT-I	5050	RT	LTR RT	Copia	Y	Y	Repbase	Y
Copia-35_AT-LTR	339	RT	LTR RT	Copia	Y	Y	Repbase	Y
Copia-4_AT-I	4196	RT	LTR RT	Copia	Y	N	Repbase	N
Copia-4_AT-LTR	499	RT	LTR RT	Copia	Y	Y	Repbase	N
CTACTACTACTA	12	SR	tri	NA	N	N	NA	N
CTAGCTAGCTAG	12	SR	tetra	NA	N	N	NA	Y
CTGACTGACTGA	12	SR	tetra	NA	N	N	NA	Y
DRL1	250	DNA	Other DNA	hAT	N	Y	Repbase	N
DT1	262	DNA	Other DNA	mariner/Tc1	Y	Y	Repbase	Y
ENDOVIR1_I	7985	RT	LTR RT	Copia	Y	Y	Repbase	Y
ENDOVIR1LTR	549	RT	LTR RT	Copia	Y	Y	Repbase	Y
GACGACGACGAC	12	SR	tri	NA	N	N	NA	N
GAGAGAGAGAGA	12	SR	di	NA	N	N	NA	N
GATCGATCGATC	12	SR	tetra	NA	N	N	NA	Y
GCAGCAGCAGCA	12	SR	tri	NA	N	N	NA	N
GCCCCCGCCCCC	12	SR	hexa	NA	N	N	NA	Y
GCCCCGCCCCGC	12	SR	penta	NA	N	N	NA	Y
GCGCGCGCGCGC	12	SR	di	NA	N	N	NA	Y
GCTAGCTAGCTA	12	SR	tetra	NA	N	N	NA	Y
GGCCCCGGCCCC	12	SR	hexa	NA	N	N	NA	Y
GGGCCCGGGCCC	12	SR	hexa	NA	N	N	NA	Y
GTACGTACGTAC	12	SR	tetra	NA	N	N	NA	Y
GTAGTAGTAGTA	12	SR	tri	NA	N	N	NA	N
GTCAGTCAGTCA	12	SR	tetra	NA	N	N	NA	Y
Gypsy-15_AT-I	8537	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
Gypsy-15_AT-LTR	432	RT	LTR RT	Gypsy	Y	Y	Repbase	Y
HARBINGER	5382	DNA	Other DNA	Harbinger	Y	Y	Repbase	N
HELITRON1	15809	DNA	Helitron	Helitron	Y	Y	Repbase	N
HELITRON2	11435	DNA	Helitron	Helitron	Y	Y	Repbase	N
HELITRON3	15333	DNA	Helitron	Helitron	Y	Y	Repbase	N
HELITRON4	17261	DNA	Helitron	Helitron	Y	Y	Repbase	N
HELITRON5	12495	DNA	Helitron	Helitron	Y	Y	Repbase	N

HELITRONY1A	1348	DNA	Helitron	Helitron	Y	Y	Repbase	Y
HELITRONY1B	1311	DNA	Helitron	Helitron	Y	Y	Repbase	Y
HELITRONY1C	3058	DNA	Helitron	Helitron	Y	Y	Repbase	N
HELITRONY1D	2541	DNA	Helitron	Helitron	Y	Y	Repbase	Y
HELITRONY1E	1291	DNA	Helitron	Helitron	Y	Y	Repbase	Y
HELITRONY2	11114	DNA	Helitron	Helitron	Y	Y	Repbase	N
HELITRONY3	5166	DNA	Helitron	Helitron	Y	Y	Repbase	Y
HELITRONY3A	3315	DNA	Helitron	Helitron	Y	Y	Repbase	N
LIMPET1	1874	DNA	Other DNA	MuDR	Y	Y	Repbase	N
M65137.1	497	SR	rDNA	NA	Y	Y	GenBank	N
META1_I	4821	RT	LTR RT	Copia	Y	Y	Repbase	Y
META1_LTR	162	RT	LTR RT	Copia	Y	Y	Repbase	Y
MI167_AT	980	Other	Other	NA	N	Y	Repbase	N
RP1_AT	286	DNA	Other DNA	Other	Y	Y	Repbase	Y
Sadhu1-1	884	RT	Non-LTR RT	SADHU	Y	Y	Repbase	N
Sadhu1-2	902	RT	Non-LTR RT	SADHU	N	Y	Repbase	N
Sadhu1-3	902	RT	Non-LTR RT	SADHU	N	Y	Repbase	N
Sadhu10-1	819	RT	Non-LTR RT	SADHU	N	Y	Repbase	Y
Sadhu2-1	876	RT	Non-LTR RT	SADHU	Y	Y	Repbase	N
Sadhu3-1	885	RT	Non-LTR RT	SADHU	N	Y	Repbase	N
Sadhu3-2	884	RT	Non-LTR RT	SADHU	Y	Y	Repbase	N
Sadhu4-1	906	RT	Non-LTR RT	SADHU	N	Y	Repbase	N
Sadhu4-2	869	RT	Non-LTR RT	SADHU	N	Y	Repbase	N
Sadhu5-1	871	RT	Non-LTR RT	SADHU	N	Y	Repbase	Y
Sadhu5-2	770	RT	Non-LTR RT	SADHU	N	Y	Repbase	N
Sadhu6-1	865	RT	Non-LTR RT	SADHU	Y	Y	Repbase	N
Sadhu7-1	886	RT	Non-LTR RT	SADHU	N	N	Repbase	N
Sadhu7-2	869	RT	Non-LTR RT	SADHU	Y	Y	Repbase	N
Sadhu8-1	881	RT	Non-LTR RT	SADHU	N	Y	Repbase	N
Sadhu9-1	1000	RT	Non-LTR RT	SADHU	N	Y	Repbase	N
SIMPLEGUY1	1068	DNA	Other DNA	Harbinger	Y	Y	Repbase	Y
SIMPLEHAT1	1059	DNA	Other DNA	hAT	Y	Y	Repbase	Y
SIMPLEHAT2	1208	DNA	Other DNA	hAT	Y	Y	Repbase	Y

TA1_AT	542	RT	LTR RT	Gypsy	Y	Y	Repbase	N
TA1-2_I	4192	RT	LTR RT	Copia	Y	Y	Repbase	N
TA1-2_LTR	515	RT	LTR RT	Copia	N	Y	Repbase	N
TA11	5976	RT	Non-LTR RT	L1	Y	Y	Repbase	N
TA12	949	RT	Non-LTR RT	L1	Y	Y	Repbase	N
TAG1	3299	DNA	Other DNA	hAT	Y	Y	Repbase	N
TAG2	3094	DNA	Other DNA	hAT	Y	Y	Repbase	N
TAG3N1	754	DNA	Other DNA	hAT	Y	Y	Repbase	Y
TATATATATATA	12	SR	di	NA	N	N	NA	Y
TCATCATCATCA	12	SR	tri	NA	N	N	NA	Y
TCGATCGATCGA	12	SR	tetra	NA	N	N	NA	Y
TGCATGCATGCA	12	SR	tetra	NA	N	N	NA	Y
TNAT1A	609	DNA	Other DNA	Other	Y	Y	Repbase	Y
TNAT2A	771	DNA	Other DNA	Other	Y	Y	Repbase	Y
TSCL	1225	RT	Non-LTR RT	Other	Y	Y	Repbase	N
VANDAL1	15093	DNA	Other DNA	MuDR	Y	Y	Repbase	Y
VANDAL10	12295	DNA	Other DNA	MuDR	Y	Y	Repbase	N
VANDAL11	14166	DNA	Other DNA	MuDR	Y	Y	Repbase	N
VANDAL12	11974	DNA	Other DNA	MuDR	Y	Y	Repbase	N
VANDAL13	12147	DNA	Other DNA	MuDR	Y	Y	Repbase	N
VANDAL14	12268	DNA	Other DNA	VANDAL	N	Y	Repbase	Y
VANDAL15	5332	DNA	Other DNA	VANDAL	Y	Y	Repbase	Y
VANDAL16	10472	DNA	Other DNA	VANDAL	Y	Y	Repbase	Y
VANDAL17	8911	DNA	Other DNA	VANDAL	Y	Y	Repbase	Y
VANDAL18	11260	DNA	Other DNA	VANDAL	Y	Y	Repbase	N
VANDAL18NA	1261	DNA	Other DNA	VANDAL	Y	Y	Repbase	Y
VANDAL18NB	1014	DNA	Other DNA	VANDAL	Y	Y	Repbase	Y
VANDAL1N1	2265	DNA	Other DNA	MuDR	Y	Y	Repbase	Y
VANDAL2	15253	DNA	Other DNA	MuDR	Y	Y	Repbase	Y
VANDAL20	12720	DNA	Other DNA	MuDR	Y	Y	Repbase	N
VANDAL21	8244	DNA	Other DNA	VANDAL	Y	Y	Repbase	Y
VANDAL22	10310	DNA	Other DNA	MuDR	Y	Y	Repbase	N
VANDAL2N1	2712	DNA	Other DNA	MuDR	Y	Y	Repbase	Y

VANDAL3	16666	DNA	Other DNA	MuDR	Y	Y	Repbase	Y
VANDAL4	18492	DNA	Other DNA	MuDR	Y	Y	Repbase	N
VANDAL5	17915	DNA	Other DNA	MuDR	Y	Y	Repbase	Y
VANDAL5A	7727	DNA	Other DNA	MuDR	Y	Y	Repbase	Y
VANDAL6	8390	DNA	Other DNA	MuDR	Y	Y	Repbase	Y
VANDAL7	12362	DNA	Other DNA	MuDR	Y	Y	Repbase	Y
VANDAL8	9577	DNA	Other DNA	MuDR	Y	Y	Repbase	Y
VANDAL9	12396	DNA	Other DNA	MuDR	Y	Y	Repbase	N
VANDALNX1	1728	DNA	Other DNA	VANDAL	N	Y	Repbase	Y

Classes: RT = Retrotransposon, DNA = DNA transposon, SAT = Satellite, SR = Simple Repeat

Table 1.S3 Fisher's exact test p-values for enrichment test for significant SNPs in pericentromere and centromere

ID	P value
18S_At3	1
25S_At3	0.81
45S_At3	1
5.8S_At3	1
AAAAATAAAAAT	0
AAACCCAAACCC	0
AAAGCAAAGCAA	1
AAAGCCAAAGCC	0
AAAGGCAAAGGC	0
AAAGGGAAAGGG	1
AAATCCAAATCC	0.22
AAATGCAAATGC	0.05
AACCCAACCCAA	0
AACCCCAACCCC	0
AAGCCAAGCCAA	0.08
AAGGGAAGGGAA	0.11
AAGGGCAAGGGC	0.98
AATCCCAATCCC	0
AATGCAATGCAA	0
AATGCCAATGCC	1
AATGGAATGGAA	0
AATTCCAATTCC	0.59
AATTGAATTGAA	0
AATTGCAATTGC	0
ACCCCACCCCAC	0
ACCCCCACCCCC	0.96
AGAGAGAGAGAG	1
AGCTAGCTAGCT	0.96
AGGCCCAGGCCC	1
AGGGGCAGGGGC	1
AR12	0
AR3	0
ARNOLD1	0
ARNOLD2	0
ARNOLD3	0
ARNOLD4	0
ARNOLDY1	0.47
ARNOLDY2	0.73
AT10MU1	0
ATCCCATCCCAT	0.83
ATCGATCGATCG	1
ATCLUST1	0.87
ATCOPI1_I	1
ATCOPI1_LTR	1
ATCOPIA11LTR	0
ATCOPIA13I	0
ATCOPIA18LTR	0
ATCOPIA20I	0
ATCOPIA20LTR	0
ATCOPIA21I	0
ATCOPIA22LTR	1
ATCOPIA23_LTR	1
ATCOPIA25LTR	1
ATCOPIA26I	0
ATCOPIA27_I	0
ATCOPIA27_LTR	0
ATCOPIA2I	0
ATCOPIA2LTR	0
ATCOPIA31_I	0.99
ATCOPIA31_LTR	1
ATCOPIA31A_LTR	0.98
ATCOPIA32_LTR	0
ATCOPIA33_LTR	0
ATCOPIA34_LTR	0
ATCOPIA36_I	0.1
ATCOPIA36_LTR	1
ATCOPIA3I	0.02
ATCOPIA40_LTR	0.11
ATCOPIA41I	0
ATCOPIA41LTR	0
ATCOPIA43LTR	0
ATCOPIA45_I	1
ATCOPIA48LTR	1
ATCOPIA49_I	0
ATCOPIA49LTR	0.29
ATCOPIA4I	0.56
ATCOPIA4LTR	1
ATCOPIA51_I	0.69
ATCOPIA52_I	0.65
ATCOPIA52LTR	0.88
ATCOPIA54LTR	0
ATCOPIA56_I	0
ATCOPIA56LTR	0
ATCOPIA57LTR	0.98
ATCOPIA58_I	0
ATCOPIA58LTR	0
ATCOPIA5LTR	1
ATCOPIA62LTR	0
ATCOPIA63LTR	1

ATCOPIA65A_I	1
ATCOPIA6I	0
ATCOPIA6LTR	0.92
ATCOPIA71LTR	1
ATCOPIA72_I	0.7
ATCOPIA72LTR	0
ATCOPIA74LTR	1
ATCOPIA75_I	1
ATCOPIA76LTR	1
ATCOPIA78_I	0
ATCOPIA78LTR	1
ATCOPIA83_I	1
ATCOPIA83LTR	1
ATCOPIA87LTR	0
ATCOPIA89LTR	1
ATCOPIA8BLTR	1
ATCOPIA93LTR	0
ATCOPIA95_I	0
ATCOPIA95LTR	0
ATCOPIA97LTR	1
ATCOPIA9LTR	0
ATDNA2T9A	0.99
ATDNA2T9B	0.97
ATDNA2T9C	0.98
ATDNAI26T9	0.98
ATDNAI27T9A	1
ATDNAI27T9B	0
ATDNATA1	0.4
ATENSAT1	0
ATENSAT2	0
ATENSPM1	0.04
ATENSPM1A	0
ATENSPM2	0
ATENSPM6	0
ATENSPM9	0
ATGGCCATGGCC	0.95
ATGGGGATGGGG	1
ATGP10_I	0
ATGP10LTR	0
ATGP11_I	0
ATGP11_LTR	0
ATGP1LTR	0.03
ATGP2I	0.98
ATGP2LTR	0.77
ATGP2N_I	1
ATGP2NLTR	0.77
ATGP3B_I	0
ATGP3B_LTR	0

ATGP4_I	0
ATGP4_LTR	0
ATGP5A_I	0
ATGP5A_LTR	0
ATGP5LTR	0
ATGP6I	0
ATGP6LTR	0
ATGP8I	0
ATGP8LTR	0
ATGP9BI	0
ATGP9BLTR	0
ATGP9LTR	0
ATHAT1	0
ATHATN1	0.87
ATHATN10	0.26
ATHATN2	0
ATHATN3	0.24
ATHATN3A	0.77
ATHATN4	0.64
ATHATN5	0.96
ATHATN7	0.67
ATHILA_I	0
ATHILA_LTR	0
ATHILA0_I	0
ATHILA3_I	0
ATHILA3_LTR	0
ATHILA4_LTR	0.4
ATHILA4A_I	0
ATHILA4A_LTR	0.96
ATHILA4B_LTR	1
ATHILA4C_I	0
ATHILA4C_LTR	0
ATHILA4D_I	0
ATHILA4D_LTR	0
ATHILA5_I	0
ATHILA5_LTR	0
ATHILA6A_I	0
ATHILA6A_LTR	0
ATHILA6B_I	0
ATHILA6C_I	0
ATHILA6C_LTR	0
ATHILA7LTR	0
ATHILA8A_I	0
ATHILA8ALTR	0
ATHILA8BLTR	0
ATHPOGON1	1
ATHPOGON2	0.99
ATHPOGON3	0.99

ATLANTYS2_I	0
ATLANTYS2_LTR	0
ATLANTYS3I	0.95
ATLANTYS3LTR	0.1
ATLINE1_1	1
ATLINE1_12	1
ATMSAT1	0
ATMUN1	1
ATMUN2	1
ATMUNX1	0.65
ATN9_1	0.01
ATRE1_I	0
ATRE1_LTR	0
ATREP1	0.97
ATREP10	0.37
ATREP10A	0.49
ATREP10B	0.59
ATREP10C	0.45
ATREP10D	0.85
ATREP11	0.61
ATREP11A	0.12
ATREP13	0.95
ATREP14	1
ATREP15	0.03
ATREP16	1
ATREP17	1
ATREP18	0
ATREP2	1
ATREP20	1
ATREP21	0.63
ATREP2A	0.98
ATREP3	1
ATREP4	0.16
ATREP5	1
ATREP6	0.98
ATREP7	0.55
ATREP8	0.98
ATREP9	0.54
ATREPX1	0.91
ATSAA5	0
ATSAB5	0
ATSAT5	0
AtSB2	0.94
AtSB3	0.65
AtSB5	0
AtSB6	0.63
ATTGGCATTGGC	0.94
ATTGGGATTGGG	0

ATTIR16T3A	0.87
ATTIRTA1	1
ATTIRX1C	0.93
ATTIRX1D	1
ATTTCCATTTCC	0
BOMZH2	0.36
BRODYAGA2	1
CASTOR_I	0
CEN_Cluster1_cons	0
CEN_Cluster3_cons	0
CEN_Cluster4_cons	0
CEN_Cluster5_cons	0
CEN_Cluster6_cons	0
CGCGCGCGCGCG	0.99
COLAR12	0
Copia-2_AT-I	1
Copia-2_AT-LTR	1
Copia-35_AT-I	0
Copia-35_AT-LTR	0
CTAGCTAGCTAG	0
DT1	0.75
ENDOVIR1_I	0.98
ENDOVIR1LTR	1
GAGAGAGAGAGA	1
GATCGATCGATC	0
GCCCCGCCCCGC	0.08
GCGCGCGCGCGC	1
GCTAGCTAGCTA	0.33
GGGCCCGGGCCC	0.45
GTACGTACGTAC	1
Gypsy-15_AT-I	0.99
Gypsy-15_AT-LTR	1
HELITRONY1A	1
HELITRONY1B	0.34
HELITRONY1D	0.46
HELITRONY1E	0.39
HELITRONY3	0.99
M65137.1	0
RP1_AT	0.8
Sadhu10-1	1
Sadhu5-1	1
TAG1	1
TAG3N1	0.2
TNAT1A	0.72
TNAT2A	1
VANDAL1	0
VANDAL14	0.28
VANDAL15	0.5

VANDAL16	0.88
VANDAL17	0
VANDAL18NB	0.26
VANDAL21	0
VANDAL5	0

VANDAL5A	0
VANDAL6	0
VANDAL7	0
VANDAL8	0
VANDALNX1	0

Table 1.S4 Proportion of significant SNPs in centromere and pericentromere

ID	Cent_1	Cent_2	Cent_3	Cent_4	Cent_5
AAAAATAAAAAT	0	0.70	0.30	0	0
AAACCCAAACCC	0	0	0	1	0
AAAGCCAAAGCC	1	0	0	0	0
AAAGGCAAAGGC	1	0	0	0	0
AACCCAACCCAA	0	0	0	0	1
AACCCCAACCCC	1	0	0	0	0
AATCCCAATCCC	0	0	0.96	0.04	0
AATGCAATGCAA	0	0	0	0.56	0.43
AATTGAATTGAA	0	0	1	0	0
AATTGCAATTGC	1	0	0	0	0
ACCCCACCCCAC	0.96	0	0	0.04	0
AR12	0	0	0	1	0
AR3	0.46	0	0.54	0	0
ARNOLD1	0	0.26	0.69	0.06	0
ARNOLD2	0	0.21	0.74	0.05	0
ARNOLD3	0	0.29	0.71	0	0
ARNOLD4	0	0.29	0.71	0	0
ATCOPIA11LTR	0	0	0	0.07	0.93
ATCOPIA13I	0	1	0	0	0
ATCOPIA18LTR	0	1	0	0	0
ATCOPIA20I	0.68	0.30	0	0.01	0
ATCOPIA20LTR	0.77	0.23	0	0	0
ATCOPIA21I	0.22	0.78	0	0	0
ATCOPIA26I	0.02	0.14	0.79	0.04	0.01
ATCOPIA27_I	0.03	0.02	0	0.04	0.90
ATCOPIA27_LTR	0	0.01	0	0.03	0.96
ATCOPIA2I	0	0.29	0.71	0	0
ATCOPIA2LTR	0	0.14	0.86	0	0
ATCOPIA32_LTR	0.05	0.95	0	0	0
ATCOPIA33_LTR	0	1	0	0	0
ATCOPIA34_LTR	0	0.19	0.50	0.28	0.03
ATCOPIA41I	0	1	0	0	0
ATCOPIA41LTR	0	1	0	0	0
ATCOPIA43LTR	0	0	0.04	0.96	0
ATCOPIA54LTR	0	0	0	1	0
ATCOPIA56_I	0	0.20	0.29	0.13	0.37
ATCOPIA56LTR	0	0.32	0	0.27	0.41
ATCOPIA58_I	0	0.05	0.77	0.18	0
ATCOPIA58LTR	0	0.11	0.68	0.21	0
ATCOPIA62LTR	0	0	1	0	0
ATCOPIA6I	0	0.96	0	0	0.04
ATCOPIA78_I	1	0	0	0	0
ATCOPIA87LTR	0	0	0	0.57	0.43
ATCOPIA93LTR	1	0	0	0	0
ATCOPIA95_I	0.36	0.50	0.03	0.11	0

ATCOPIA95LTR	0.86	0	0.07	0.07	0
ATCOPIA9LTR	0	0.43	0	0.57	0
ATDNAI27T9B	0	0	0	0	1
ATENSAT1	0	0	0	1	0
ATENSAT2	0	0	0	1	0
ATENSPM1A	0	1	0	0	0
ATENSPM2	0.86	0	0	0.14	0
ATENSPM6	0.03	0.97	0	0	0
ATENSPM9	1	0	0	0	0
ATGP10_I	0.37	0	0.63	0	0
ATGP10LTR	0	0	1	0	0
ATGP11_I	0	0.32	0	0.68	0
ATGP11_LTR	0.07	0.93	0	0	0
ATGP3B_I	0	0.55	0	0	0.45
ATGP3B_LTR	0	0	0	0	1
ATGP4_I	0	0.65	0	0.25	0.10
ATGP4_LTR	0	0	0	0	1
ATGP5A_I	0	0.01	0.28	0.19	0.51
ATGP5A_LTR	0	0.01	0.41	0.25	0.33
ATGP5LTR	0	0	0.47	0.07	0.46
ATGP6I	0.02	0.23	0.05	0.71	0
ATGP6LTR	0.01	0.20	0.08	0.71	0
ATGP8I	0	0	0.19	0.01	0.80
ATGP8LTR	0	0.02	0.09	0.02	0.87
ATGP9BI	0	0	0	0	1
ATGP9BLTR	0	0	0	0	1
ATGP9LTR	0	0	0	0	1
ATHAT1	0	0.03	0.11	0.86	0
ATHILA_I	0	0	0.41	0.39	0.20
ATHILA_LTR	0	0	0.61	0.33	0.06
ATHILA0_I	0.31	0.66	0	0.03	0
ATHILA3_I	0	0	0	0.97	0.03
ATHILA3_LTR	0	0	0	0.90	0.10
ATHILA4C_I	0	0	0	0.80	0.19
ATHILA4C_LTR	0.01	0	0	0.54	0.45
ATHILA4D_I	0	0.62	0	0.18	0.20
ATHILA4D_LTR	0.11	0.80	0	0.02	0.07
ATHILA5_I	0	0	0.98	0.01	0.01
ATHILA5_LTR	0	0	0.99	0.01	0
ATHILA6A_I	0	0	0.05	0	0.95
ATHILA6A_LTR	0	0	0.03	0	0.97
ATHILA6B_I	0	0	0.01	0	0.99
ATHILA6C_I	0.44	0.37	0	0.01	0.19
ATHILA6C_LTR	0.15	0	0.85	0	0
ATHILA7LTR	0	0.89	0	0	0.11
ATHILA8A_I	0.75	0	0	0.08	0.17
ATHILA8ALTR	0	0	0	1	0
ATHILA8BLTR	0	0	0	0	1

ATLANTYS2_I	0	0	1	0	0
ATLANTYS2_LTR	0.24	0	0.72	0.04	0.01
ATMSAT1	0	1	0	0	0
ATRE1_I	0	0	0	1	0
ATRE1_LTR	0	0	0	1	0
ATREP18	1	0	0	0	0
ATSAA5	0	0	0	0	1
ATSAB5	0	0	0	0	1
ATSAT5	0	0	0	0	1
AtSB5	0	1	0	0	0
ATTGGGATTGGG	0	0	1	0	0
ATTTCCATTTCC	0	0	1	0	0
CASTOR_I	0.61	0.39	0	0	0
CEN_Cluster1_cons	0.26	0.19	0.26	0.07	0.22
CEN_Cluster3_cons	0	0	0	1	0
CEN_Cluster4_cons	0.27	0.21	0.26	0.06	0.20
CEN_Cluster5_cons	0.99	0	0	0	0
CEN_Cluster6_cons	0.98	0.01	0	0.01	0
COLAR12	0	0.01	0.01	0.97	0.01
Copia-35_AT-I	0.61	0	0.39	0	0
Copia-35_AT-LTR	0.09	0	0.91	0	0
GATCGATCGATC	1	0	0	0	0
VANDAL1	0	0.23	0.23	0	0.54
VANDAL17	0	0	1	0	0
VANDAL21	0	1	0	0	0
VANDAL5	0	0.03	0.18	0.09	0.71
VANDAL5A	0	0	0.49	0.09	0.42
VANDAL6	0	0.82	0.18	0	0
VANDAL7	0	0.09	0.35	0.56	0
VANDAL8	0	0	0	1	0
VANDALNX1	0.95	0	0	0.05	0

Table 1.S5 Enriched gene ontology terms for loci within 10 KB of SNPs focal in all 3 meta-GWA

GO.ID	Term	Annotated	Significant	Expected	P value	Enrichment
GO:0006782	protoporphyrinogen IX biosynthetic process	15	4	0.41	0058	3.24
GO:0006468	protein phosphorylation	1132	43	30.75	0220	2.66
GO:0009554	megasporogenesis	12	3	0.33	0365	2.44
GO:0044237	cellular metabolic process	9720	281	264.01	0636	2.20
GO:0030148	sphingolipid biosynthetic process	41	5	1.11	0852	2.07
GO:0033260	nuclear DNA replication	16	3	0.43	0858	2.07
GO:0006271	DNA strand elongation involved in DNA replication	16	3	0.43	0858	2.07
GO:0002221	pattern recognition receptor signaling pathway	16	3	0.43	0858	2.07
GO:0045087	innate immune response	371	13	10.08	0.01042	1.98
GO:0048544	recognition of pollen	50	5	1.36	0.01126	1.95
GO:0006807	nitrogen compound metabolic process	8206	249	222.89	0.01626	1.79
GO:0042761	very long-chain fatty acid biosynthetic process	21	3	0.57	0.01842	1.73
GO:0010286	heat acclimation	58	5	1.58	0.02043	1.69
GO:0006672	ceramide metabolic process	27	3	0.73	0.02864	1.54
GO:0030149	sphingolipid catabolic process	10	2	0.27	0.02868	1.54
GO:0071456	cellular response to hypoxia	239	12	6.49	0.03081	1.51
GO:0010582	floral meristem determinacy	26	3	0.71	0.03261	1.49
GO:0000338	protein deneddylation	11	2	0.3	0.03444	1.46
GO:0006621	protein retention in ER lumen	11	2	0.3	0.03444	1.46
GO:0031930	mitochondria-nucleus signaling pathway	11	2	0.3	0.03444	1.46
GO:0080147	root hair cell development	99	5	2.69	0.03595	1.44
GO:0001731	formation of translation preinitiation complex	12	2	0.33	0.04059	1.39
GO:0043486	histone exchange	12	2	0.33	0.04059	1.39
GO:0006122	mitochondrial electron transport, ubiquinol to cytochrome c	12	2	0.33	0.04059	1.39
GO:0009414	response to water deprivation	398	17	10.81	0.04285	1.37

GO:0010262	somatic embryogenesis	13	2	0.35	0.04713	1.33
GO:0044092	negative regulation of molecular function	133	4	3.61	0.04731	1.33
GO:0050801	ion homeostasis	291	7	7.9	0.04766	1.32
GO:0009056	catabolic process	1529	32	41.53	0.04885	1.31

Table 1.S6 Loci associated in multiple meta-GWA

SNP ID	Minor	Major	MAF	Chr	Start	End	Classes	Candidate
1:76313	A	G	0.209	1	62906	95120	RT,SR	
1:241262	G	A	0.015	1	227796	248701	RT,DNA	AT1G01690
1:2258053	T	C	0.042	1	2238867	2272685	RT,DNA,SR	AT1G07370
1:3088050	T	C	0.025	1	3070179	3107842	DNA,SR	
1:3231112	G	C	0.029	1	3211150	3250169	RT,DNA,SR	
1:3304695	G	A	0.026	1	3288658	3321865	RT,DNA,SR	
1:4566906	T	A	0.144	1	4546926	4581449	RT,DNA	AT1G13330
1:4950329	T	A	0.077	1	4932942	4969207	RT,DNA,SR	AT1G14460
1:5309667	T	C	0.024	1	5291077	5329404	RT,DNA,SR	
1:5739467	A	T	0.354	1	5727989	5759137	RT,DNA	
1:6709908	T	G	0.049	1	6689992	6709908	RT,DNA,SR	
1:7347556	C	T	0.011	1	7343297	7347556	RT,DNA	
1:8187625	A	G	0.026	1	8168557	8203974	RT,DNA	
1:8618647	T	G	0.013	1	8599419	8635321	RT,DNA,SR	
1:8733780	C	T	0.036	1	8714506	8733793	RT,DNA	
1:9103927	C	T	0.011	1	9089436	9120907	RT,DNA	
1:9182192	T	G	0.012	1	9167429	9201730	RT,DNA	
1:9244929	A	G	0.01	1	9226389	9254799	RT,DNA	
1:10369395	T	C	0.02	1	10354051	10384075	DNA,SR	
1:10493327	C	G	0.03	1	10473645	10510516	RT,DNA,SR	
1:10583180	A	G	0.026	1	10576673	10585507	RT,DNA	
1:10601940	A	G	0.035	1	10582206	10618749	RT,DNA	
1:10653576	T	C	0.021	1	10633693	10673336	DNA,SR	
1:11905849	A	G	0.012	1	11886170	11923833	RT,DNA	
1:11975957	C	T	0.013	1	11967293	11993027	RT,DNA,SR	
1:12031437	T	A	0.012	1	12014686	12047473	DNA,SR	
1:12206558	A	G	0.01	1	12187278	12221492	RT,DNA,SR	
1:12259542	A	T	0.012	1	12243144	12270264	RT,DNA	
1:12278987	A	C	0.012	1	12260750	12286307	RT,DNA,SR	
1:13145601	G	T	0.011	1	13131296	13163879	RT,DNA	
1:13288090	G	A	0.011	1	13282464	13306541	RT,DNA	

1:14010281	G	C	0.021	1	13994064	14027154	RT,DNA,SR	
1:14278144	T	C	0.011	1	14275772	14281511	RT,DNA	
1:15917161	T	C	0.038	1	15898084	15935543	RT,DNA,SR	
1:16460839	T	C	0.064	1	16447448	16466294	RT,DNA	
1:16507351	G	A	0.013	1	16487789	16509398	RT,DNA	
1:16850163	T	G	0.011	1	16832215	16869130	RT,DNA	
1:16837549	A	T	0.013	1	16836933	16852959	RT,DNA,SR	
1:18037548	A	T	0.076	1	18018559	18054194	RT,SR	
1:18078920	T	A	0.092	1	18059475	18098828	RT,SR	
1:18106920	T	C	0.011	1	18089697	18123521	RT,DNA,SR	
1:18176289	T	A	0.012	1	18164124	18192562	RT,DNA,SR	
1:18223101	A	G	0.011	1	18216002	18223101	RT,DNA,SR	AT1G49250
1:18280742	A	G	0.011	1	18274161	18280742	RT,SR	
1:18319299	G	C	0.011	1	18313981	18319299	RT,DNA,SR	
1:18699009	T	C	0.012	1	18679844	18707798	RT,DNA,SR	AT1G50410
1:18807598	G	A	0.029	1	18787832	18824504	RT,DNA	
1:18822307	T	C	0.013	1	18803063	18842103	RT,DNA,SR	AT1G50840
1:18882244	G	T	0.012	1	18864872	18898274	RT,DNA,SR	
1:18985974	T	C	0.011	1	18978989	18990984	RT,SR	
1:19025674	A	G	0.011	1	19019278	19045501	RT,SR	AT1G51355
1:19034793	G	A	0.025	1	19020723	19052110	RT,DNA,SR	
1:19079755	G	T	0.02	1	19066088	19097418	RT,DNA,SR	AT1G51450
1:19169340	C	T	0.015	1	19151073	19187540	RT,DNA,SR	
1:19238002	T	C	0.018	1	19230629	19244398	RT,DNA,SR	
1:19270100	A	T	0.023	1	19270100	19274479	RT,DNA	
1:19332352	G	T	0.012	1	19332352	19334565	RT,DNA,SR	
1:19436244	A	G	0.011	1	19423873	19443104	RT,SR	
1:19545145	A	T	0.017	1	19527855	19562193	RT,DNA,SR	AT1G52500
1:19690981	A	T	0.056	1	19671812	19710545	RT,DNA	
1:19758847	G	A	0.026	1	19739943	19778004	RT,DNA,SR	AT1G52990
1:21362733	G	A	0.013	1	21344585	21381438	DNA,SR	
1:21415238	A	G	0.013	1	21404267	21415238	DNA,SR	AT1G57820
1:22072139	G	A	0.013	1	22052326	22090592	RT,DNA,SR	
1:22661361	C	T	0.022	1	22645809	22679677	RT,DNA,SR	AT1G61410

1:23131666	G	A	0.062	1	23117775	23141102	RT,DNA	
1:23175924	C	A	0.029	1	23158820	23193109	RT,DNA,SR	
1:23305482	C	T	0.025	1	23286156	23323584	DNA,SR	AT1G62886
1:24114276	G	T	0.012	1	24109712	24133542	RT,SR	
1:25367176	T	C	0.028	1	25349624	25386683	RT,DNA	
1:26234197	A	C	0.011	1	26217646	26250616	RT,DNA,SR	A1G69690
1:26257074	C	G	0.033	1	26240534	26275148	RT,DNA,SR	AT1G69770
1:26304175	G	T	0.021	1	26284929	26322800	RT,DNA,SR	
1:26300526	A	G	0.017	1	26284929	26305858	RT,DNA	
1:26322840	T	G	0.021	1	26305858	26342493	RT,DNA,SR	
1:26360505	G	C	0.018	1	26342252	26377703	RT,DNA,SR	
1:26410726	A	G	0.02	1	26391336	26428866	RT,DNA	
1:26455954	T	G	0.02	1	26437143	26475450	RT,DNA	
1:26685140	A	G	0.065	1	26666621	26704401	RT,DNA	
1:26879257	G	A	0.084	1	26867008	26886642	RT,DNA	AT1G71260
1:27481441	T	C	0.011	1	27474210	27497963	RT,DNA	
1:27560902	T	G	0.027	1	27542300	27575762	RT,DNA	
1:28458773	A	T	0.032	1	28440863	28473387	DNA,SR	
1:28594205	T	A	0.033	1	28577787	28608236	RT,DNA,SR	
1:28630032	T	C	0.034	1	28620225	28630032	RT,DNA,SR	
1:28674712	A	G	0.048	1	28659812	28692002	RT,DNA	
1:28698938	C	A	0.03	1	28679297	28718358	RT,DNA	AT1G76440
1:28719307	G	A	0.032	1	28699380	28738831	RT,DNA	
1:28952249	T	G	0.026	1	28932428	28952249	RT,DNA,SR	
1:28974054	T	A	0.023	1	28974054	28977799	RT,DNA,SR	
1:29002503	A	G	0.023	1	29002503	29008044	RT,DNA,SR	
1:29093335	T	A	0.017	1	29077078	29102608	RT,DNA,SR	
1:29157988	A	G	0.062	1	29141679	29177222	RT,DNA,SR	AT1G77600
1:29181570	G	A	0.069	1	29167049	29195854	RT,DNA	
1:29905689	C	T	0.067	1	29886988	29923899	DNA,SR	
1:19305855	A	G	0.012	1	19305855	19305855	RT,DNA	
1:25645494	C	T	0.011	1	25645494	25645494	RT,DNA	
1:12749562	C	G	0.011	1	12749562	12749562	RT,DNA,SR	AT1G34770
1:14225388	T	G	0.012	1	14225388	14225388	RT,DNA,SR	

2:607389	A	T	0.011	2	606872	608072	RT,DNA	
2:1294500	T	C	0.014	2	1278080	1314232	RT,DNA	
2:1358129	C	T	0.013	2	1339579	1363713	RT,DNA	
2:1400578	G	T	0.044	2	1382950	1416081	RT,DNA	
2:1624836	TA	T	0.011	2	1624831	1625883	RT,SR	
2:2034457	C	T	0.011	2	2034457	2038687	DNA,SR	
2:2060726	A	G	0.012	2	2054583	2069857	RT,DNA	
2:2183825	G	T	0.013	2	2183825	2190849	DNA,SR	
2:2260838	G	A	0.017	2	2260838	2270178	DNA,SR	
2:2580914	A	G	0.013	2	2562265	2586064	RT,DNA	AT2G06510
2:2995161	A	G	0.015	2	2977076	2995161	RT,DNA,SR	
2:4830692	T	C	0.063	2	4810977	4849593	RT,SR	
2:5772191	A	T	0.016	2	5767642	5789915	RT,DNA	
2:6016565	A	G	0.012	2	5996588	6019066	RT,DNA	
2:6022790	A	C	0.03	2	6022384	6041489	RT,DNA	
2:6212583	G	C	0.014	2	6198001	6229967	RT,DNA	AT2G14540
2:6305702	T	C	0.013	2	6300698	6325147	RT,SR	
2:6361770	T	C	0.012	2	6359656	6377347	RT,DNA,SR	
2:6647687	A	G	0.013	2	6638695	6664957	RT,DNA	
2:6714177	T	A	0.012	2	6698866	6732862	RT,DNA,SR	AT2G15400
2:7548775	A	G	0.044	2	7531059	7561219	RT,DNA	
2:7690375	A	G	0.011	2	7690375	7707586	RT,DNA,SR	
2:8898759	A	G	0.033	2	8898759	8911158	RT,SR	
2:8995807	C	G	0.031	2	8978763	9012134	RT,SR	AT2G20980
2:9202914	A	G	0.046	2	9184218	9222668	RT,SR	AT2G21450
2:9592884	A	G	0.018	2	9573066	9611472	RT,DNA,SR	
2:9882413	A	C	0.014	2	9863420	9894170	RT,DNA	
2:9911192	C	T	0.013	2	9894170	9912324	RT,DNA	
2:10374711	A	G	0.015	2	10355714	10382269	RT,DNA	
2:10795893	C	A	0.033	2	10777899	10796158	RT,DNA	
2:10803367	T	C	0.011	2	10803367	10819677	RT,DNA	AT2G25360
2:11096053	A	T	0.013	2	11080769	11096054	RT,SR	
2:11108360	G	C	0.018	2	11093205	11126714	RT,DNA	
2:11564680	T	C	0.012	2	11557956	11579602	RT,DNA	

2:11845993	C	G	0.022	2	11832733	11859329	DNA,SR	
2:12641939	G	T	0.021	2	12626731	12650745	DNA,SR	AT2G29570
2:12687596	G	T	0.02	2	12669305	12704061	DNA,SR	AT2G29680
2:12923473	C	G	0.025	2	12903554	12942472	RT,DNA,SR	AT2G30280
2:14228762	C	G	0.019	2	14219320	14243367	RT,DNA,SR	AT2G33640
2:15236838	T	G	0.044	2	15220691	15255732	RT,DNA,SR	
2:16014238	C	A	0.06	2	15994345	16032390	RT,DNA	
2:16078180	G	A	0.011	2	16078180	16089402	RT,DNA	
2:16606937	T	A	0.042	2	16606937	16622892	RT,DNA	
2:17061948	C	T	0.04	2	17046243	17079822	RT,DNA,SR	
2:17265036	T	C	0.013	2	17251627	17283098	RT,DNA,SR	AT2G41460
2:17294955	T	C	0.012	2	17280925	17301780	DNA,SR	AT2G41460
2:17669397	G	T	0.011	2	17667460	17688881	RT,SR	
2:17806720	A	G	0.017	2	17789983	17817534	RT,DNA	
2:17834472	T	G	0.013	2	17817534	17837579	RT,SR	
2:17916129	T	C	0.015	2	17897808	17928712	RT,DNA,SR	
2:18019384	A	T	0.012	2	18001644	18034341	RT,DNA	
2:18564650	T	C	0.024	2	18545490	18581500	RT,DNA	
2:18721683	G	C	0.026	2	18706077	18732453	RT,DNA	
2:19031592	C	T	0.012	2	19012063	19042132	RT,DNA,SR	
2:19376913	A	G	0.02	2	19357275	19393615	RT,DNA,SR	AT2G47210
2:19400348	T	A	0.019	2	19383289	19419503	RT,DNA	
2:16619477	T	C	0.02	2	16619477	16619477	RT,SR	AT2G39830
3:213319	C	G	0.068	3	201568	231580	RT,SR	
3:832376	C	T	0.012	3	812456	844647	RT,DNA	
3:1243127	C	G	0.011	3	1232801	1263026	RT,DNA	
3:1974111	C	A	0.273	3	1954680	1991150	RT,DNA,SR	
3:2020135	A	C	0.07	3	2000761	2038961	RT,SR	
3:2415720	G	A	0.024	3	2407824	2432403	RT,DNA	AT3G07610
3:3034610	A	G	0.027	3	3014773	3053766	RT,DNA	
3:3055283	C	A	0.064	3	3035723	3075252	RT,DNA,SR	
3:3277836	A	T	0.027	3	3257979	3296572	RT,DNA	AT3G10525
3:3535648	A	G	0.033	3	3526557	3554513	RT,DNA,SR	
3:3579102	T	G	0.019	3	3571597	3590592	RT,DNA,SR	

3:3619259	C	A	0.019	3	3599370	3633049	RT,SR	
3:3723049	A	G	0.018	3	3705834	3727277	RT,SR	AT3G11770
3:4079946	C	A	0.02	3	4060785	4095486	RT,DNA,SR	
3:4209710	T	C	0.063	3	4189727	4228131	RT,DNA,SR	
3:4555488	G	C	0.018	3	4549458	4556640	RT,DNA,SR	
3:4634563	T	C	0.065	3	4616320	4652813	RT,DNA,SR	
3:5377114	T	A	0.011	3	5366504	5386441	RT,DNA	
3:6239853	A	T	0.013	3	6220659	6258615	RT,DNA	
3:6292094	G	A	0.013	3	6273524	6296391	RT,DNA,SR	
3:7002570	A	G	0.031	3	6989124	7020149	DNA,SR	
3:7535685	G	C	0.012	3	7515866	7541426	RT,SR	
3:7586182	T	C	0.011	3	7572697	7588935	RT,SR	
3:7700021	G	T	0.011	3	7683157	7715899	RT,DNA	
3:7898709	A	G	0.011	3	7895042	7912316	RT,DNA,SR	
3:7941756	G	A	0.012	3	7928006	7941846	DNA,SR	
3:9003354	T	A	0.014	3	9003354	9004094	RT,DNA,SR	
3:9035511	T	C	0.011	3	9030845	9051009	RT,DNA	
3:9058583	G	A	0.018	3	9044701	9064145	RT,DNA,SR	AT3G24810
3:9128095	A	C	0.014	3	9127516	9132368	RT,DNA,SR	
3:9158855	T	A	0.016	3	9139278	9171686	RT,DNA,SR	AT3G25100
3:9198031	A	G	0.02	3	9185136	9216390	DNA,SR	AT3G25270
3:9223726	G	A	0.012	3	9204090	9225964	RT,DNA,SR	AT3G25270
3:9249465	T	G	0.012	3	9246243	9257006	RT,DNA,SR	
3:9265714	T	C	0.24	3	9250910	9271653	RT,DNA	
3:9276255	A	G	0.025	3	9258686	9296117	RT,DNA,SR	
3:10804681	T	C	0.07	3	10785308	10824323	RT,DNA	
3:11242146	A	G	0.019	3	11225791	11261181	RT,DNA	
3:11268014	A	G	0.02	3	11260086	11278805	RT,DNA,SR	
3:11532253	T	G	0.012	3	11513409	11549886	RT,SR	
3:14112390	A	G	0.012	3	14093496	14117256	RT,DNA	
3:14900288	G	T	0.016	3	14881057	14920078	RT,SR	
3:15395193	A	G	0.013	3	15379839	15404746	RT,DNA	
3:15662430	A	T	0.013	3	15656123	15663296	RT,DNA	
3:16831631	A	T	0.012	3	16817411	16836872	RT,DNA	

3:17344176	G	T	0.017	3	17325386	17354518	RT,DNA,SR	
3:18940486	T	G	0.013	3	18935010	18958913	RT,DNA,SR	
3:18994145	A	C	0.049	3	18977688	19011591	RT,DNA,SR	
3:19063521	A	G	0.011	3	19063521	19073543	RT,SR	
3:19699451	T	A	0.013	3	19699439	19702974	RT,DNA,SR	
3:19768072	T	G	0.013	3	19751449	19773255	RT,DNA,SR	
3:19817199	A	C	0.011	3	19803801	19819062	RT,DNA	
3:20269213	G	A	0.026	3	20254643	20286389	RT,DNA	AT3G54760
3:20336718	T	G	0.025	3	20316779	20355165	RT,DNA	
3:20365685	G	A	0.016	3	20347292	20385582	RT,DNA	
3:20838143	T	C	0.039	3	20820798	20857425	RT,DNA	
3:22956248	T	C	0.012	3	22938461	22959576	RT,DNA,SR	
3:23004330	C	T	0.011	3	22993755	23016057	RT,DNA,SR	
3:23047402	A	G	0.015	3	23028138	23051386	RT,DNA,SR	
3:23093410	T	C	0.017	3	23093410	23100192	RT,SR	
3:23152265	T	C	0.013	3	23136572	23164902	RT,DNA,SR	
3:7865129	A	C	0.017	3	7865129	7865129	RT,DNA	
3:8932720	A	C	0.017	3	8932720	8932720	RT,SR	
3:9154970	G	A	0.013	3	9154970	9154970	RT,DNA,SR	
4:244511	C	A	0.014	4	242714	255477	DNA,SR	
4:582977	G	A	0.033	4	565535	598046	RT,SR	
4:899276	A	G	0.01	4	879404	918891	RT,DNA	AT4G02060
4:974970	C	T	0.016	4	968907	989232	RT,DNA	
4:1080513	T	G	0.139	4	1060515	1093922	RT,SR	AT4G02460
4:1111463	A	G	0.013	4	1093516	1112681	RT,SR	
4:2042003	A	T	0.029	4	2022858	2048135	RT,DNA,SR	
4:2283154	G	A	0.011	4	2263389	2300801	RT,DNA	
4:2282882	C	T	0.03	4	2273571	2300276	DNA,SR	
4:2527274	G	A	0.031	4	2508068	2546737	DNA,SR	AT4G04957
4:2628940	C	A	0.058	4	2611630	2639474	RT,DNA	
4:2916831	C	G	0.011	4	2899623	2919152	RT,DNA,SR	
4:3382145	A	G	0.03	4	3364877	3385677	RT,DNA	
4:4202674	T	A	0.228	4	4186597	4204687	RT,DNA	
4:4869393	G	C	0.022	4	4860246	4879683	RT,DNA,SR	

4:5251754	T	C	0.029	4	5233065	5270416	RT,DNA,SR	
4:5603298	C	T	0.073	4	5592302	5623220	RT,DNA,SR	
4:5648561	C	G	0.021	4	5646191	5655413	RT,DNA	
4:6526825	A	C	0.016	4	6521003	6542761	RT,DNA,SR	
4:7753711	T	C	0.012	4	7753472	7767273	RT,DNA,SR	
4:8487923	A	T	0.011	4	8468193	8506829	RT,DNA,SR	
4:8584026	A	G	0.012	4	8567927	8601653	RT,DNA,SR	
4:9302563	T	C	0.02	4	9293021	9319935	RT,DNA	
4:9333986	T	C	0.012	4	9333986	9348911	RT,DNA,SR	
4:9352775	G	A	0.05	4	9345279	9370879	RT,SR	
4:9743085	T	G	0.01	4	9743085	9758499	RT,DNA,SR	
4:9908508	G	A	0.011	4	9894290	9923357	RT,DNA	
4:10041117	C	A	0.019	4	10021600	10059969	RT,DNA	
4:10077488	A	C	0.02	4	10060050	10094382	RT,DNA	
4:10139581	A	T	0.014	4	10120870	10153466	DNA,SR	
4:10234320	G	A	0.024	4	10216654	10253427	RT,DNA	
4:10407897	T	G	0.011	4	10407897	10423449	RT,DNA	AT4G19020
4:10501457	T	A	0.011	4	10483168	10501457	RT,DNA,SR	
4:10579146	T	C	0.012	4	10563036	10587909	RT,SR	
4:10585976	A	T	0.011	4	10566678	10589596	RT,DNA,SR	
4:10822865	A	T	0.014	4	10810862	10841018	RT,DNA	
4:10862971	G	T	0.011	4	10844403	10880014	DNA,SR	AT4G20010
4:12475889	C	T	0.021	4	12457973	12475889	RT,DNA,SR	
4:12504039	G	A	0.021	4	12504039	12519661	RT,DNA,SR	
4:12769867	A	C	0.018	4	12757664	12781578	RT,SR	
4:13027938	C	T	0.011	4	13026548	13046576	RT,DNA	AT4G25540
4:13089958	A	G	0.016	4	13081014	13109653	RT,DNA,SR	
4:13224201	G	A	0.049	4	13205730	13244180	RT,SR	AT4G26110
4:13521314	T	A	0.06	4	13511928	13522743	RT,DNA	
4:13710571	T	G	0.011	4	13710571	13718088	RT,DNA	
4:14520637	C	G	0.019	4	14505380	14539815	DNA,SR	AT4G29560
4:14570491	C	T	0.026	4	14554267	14585849	RT,DNA,SR	
4:14565920	T	A	0.029	4	14555350	14585669	RT,DNA,SR	
4:14851621	A	T	0.037	4	14834633	14865184	RT,DNA,SR	

4:15287809	A	C	0.048	4	15268393	15306110	DNA,SR	
4:15314318	C	T	0.054	4	15295620	15320671	DNA,SR	
4:15346286	C	G	0.011	4	15327906	15359136	RT,DNA,SR	
4:17564027	G	A	0.043	4	17557285	17579710	RT,DNA	
4:17851000	T	C	0.02	4	17839837	17863383	RT,DNA	
4:18030313	A	G	0.014	4	18027692	18047957	RT,DNA,SR	AT4G28600
4:18349379	T	A	0.016	4	18338868	18362067	RT,SR	
4:18376961	T	C	0.017	4	18358660	18392713	RT,SR	
4:2316796	A	G	0.012	4	2316796	2316796	RT,DNA	
4:13120982	T	A	0.012	4	13120982	13120982	DNA,SR	
5:23535	C	A	0.028	5	6940	42208	RT,DNA	
5:234533	T	G	0.027	5	234533	254377	RT,DNA	AT5G01630
5:255518	T	C	0.029	5	248031	266284	RT,DNA	
5:357120	C	T	0.017	5	341222	375360	RT,DNA,SR	
5:417835	A	C	0.028	5	407072	434053	RT,DNA	
5:757288	T	C	0.015	5	738542	776307	RT,DNA	
5:1157814	T	C	0.041	5	1139375	1162975	RT,DNA	
5:1347197	T	A	0.025	5	1337830	1362643	RT,DNA	
5:1526188	A	C	0.028	5	1509736	1538301	RT,DNA	
5:2477945	A	T	0.026	5	2471378	2492989	RT,DNA	
5:2676353	G	A	0.019	5	2659328	2692452	RT,DNA,SR	
5:2868999	A	G	0.025	5	2850324	2888932	RT,DNA	
5:4184791	C	A	0.015	5	4167905	4203430	RT,DNA,SR	
5:4299746	T	G	0.012	5	4299746	4319189	RT,DNA,SR	
5:4428616	T	A	0.014	5	4410086	4430832	DNA,SR	
5:4497094	G	A	0.021	5	4486064	4516970	DNA,SR	AT5G13960
5:4560889	C	T	0.013	5	4542908	4576523	RT,DNA,SR	AT5G14170
5:4592992	T	A	0.014	5	4576523	4610486	RT,DNA,SR	
5:5897900	A	C	0.014	5	5886672	5906533	RT,DNA	
5:7063428	C	A	0.016	5	7048418	7082428	RT,DNA,SR	AT5G20850
5:7960299	A	T	0.017	5	7944268	7972804	RT,DNA,SR	AT5G23610
5:8523052	C	A	0.012	5	8511580	8541670	RT,DNA,SR	AT5G24850
5:8674612	A	T	0.011	5	8655731	8679183	RT,DNA,SR	
5:8703859	T	C	0.011	5	8703859	8712522	RT,DNA,SR	

5:8989342	T	A	0.011	5	8970620	9005756	RT,DNA,SR	
5:9975947	C	A	0.017	5	9970048	9992226	RT,DNA	
5:10258546	A	G	0.014	5	10241425	10273930	RT,DNA,SR	
5:10602491	T	C	0.013	5	10596337	10605925	DNA,SR	
5:10636839	C	A	0.011	5	10617570	10636839	RT,DNA,SR	
5:12198566	T	A	0.019	5	12194965	12212942	RT,DNA	
5:12599433	A	T	0.013	5	12589256	12610528	RT,DNA	AT5G33330
5:13248640	C	T	0.012	5	13228774	13258144	RT,DNA,SR	
5:14284875	C	A	0.039	5	14273446	14304819	RT,DNA,SR	
5:14861652	C	T	0.035	5	14841669	14877612	DNA,SR	
5:15777106	A	G	0.011	5	15776723	15788076	RT,DNA	
5:16016004	G	T	0.012	5	16003127	16016004	RT,DNA,SR	
5:16083969	C	T	0.013	5	16079858	16083969	DNA,SR	
5:16804885	A	G	0.063	5	16785265	16823059	RT,SR	
5:16853514	C	T	0.011	5	16845232	16865454	RT,DNA	
5:17138152	T	C	0.014	5	17132259	17155727	RT,DNA	
5:17198666	T	A	0.085	5	17179552	17217008	RT,DNA	AT5G42905
5:17446300	C	A	0.024	5	17446300	17461067	RT,DNA	
5:17472749	T	C	0.022	5	17455605	17492651	RT,DNA	AT5G43500
5:17503932	T	C	0.02	5	17489449	17512686	RT,DNA	
5:17544726	G	C	0.024	5	17530524	17551915	RT,DNA	
5:17759064	A	G	0.011	5	17744880	17762054	DNA,SR	
5:17810695	T	C	0.011	5	17810695	17816336	DNA,SR	
5:17937495	G	A	0.049	5	17918295	17948909	RT,DNA	
5:18011110	C	T	0.013	5	18011110	18012650	RT,SR	AT5G44635
5:18456726	T	C	0.028	5	18451699	18470638	RT,DNA,SR	
5:18535826	T	C	0.021	5	18535826	18544383	DNA,SR	AT5G45720
5:18566811	A	T	0.018	5	18561231	18586628	RT,DNA,SR	
5:19206527	A	C	0.033	5	19187136	19220248	RT,DNA,SR	
5:19207920	C	T	0.018	5	19188015	19227434	RT,DNA	
5:19730405	C	T	0.067	5	19722699	19748688	RT,DNA,SR	
5:19812860	A	G	0.039	5	19796536	19832858	RT,SR	
5:19913612	C	G	0.011	5	19901428	19913616	DNA,SR	AT5G49110
5:20989739	C	T	0.021	5	20978805	21005651	RT,DNA	

5:21039880	G	A	0.012	5	21020000	21056210	RT,DNA	AT5G51795
5:22249852	T	A	0.047	5	22236512	22258818	RT,DNA	AT5G54770
5:22373013	A	C	0.014	5	22373013	22384830	RT,DNA	
5:22448142	T	G	0.011	5	22433785	22467851	RT,DNA	AT5G55390, AT5G55310
5:22612999	C	T	0.012	5	22594229	22612999	RT,SR	
5:23911727	G	A	0.012	5	23892816	23915600	RT,DNA,SR	
5:23996577	T	A	0.011	5	23978319	24010133	DNA,SR	
5:24875205	G	C	0.02	5	24856219	24893603	RT,DNA,SR	
5:24942797	T	C	0.038	5	24928293	24962239	RT,DNA	
5:24950157	G	A	0.012	5	24934076	24969156	RT,DNA	
5:25682366	G	C	0.059	5	25662490	25700604	DNA,SR	
5:25852153	C	A	0.024	5	25833709	25871684	RT,DNA,SR	AT5G64630
5:26010945	C	G	0.108	5	25992553	26026445	RT,SR	
5:26159124	T	A	0.062	5	26139851	26176699	DNA,SR	
5:26171410	C	G	0.013	5	26155037	26184892	DNA,SR	
5:26400787	A	C	0.019	5	26381294	26414080	DNA,SR	AT5G66030
5:26499298	G	A	0.021	5	26479848	26516822	RT,DNA,SR	
5:26703057	G	A	0.012	5	26688094	26718203	RT,DNA,SR	
5:26738194	G	A	0.013	5	26718203	26743630	RT,DNA,SR	
5:26785380	A	T	0.013	5	26783418	26785380	RT,DNA,SR	AT5G67100
5:26815557	A	T	0.014	5	26806262	26815557	DNA,SR	
5:26908279	C	A	0.013	5	26895931	26913504	DNA,SR	
5:26951727	G	A	0.013	5	26940172	26951727	RT,DNA,SR	AT5G67580
5:16646832	G	T	0.011	5	16646832	16646832	RT,DNA	

RT = Retrotransposon, DNA = DNA transposon, SR = Simple Repeat

Chapter 2: Subgenome diversification following allopolyploidization in the cosmopolitan weed *Capsella bursa-pastoris*

Abstract

Polyploidy is a driver of evolutionary novelty in flowering plants. However, the genomic changes that occur after the hybridization of two species to produce a polyploid lineage i.e. an allopolyploid, remain poorly characterized. Here, we present novel genome assemblies for the allotetraploid species *Capsella bursa-pastoris* and its two subgenome donor lineages *Capsella orientalis* and *Capsella rubella* (selfing species recently derived from subgenome donor *Capsella grandiflora)*. We use these assemblies to catalog the pattern of structural variants (SVs) between subgenomes and parental genomes and show that the pattern of variation in subgenomes is defined by thousands of small SVs and not large-scale chromosomal rearrangements. Further, we examine the pattern of population structure in a global sample of *C. bursa-pastoris* and confirm that genetic variation in this species is best explained by two groups defined by adaptation to either warm, Mediterranean-like climates or cool, continental climates. Finally, we map the genetic basis of environmental adaptation in *bursa-pastoris* and show that environmental variation is correlated with differences in flowering time across the species range. Our work lends new insight into the evolutionary forces acting upon subgenomes in an allopolyploid context in short evolutionary timescales after polyploid formation and investigates the genetic loci implicated in environmental adaptation.

Introduction

Polyploidy is an important force in genome evolution in both plants [1] and animals [2]. Nearly all extant eukaryotic lineages have experienced polyploidy followed by diploidization in the ancient past [3,4]. Though once thought to be an “evolutionary dead end” [5], polyploidy is now considered to be an important driver of evolutionary novelty and subsequent species diversification [6]. However, most polyploids were formed in the ancient past or have subsequently undergone diploidization, obscuring the genome evolutionary processes occurring in young polyploids.

Polyploids form either by whole genome duplication within a species (autopolyploidy) or by hybridization between two species followed by whole genome duplication (allopolyploidy) [7]. The combination of distantly related genomes in allopolyploids has the potential to disrupt gene expression [8,9], drive transposon activation [10–12], and seed large scale genome rearrangements [13,14]. These rapid and potentially deleterious side effects of allopolyploidization are termed “genomic shock,” [10]. While genomic shock has been observed in both synthesized and natural polyploid lineages [15,16], the phenomenon does not appear to be universal among novel polyploids [17,18].

If a polyploid survives the chaotic formative event, polyploidy may accelerate adaptation to novel environments [19]. In the case of an allopolyploid, the genome may contain loci pre-adapted to the environments inhabited by the progenitors and higher genetic diversity that can be subsequently selected upon to enable adaptation [20]. Polyploidy has also been linked to changes in reproduction such as a loss of self-incompatibility [21], which can aid colonization.

In the long term, polyploid lineages undergo a slow process of diploidization. During this process, the genome undergoes extensive rearrangement usually leading to a reduction in genome size and chromosomal number [22–24]. Duplicated genes experience either neofunctionalization, subfunctionalization, or are lost, leading to lineage diversification [23]. Paleopolyploidy has been detected in many plant lineages including in the ancestor to all flowering plants [4] and ongoing diploidization has been speculated to be a mechanism driving selection for reduction in genome size over time [25,26].

The allotetraploid *Capsella bursa-pastoris* (L.) Medik (2n = 4x = 32) is one of the world's most successful plant species, having colonized disturbed habitats on six of seven continents. *C. bursa-pastoris* is a self-compatible, annual species that is the result of hybridization of progenitor species *Capsella orientalis* (maternal donor) and *Capsella grandiflora* (paternal donor) that formed between 100,000 to 300,000 years ago on the northern coast of the Black Sea in Southeast Europe [27,28]. Unlike its progenitor species which have limited ranges in Eurasia [29], *C. bursa-pastoris* has a cosmopolitan distribution and is found worldwide with the exception of in the tropics and Antarctica [30,31]. The species is an excellent colonizer; though it was introduced to the Americas only a few centuries ago, it has become a very common weedy species [32].

In this work, we characterize the effects of allopolyploidy on the genome of *C. bursa-pastoris*. We begin by assembling and comparing high quality reference genomes from each diploid ancestral lineage and from *C. bursa-pastoris* itself. We then use this new set of genomes to explore the genetic mechanisms that allowed *C. bursa-pastoris* to colonize such a wide array of environments.

Results

Near chromosome-scale genome assemblies for C. bursa-pastoris, C. rubella, and C. orientalis

We produced *de novo* genome assemblies for *C. bursa-pastoris* and its two parental subgenome donors, *C. rubella* and *C. orientalis* (Table 2.S1). The *C. bursa-pastoris* 721-48 assembly is highly contiguous, consisting of 278,339,433 bp (~71% of predicted 1C genome size of 391.2 Mbp [33]) assembled into 77 scaffolds with an N50 of 17,543,583 (Table 2.1). Compared to a previously published genome assembly for this species [34], the assembly presented here is over 9.9 Mbp longer, with a 106 fold change reduction in the number of scaffolds, and a nearly 28 fold increase in N50. The new *C. bursa-pastoris* assembly is also highly complete, containing 99.4% of complete BUSCO genes (Table 2.1, Table 2.S2).

The new *C. rubella* 721-48 genome assembly also improves upon the currently available assembly [35]. The assembly consists of 158,571,049 bp (~73% of predicted 1C genome size of 215 Mbp [33]) assembled into 129 scaffolds with an N50 of 17,600,677, which is over 23 Mbp more assembled sequence than the previous assembly with a 6.6 fold reduction in the number of scaffolds and a substantial increase in N50 (Table 2.1). The assembly of the gene space is near complete, with 99% of BUSCO assembled completely (Table 2.S2).

The *C. orientalis* 2007-03 assembly is considerably more complete than the currently available assembly [36]. The full assembly was 136,180,346 bp in size spread across 32 scaffolds and contains nearly 99% complete BUSCO genes (Table 2.1, Table

2.S2). In sum, the three novel genome assemblies presented here are highly contiguous and represent nearly complete assemblies of the genic regions of the genome.

Effect of allopolyploidization on subgenome architecture

The high quality reference genomes of *C. bursa-pastoris* and its parental lineages *C. orientalis* and *C. grandiflora/rubella* provide an excellent opportunity to examine the evolution of subgenomes in an allopolyploid context over relatively short evolutionary time. For this analysis, we produced whole genome alignments between each subgenome and its respective progenitor species to identify the evolutionary pattern of the *C. bursa-pastoris* subgenomes since polyploid formation.

In the uniquely aligning sequence, we identified a total of 144,111 structural variants between the *C. bursa-pastoris* reference genome and the *C. rubella* and *C. orientalis* genomes. The structural variants were not equally distributed across the two subgenomes, with 28,616 insertions, 20,921 deletions, 2,557 translocations, and 447 inversions found in the CbpCo subgenome and 42,499 insertions, 41,132 deletions, 7,018 translocations, and 921 inversions in the CbpCg subgenome (Figure 2.1A-B). The number of structural variants in the CbpCg subgenome was still greater than CbpCo when normalizing for the differences in genome size between subgenomes (Figure 2.S1).

The distribution of sizes across variant types was comparable across the species. Deletions tended to be largest (median lengths for CbpCo and CbpCg, respectively: 382, 405), followed by insertions (355, 306), inversions (74, 86) and translocations (30, 45) (Figure 2.1C). Overall, the frequency of structural variants per window was non-random across the genome and positively correlated with frequency of repeats per window (R = -0.52 to -0.07 between SV classes) and negatively correlated with the frequency of genes per window (R = 0.17 to 0.39 between SV classes).

We observed 1,042,229 SNPs in the CbpCo subgenome and 2,204,354 in the CbpCg subgenome compared to the *C. orientalis* and *C. rubella* genomes, respectively. Despite more than 2 X the number of SNPs in CbpCg compared to CbpCo, the SNP mutation spectrums were nearly identical between the two subgenomes (Figure 2.1D). As expected, transitions were observed at a much higher rate than transversions. The ratio of nonsynonymous to synonymous sites in CbpCo was 0.97 compared to 0.83 in CbpCg, suggesting that purifying selection has been stronger in the CbpCg subgenome than in CbpCo in the shared polyploid environment.

Gene content evolution across C. bursa-pastoris subgenomes

To identify functional consequences of structural variation in the *C. bursa-pastoris* subgenomes, we examined copy number changes for genes with homologs in both parental donor genomes. Of the 20,582 genes with a homolog in both subgenomes, there were 14,976 orthologs that did not change in copy number in the subgenomes, and 5,605 genes with copy number change in one or both subgenomes (Figure 2.1E-G). There were more genes with an increase of copy number in CbpCo compared to CbpCg (631 vs. 535) and genes typically increased by a single copy (median copy number change 1) and in just one of the subgenomes (Figure 2.1E). Genes with an increase in copy number were enriched for 46 GO terms (Table 2.S3, $p < 0.05$). Among the top 10 GO terms with highest enrichment were histone H3-K9 demethylation, nitrile biosynthetic process, cellular response to heat, photoprotection, and response to UV-B. While the latter three GO terms are all involved in response to abiotic stress, H3-K9 methylation is involved in the repression of repetitive sequences [37] and nitrile is involved in plant immune response to biotic stress [38].

The predominant fate of homologs in both parental donor genomes that experienced change in copy number was to experience copy number decrease or loss in subgenomes. Of genes found at greater than one copy in the donor genomes, there were more genes with copy number loss in the CbpCg subgenome compared to CbpCo (310 vs. 196, Figure 2.1F). However, the most striking pattern of copy number variation in subgenomes compared to donor genomes was copy number loss, with the vast majority of genes lost in both subgenomes (567 in CbpCo, 792 in CbpCg, 2741 in both, Figure 2.1G). Orthologs lost in both subgenomes were enriched for 111 GO terms (Table 2.S4, $p < 0.05$). The GO term with the top enrichment was syncytium formation, which is interesting since polyploid cells resemble syncytium [39]. Among the enriched GO terms were numerous terms related to response to biotic and abiotic stress such as response to stress, response to insect, stress granule assembly, response to oomycetes, detoxification, water homeostasis, cellular response to freezing, cellular response to ozone, and cellular oxidant detoxification.

In addition to genes found in both parental donor lineages, we examined the fate of genes unique to a parental donor lineage in the subgenomes (Figure 2.1H-I). Of the 4,566 genes unique to Co and 4,550 genes unique to Cr, the majority of unique genes were lost in their respective subgenomes. We also observed a small number of genes

(170 from Co, 144 from Cg) that were lineage specific and translocated to the other subgenome.

Our analysis suggests that copy number variation of progenitor genes has affected upwards of 27% of orthologous genes in the *C. bursa-pastoris* subgenomes. We also showed that the genes that have undergone copy number variation in the polyploid subgenomes have functional enrichment, suggesting that the process is at least partially driven by selection.

Repeat content evolution across C. bursa-pastoris subgenomes

In addition to gene content, we examined the copy number and sequence quantity of repetitive sequences in both donor genomes and their respective subgenomes. Overall, we observed copy number increase of transposons of all classes in CbpCo compared to *C. orientalis*, and copy number decrease across all classes in CbpCg compared to *C. grandiflora*/ *C. rubella* (Figure 2.1J). Copy number variation in LTR retrotransposons is mostly due to losses of Copia superfamily elements in CbpCg, which together account for more than 14 Mbp of sequence difference between *C. rubella* and CbpCg (Figure 2.S2-S3). The increase in LTR retrotransposons in CbpCo is also caused by increased copy number of Copia superfamily elements. Also of note is a large loss of TIR Mutator elements in CbpCg compared to *C. rubella*.

Taken together, our analyses suggest that the subgenomes of *C. bursa-pastoris* have evolved by many small structural variants and have not undergone large-scale reshuffling since allopolyploid formation. Our work suggests that the CbpCg subgenome has evolved at a faster rate than the CbpCo subgenome and that the two subgenomes have been subject to different selection pressures. Based on our results, we predict that the strength of purifying selection has increased on the CbpCg subgenome and relaxed on the CbpCo subgenome compared to the parental lineages.

Population structure in worldwide C. bursa-pastoris

Subsequent to formation, *C. bursa-pastoris* spread towards the Mediterranean Sea in Europe before later spreading towards Asia [40]. This was followed by a much more recent introduction to other regions of the world such as the Americas and Africa, presumably via introduction by European colonizers [30,32,41–43]. We next set out to use our newly generated *C. bursa-pastoris* reference genome to understand the global pattern of genetic relationships in this species. Using a reduced-representation sequencing approach, we genotyped 1,441 samples spanning every continent except for Antarctica. After filtering (see Materials and Methods), we retained 1,251 samples genotyped for 30,668 SNPs for subsequent analysis.

Population structure analysis using ADMIXTURE indicated K = 2 to be the most likely number of subpopulations per the delta K method [44] (Figure 2.S4). Using a 70% admixture proportion threshold, we assigned 671 samples to Cluster, 1, 559 samples to Cluster 2, and considered 21 samples to be Admixed. The two subpopulation clusters are separated by a strong latitudinal gradient, with 95% of samples assigned to Cluster 1 found at 34.65 N or above and 95% of samples assigned to Cluster 2 found at 42.35 N or below (Figure 2.2A). The intermediate range between the two latitudinal lines appears to represent a zone where samples from the clusters have hybridized with over half (22 / 42) of the Admixed samples occurring between these latitudes worldwide. Principal component analysis of allele frequencies separates the two subpopulation clusters with no overlap of individuals from Cluster 1 and Cluster 2 on the first two principal components (Figure 2.2B).

Modeling population structure with additional subpopulations did not yield much new insight into the patterns of subpopulation differentiation in *C. bursa-pastoris*. Considering K = 3 assigns samples from Cluster 1 to the new Cluster 3, with Cluster 3 accessions relegated to Eastern and Southern Asia and defined by being early flowering similar to samples in Cluster 2 (Figure 2.S5). At K = 4, most samples were considered to be admixed, with samples assigned to only two clusters.

Concurrent with the latitudinal separation of the subpopulation clusters, we also observed differences in the climate at sample collection sites between the clusters. While the majority of samples were collected in mild Mediterranean-like climates (Köppen Climate Type C, temperate), we observed that about half of samples belonging to Cluster 1 were collected in either continental (type D) or polar (type E) climates and that many samples from Cluster 2 were collected in dry (type B) climate (Figure 2.2C). Admixed samples were found only in temperate or dry climates.

We identified loci in the genome that have been differentially selected between the two clusters and are responsible for population stratification using the XP-CLR statistic [45]. The top 1% of 100 KB non-overlapping windows contained genes significantly enriched for numerous GO terms related to abiotic stress response (e.g. response to cadmium ion, response to water deprivation, regulation of removal of superoxide radicals), biotic stress response, (e.g. trehalose biosynthetic process, cyanate catabolic process) response to the environment (e.g. vernalization response, cellular response to light stimulus, chloroplast accumulation movement), and development (e.g. gynoecium development, regulation of meristem development, and root system development) (Figure 2.S6, Table 2.S5). Our results suggest that these processes are important for differential adaptation of the two subpopulation clusters to their ranges.

Phenotypic distribution between subpopulations

The two subpopulations had differences in phenotypic distribution in a common garden experiment conducted in the Botanical Garden in Osnabrück, Germany from May to July 2015 [31]. In the common garden, Cluster 2 samples had earlier flowering (Figure 2.2D), more basal branches, and better germination success compared to samples in Cluster 1 (Figure 2.2F). We also observed differences in the frequencies of leaf shape morphologies between the clusters ($\chi2 = 30.318$, df = 4, p-value = 4.216e-06), with heteris and simplex shapes at higher frequency in Cluster 2 and tenuis shape at higher frequency in Cluster 1 (Figure 2.2G). We did not observe statistically significant differences in plant height or seed weight between the clusters. However, we did notice that seed weight was substantially higher in Admixed samples compared to both clusters (Figure 2.S7). We also found that Cluster 2 samples have reduced genome size compared to cluster 1 samples, with admixed samples having intermediate genome size between the two clusters (Figure 2.2H).

Taken together, our results suggest that population structure in *C. bursa-pastoris* is defined by two major clusters of samples with differences in the distribution of allele frequencies, geography, and phenotype. Cluster 1 samples are found in cooler climates, have late flowering, and reduced biomass compared to samples from Cluster 2. Cluster 2 consists of samples found in temperate and dry climates with earlier flowering and is the predominant cluster found outside Eurasia. The differences in climate habitat and phenotype between the two clusters suggests that Cluster 1 and Cluster 2 samples likely represent different ecotypes of *C. bursa-pastoris.*

Genetic history of colonization

Although the species probably originated around the north coast of the Black Sea [28], *C. bursa-pastoris* is a cosmopolitan species that has been found growing in the wild on all continents except Antarctica. Most regions outside of Europe consist exclusively of samples from Cluster 2 except for the Americas and in Great Britain and Ireland (Figure 2.2A). To gain insight into the history of migration in regions containing both subpopulation clusters, we calculated the mean genetic distance for samples in a focal region for each sample in the dataset. Since migration outside of Europe has been rapid and recent (within the last 1000 years), if colonization of a continent was due to the migration of a single lineage which then diverged into the Cluster 1 and Cluster 2 ecotypes (i.e. repeatedly adapted) we expect samples in a region to be more closely related to each other than samples from some other region.

The colonization of North and South America appears to have been by at least two distinct lineages: one lineage from Cluster 1 (found primarily outside the West coast of North America) and the other from Cluster 2 (found along the West coast of both North America and South America) (Figure 2.3A-B). The Cluster 1 samples appear to be most closely related to Cluster 1 samples present in West, Central, and Eastern Europe.

The Cluster 2 samples appear to be very closely related to samples collected in South America, the Southern tip of Africa, Sri Lanka, and Oceania and only moderately related to samples present in the Iberian peninsula of Southern Europe. The pattern of close relatedness between Cluster 2 samples on the West Coast of North America and the other locations separated by oceans is consistent with the hypothesis that the migration of *C. bursa-pastoris* was mitigated by humans during exploration expeditions originating from the Iberian peninsula [41,46]. This result is further corroborated by the fact that the lone sample from New Zealand off the mainland of Oceania is more closely related to samples in Southern Africa than samples on the mainland of Oceania (Figure 2.S8).

The samples from Japan have strong genetic similarity to a small number of samples found across Eastern and Southern Asia and represent the early flowering Cluster 3 (K = 3) samples described previously (Figure 2.3C). Great Britain and Ireland appear to have been colonized separately (and probably repeatedly) by Cluster 1 and Cluster 2 lineages (Figure 2.3D). The Cluster 2 samples in Iceland appear to be highly diverged, but most closely related to samples from Western and Northern Europe (Figure 2.S9).

Genetic basis of environmental adaptation

The near global distribution of *C. bursa-pastoris* makes it a prime system to study the genetic basis of environmental adaptation. A principal component analysis of the 19 worldclim2 bioclimatic variables [47] represented 62% of the variation in climate between samples on the first two principal components (Figure 2.4A, Figure 2.S10). PC 1, which is primarily explained by differences in variables describing temperature, also distinguishes the two subpopulation clusters described previously (Figure 2.4A-B). In contrast, PC 2 appears to be driven by the variables describing precipitation.

Of the phenotypes measured in the common garden experiment, only days to flowering and number of basal branches were significantly correlated with PC 1, while plant height was correlated with PC 2 ($p < 0.05$, Figure 2.S11). The relationship between flowering and PC 1 was the strongest, with PC 1 (temperature) explaining 20% of the variation in flowering time (Figure 2.4C). We also noted that genome size was correlated with both PC 1 and flowering ($R = -0.54$, $R = 0.51$, respectively).

We examined the genetic basis of environmental adaptation by treating both PC 1 and PC 2 as "phenotypes" in genome-wide association mapping (Figure 2.4D-E). After collapsing significant SNPs that were linked, we identified 45 regions of the genome associated with variation along PC 1 and 90 regions associated with PC 2 (Table 2.S6). Of these, 87 regions were associated uniquely with either PC 1 or PC 2 and 24 regions were associated in both GWA (Figure 2.4D-E). The closest genes to SNPs significantly associated with PC 1 were enriched for 16 biological process gene ontology (GO) terms (Figure 2.4F, Table 2.S7). The majority of enriched GO terms describe biological processes that have a role in plant reproduction such as DNA demethylation, double fertilization, inflorescence development, and brassinosteroid signaling. The closest genes to SNPs significantly associated with PC 2 were enriched for 38 biological process gene ontology (GO) terms, 5 of which were also associated with PC 1 and reflect the genes under the shared GWA peaks (Figure 2.4G, Table 2.S6-S7). Unique enriched GO terms for PC 2 include biological processes involved in nutrient uptake from the soil (e.g. hypoxanthine transport, arsenate ion transmembrane transport, response to hydrogen peroxide, sodium ion import across plasma membrane) and response to light (response to high light intensity, photosystem I assembly).

In addition to the GO analysis, we also manually examined the genes present under significant peaks for bioclimatic GWA. We identified numerous interesting candidate genes that appear to have linked variation associated with variation in climate. For brevity, we here profile three loci that were associated with variation along both PC 1 and PC 2 and are thus strong candidate loci implicated in environmental adaptation. A full list of all associated regions and candidate genes is available in Table 2.S6 and Table 2.S9, respectively). The SNP with the lowest p value in the PC 1 GWA and was among the top SNPs in the PC 2 GWAS was SCF_14:15183887. This SNP is 653 bp downstream of g39808, a homolog of *AT4G11560 (REPRESSOR OF VERNALIZATION 1)*, which is a transcription factor that regulates flowering time by preventing the expression of flowering genes [48]. SCF_14:15377114 is a synonymous variant in g39842, a homolog of *AT4G11890 (ABA- AND OSMOTIC-STRESS-INDUCIBLE RECEPTOR-LIKE CYTOSOLIC KINASE1),* a gene that regulates abscisic acid and osmotic stress signal transduction. SCF_9:8559318 is a splice region variant of g25003, a homolog of *AT1G20870 (INCREASED DNA METHYLATION 3)* and heat shock (HSP20-like chaperones superfamily) gene.

Discussion

In this work, we leveraged novel genome assemblies of three Capsella species along with a collection of over 1,200 genotyped *C. bursa-pastoris* individuals to determine the evolutionary trajectory of the two *C. bursa-pastoris* subgenomes and the role that genetic variation in this species has played in global adaptation. Our analyses show that the subgenomes of *C. bursa-pastoris* are relatively well-preserved and free of large scale genomic rearrangements compared to the progenitor lineages, as has been observed in other systems such as *Arabidopsis suecica* [17], *Coffea arabica* [49], and numerous allopolyploid species of Gossypium [18]. Therefore, we conclude that *C. bursa-pastoris* has not undergone "genomic shock" [10] upon polyploidization. Instead, the subgenomes have experienced thousands of small structural variants that affect the copy number of many genes and repetitive sequences, likely through homeologous recombination. Our work shows that genes that are duplicated or lost appear to be non-random in regards to function as reported previously [27] and constitute many genes involved in the response to various biotic and abiotic stresses, likely in response to adaptation to novel environments. We also observed a preference for insertions compared to deletions, which suggests that neofunctionalization and subfunctionalization were the prevailing modes of gene evolution in *C. bursa-pastoris*.

Based on comparative analysis between CbpCg and *C. rubella*, we report here that the CbpCg subgenome appears to have experienced more rapid evolution than the CbpCo subgenome. However, we admit that this result is likely biased due to the strong bottleneck effect upon speciation of self-compatible *C. rubella* from self-incompatible *C. grandiflora* between 30 - 50 KYA and the high nucleotide diversity present within *C. grandiflora* compared to *C. rubella* [50]. It is also possible that this signal is caused by interspecific hybridization between *C. bursa-pastoris* and its progenitors [27,51–53].

Population structure in *C. bursa-pastoris* appears to be explained by two groups defined by adaptation to either a wet continental (Cluster 1) or dry temperate (Cluster 2) climate. The two subpopulation clusters described in the present study mirror those described previously by [30], but we wish to point out that the assortment of individuals by climate type is incomplete, with many samples belonging to Cluster 1 also found in temperate climates. However, the two clusters have near distinct geographic distributions and hybrids, i.e. admixed individuals, appear to be rare even in the shared range, suggesting that the two lineages are either reproductively isolated or experience genetic incompatibility. Considered together with the observations of differences in genome size between clusters and admixed individuals having increased seed size suggestive of hybrid vigor, we propose that the two subpopulation clusters likely represent distinct subspecies of *C. bursa-pastoris* and therefore bursa-pastoris should be considered to be a species complex. However, the origin of the two subpopulations remains obscure. Recent work has speculated that the Mediterranean lineage (Cluster 2) is the result of gene flow from *C. grandiflora* or *C. rubella* into *C. bursa-pastoris* through a triploid bridge *C. gracilis* [28], but it is also possible that this lineage is just an independent formation of the polyploid and is not derived from the Eurasian lineage.

Nevertheless, the phenotypic hallmark of climate adaptation appears to be modulation of flowering time in response to temperature, where individuals in warmer climates tend to flower earlier than individuals in cooler climates. We hypothesize that the colonization success of *C. bursa-pastoris* is likely due to the human-mediated dispersal of near pre-adapted genotypes out of Eurasia that have further adapted to the colonized microclimates by evolving variation affecting flowering time. Our genome-wide association mapping for variation in climate identified numerous candidate loci that represent promising targets for future study.

Materials and Methods

Genome assembly and annotation

The novel *Capsella bursa-pastoris*, *Capsella rubella*, and *Capsella orientalis* genome assemblies described herein were assembled and annotated by Detlef Weigel's laboratory at the Max Planck Institute for Biology Tübingen. The accessions used for the assemblies are described in Table 2.S1.

BUSCO

To assay genome assembly completeness, conserved single copy orthologous genes were identified using BUSCO 5.2.2 ran with default settings and the brassicales_odb10 lineage dataset [54].

Comparative genomics

Genome assemblies were aligned in a pairwise fashion using the nucmer program included in MUMmer 4.0 [55] using the default parameters. Structural variants were identified in 1-to-1 alignments using the dnadiff command in the MUMmer package. Homologs were identified between genome assemblies using the synteny-aware approach implemented in GENESPACE 0.9.3 [56], which uses orthofinder 2.5.4 for homolog identification [57,58]. Effect of SNPs between genomes was determined by annotating the inter-genome SNP data with Ensembl Variant Effect Predictor v. 95 [59].

Gene ontology enrichment analyses

All gene ontology (GO) enrichment analyses were performed with topGO 2.46.0 [60] using the weight01 algorithm and Fisher's exact test considering terms with $p < 0.05$ to be significantly enriched. Gene ontology mappings for *C. bursa-pastoris, C. orientalis*, and *C. rubella* genes were determined by identifying homologs in the *Arabidopsis thaliana* Araport 11 annotation [61] using orthofinder 2.5.4 [57,58] ran with default parameters. For the GO analyses for GWA significant SNPs, the closest genes were identified using bedtools 2.29.2 [62].

Repetitive sequence annotation

Genome assemblies were annotated for repetitive sequences using the "panTE" approach of the Extensive *de novo* TE Annotator (EDTA) 2.0 [63]. First, a panTE library was constructed by individually annotating the *Arabidopsis lyrata* v.1.0 [25], *Arabidopsis thaliana* TAIR10 [64], Cbp2-2, Cr145, and Co39 genome assemblies and clustering the repetitive sequence libraries with the make_panTElib.pl script using default parameters. The panTE library was then used as a custom repeat library to annotate the Capsella genome assemblies using the "final" step of the EDTA pipeline.

Variant calling in whole genome sequencing data

Whole genome sequence reads were mapped to the respective genome assemblies with bwa-mem2 v. 2.0 [65]. SAM alignments were converted to sorted BAM format with samtools 1.10 [66]. Sequencing duplicates were marked with Picard MarkDuplicates [67] as implemented in GATK 4.1.8.1 [68]. Variants were called per sample with GATK

HaplotypeCaller in GVCF mode and then jointly genotyped per cohort with GenotypeGVCFs.

Raw genotypes were filtered with GATK 4.1.8.1 [68], bcftools 1.10 [66] and vcftools 0.1.15 [69] to exclude multiallelic sites and sites meeting the following conditions: QD < 2, FS > 60, SOR > 3, MQ < 40, MQRankSum < -12.5, ReadPosRankSum < -8.0. We also filtered sites with > 5% heterozygous genotypes (excluding *grandiflora)*, with > 5% missing calls, and with site depth > Q3 + 1.5 IQR depth across all remaining sites.

RAD-sequencing and variant calling

Sample collection, DNA extraction, and RAD-sequencing library construction is described in [70].

Read were demultiplexed and variants were called with the reference-based pipeline implemented in Stacks 2.60 [71]. For the barcode parsing step, barcodes were rescued and reads with uncalled bases or low quality were removed. Processed reads were mapped to the *Capsella bursa-pastoris* assembly with bwa-mem2 v. 2.0 [65] and SAM formatted alignments converted to sorted BAM format with samtools 1.10 [66]. Raw variants were called with the reference-based pipeline (i.e. ref_map.pl) of Stacks 2.60 [71]. Samples with mapping preference to either subgenome or with greater than 5% of raw heterozygous calls were disqualified from analysis at this step. Sites were initially filtered to allow only sites called in 60% or more samples with a minimum minor allele frequency of 1% and maximum heterozygosity of 5%. Samples with greater than 50% missing calls after the initial site filters were applied were disqualified from further analysis and the site filters were then reapplied to the raw variant calls to produce the final filtered callset.

Population structure analyses

SNPs were pruned using Stacks populations module and analyzed for population structure using ADMIXTURE v. 1.3.0 [72] considering K = 1 - 20 and 10 replicates per K. ADMIXTURE runs were aggregated and visualized with R package pophelper v. 2.3.1 [73]. The number of populations was determined according to the Evanno method [44]. Samples were assigned to subpopulations that explained 70% or more of ancestry. Principal component analysis of scaled allele frequencies was performed using the adegenet v. 2.1.5 R package [74]. Mean allele frequencies were substituted for missing values. Köppen climate classifications were extracted from sample coordinates using the LookupCZ function from the kgc 1.0.0.2 R package [75] at "coarse" resolution.

The regions of the genome under selection in the subpopulation clusters were identified by calculating the XP-CLR statistic [45] in 100 KB windows containing 2 or more SNPs using the xpclr v. 1.1.2 python module [76].

Common garden phenotyping data was produced by [70]. Leaf shapes were defined by [77]. Differences in quantitative phenotype distribution between subpopulations were identified using the Wilcoxon Rank Sum test and differences in leaf shape frequency were identified using Fisher's Exact Test implemented in R [78].

Hamming genetic distance matrix was calculated using plink 1.9 [79].

Genome-wide association

Genotypes were imputed with STITCH 1.6.6 [80] considering 30 haplotypes and 100 generations. The number of haplotypes (K) was determined empirically by comparing the mean and median INFO_SCORE across values of K = 4-30 in intervals of 2 for SCF_1. Imputed genotypes were converted to plink binary format using plink 1.90 [79]. Mixed linear models including a centered kinship matrix were fitted with GEMMA v. 0.98.5 [81]. Quantitative common garden-measured phenotypes were log-transformed and qualitative phenotypes were coded using “case/control” dummy variables prior to analysis. Environmental variables were extracted from WORLDCLIM 2 [47] at 2.5 minute resolution. A Bonferroni-adjusted p value threshold at alpha of 0.05 was used to determine significance. Significant SNPs were collapsed into “associated regions” by grouping SNPs with LD $R^2 > 0.60$. The tag SNP was considered to be the SNP with the lowest p value among linked SNPs.

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Figures and Tables

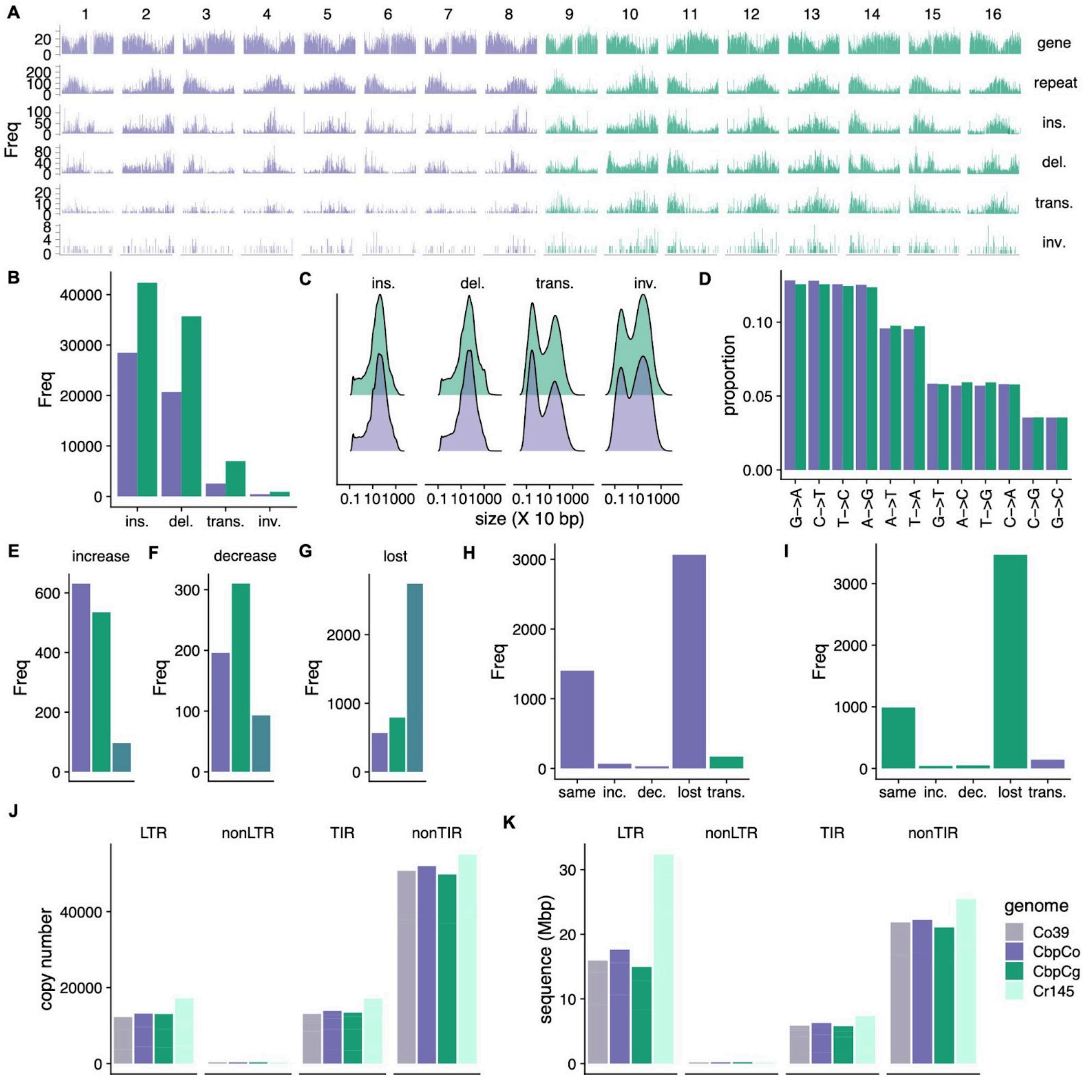

Figure 2.1 Patterns of structural variation in C. bursa pastoris subgenomes

A) Abundance of genes, repeats, insertions (ins.), deletions (del.), translocations (trans.) and inversions (inv.) in 100 KB non-overlapping windows across the CbpCo (purple) and CbpCg (green) subgenomes. B) Total abundance of structural variations (SV). C) Distributions of SV length. Data plotted on the log scale. D) SNP frequency spectra. E-G) Abundance of genes found in both donor lineages undergoing copy number increase (E), decrease (excluding loss, F), or loss (G) in one or both subgenomes (teal). H) Copy number variation in genes unique to Co lineage. I) Copy number variation in genes unique to Cg/Cr lineage). J) Transposon copy number per genome by class. LTR and nonLTR are class I elements while TIR and nonTIR are class II elements. K) Sequence content per genome attributed to transposons.

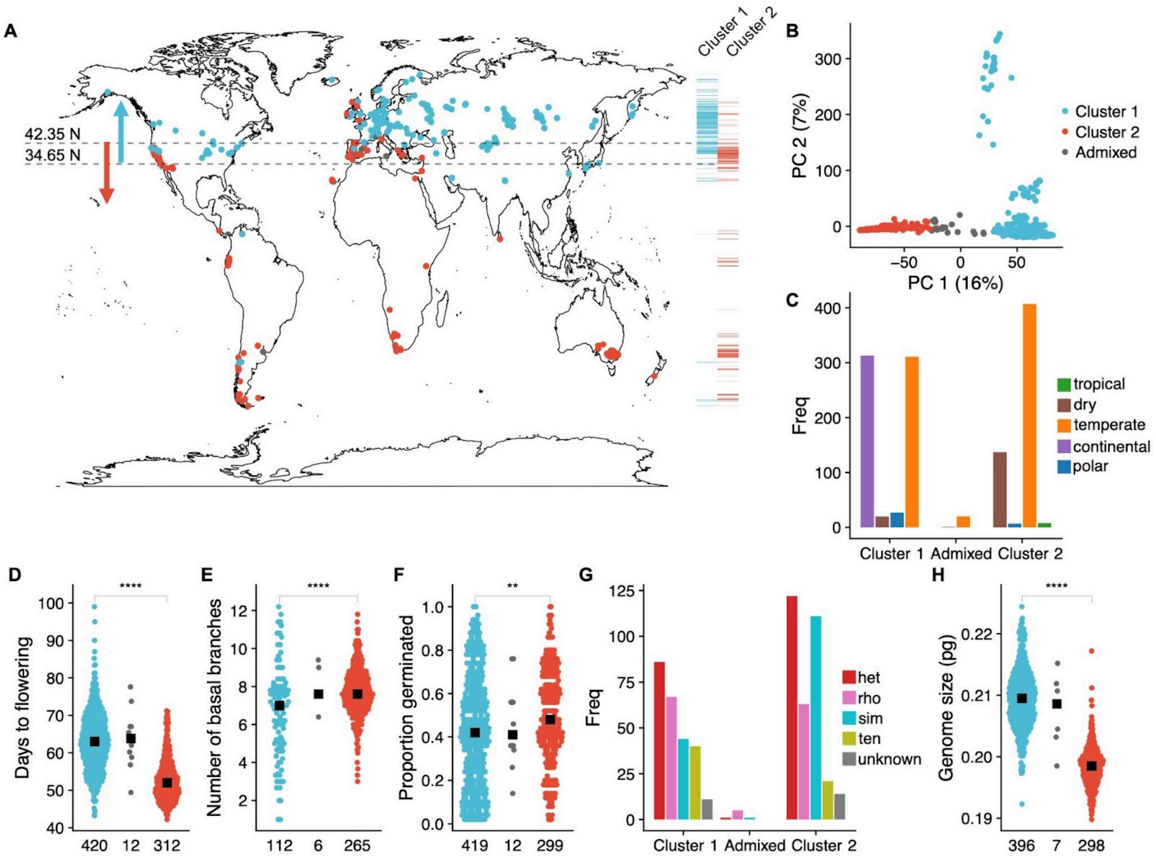

Figure 2.2 Population structure of a global sampling of C. bursa-pastoris

A) Collection sites by subpopulation assignment. Rug plot represents latitudinal distribution of samples. B) Principal component analysis of allele frequencies. C) Köppen climate classification frequencies by subpopulation. D-F) Distribution of quantitative phenotypes in a common garden experiment. Black squares denote the group medians and numbers below the X axes indicates the number of observations per group. G) Frequencies of leaf shape in a common garden experiment. Leaf shapes: heteris (het), rhomboidea (rho), simplex (sim), tenuis (ten). H) Flow-cytometry derived genome size estimates.

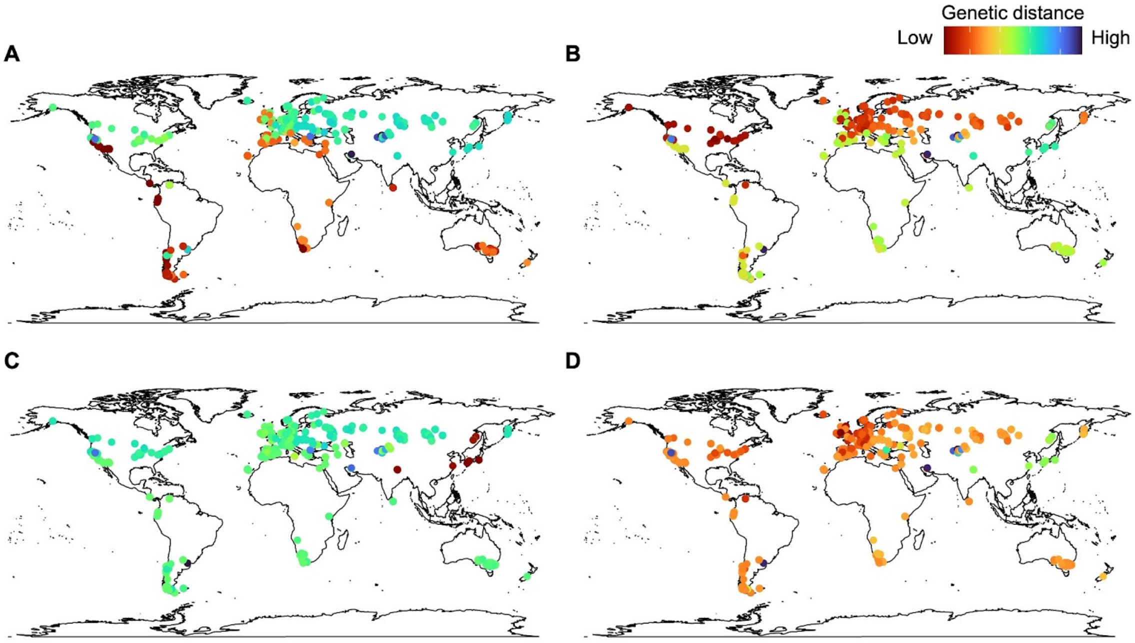

Figure 2.3 Mean genetic distance from focal locations

Mean genetic distance by geography compared to samples from A) the West Coast of North America B) other North American samples C) Japan D) Great Britain and Ireland.

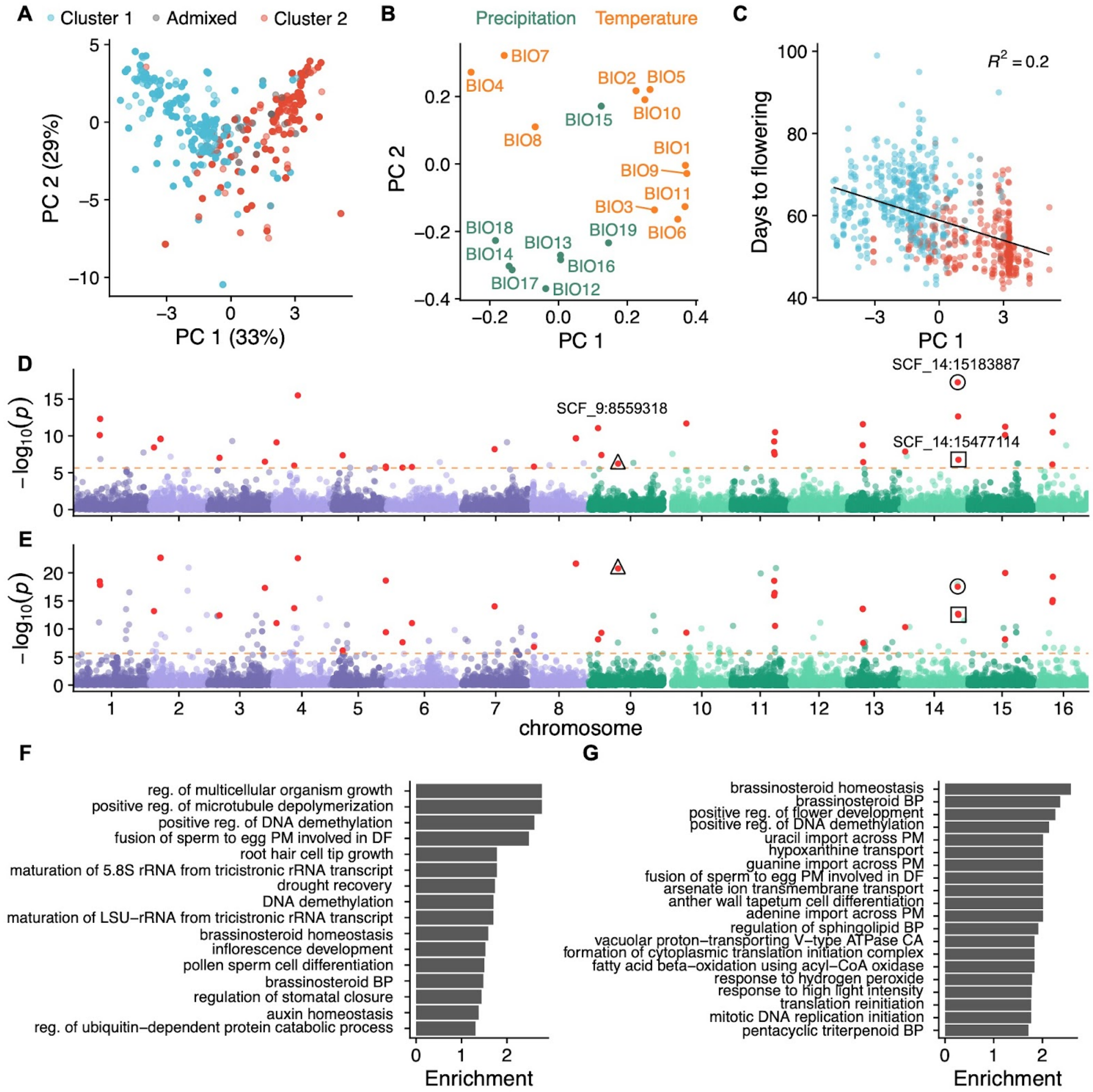

Figure 2.4 Genetic basis of climate adaptation

A) Principal component analysis of 19 worldclim2 bioclimatic variables. Samples colored according to admixture group assignments. B) Loadings of bioclimatic variables along PCs 1-2. Variables are colored by whether they describe temperature or precipitation. C) Relationship between flowering time and PC 1. D) Genome-wide association mapping manhattan plot for PC 1. Horizontal line indicates Bonferroni-adjusted significance threshold at alpha = 0.05. Highlighted SNPs were significant in both PC 1 and PC 2 GWA. E) Genome-wide association mapping manhattan plot for PC 2. F) Enrichment (-log10 p value) of significant ($p < 0.05$) biological process gene ontology terms for closest genes to PC 1 significant SNPs. G) Enrichment of significant gene ontology terms for closest genes to PC 2 significant SNPs. Abbreviations: reg. = regulation, PM = plasma membrane, DF = double fertilization, BP = biological process.

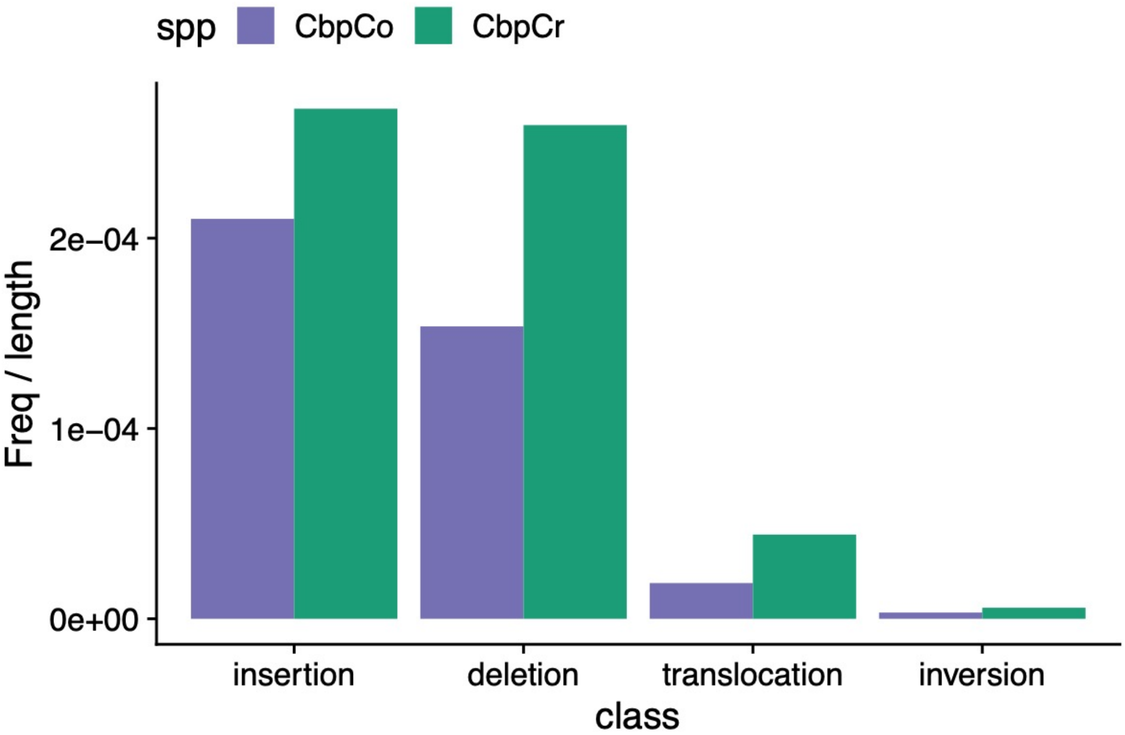

Figure 2.S1 Normalized counts of structural variants by Cbp subgenome

Number of structural variants normalized by subgenome length.

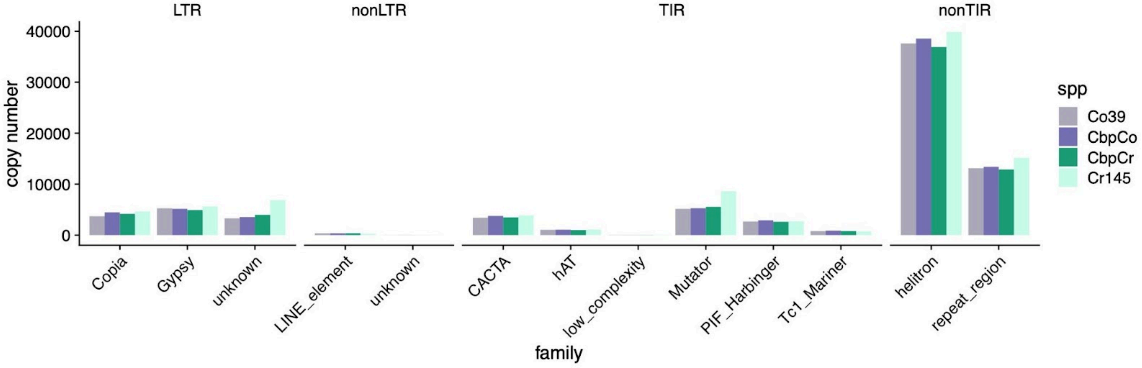

Figure 2.S2 Transposon copy number per genome.

CbpCo and CbpCr refer to the subgenomes of Cbp. Class I retrotransposons: LTR and nonLTR. Class II DNA transposons: TIR and nonTIR.

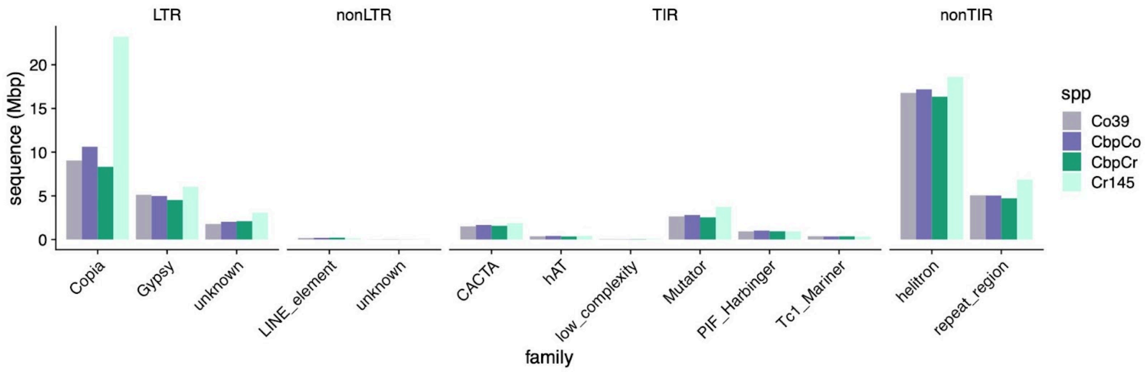

Figure 2.S3 Repetitive sequence by transposon superfamily per genome.

CbpCo and CbpCr refer to the subgenomes of Cbp. Class I retrotransposons: LTR and nonLTR. Class II DNA transposons: TIR and nonTIR.

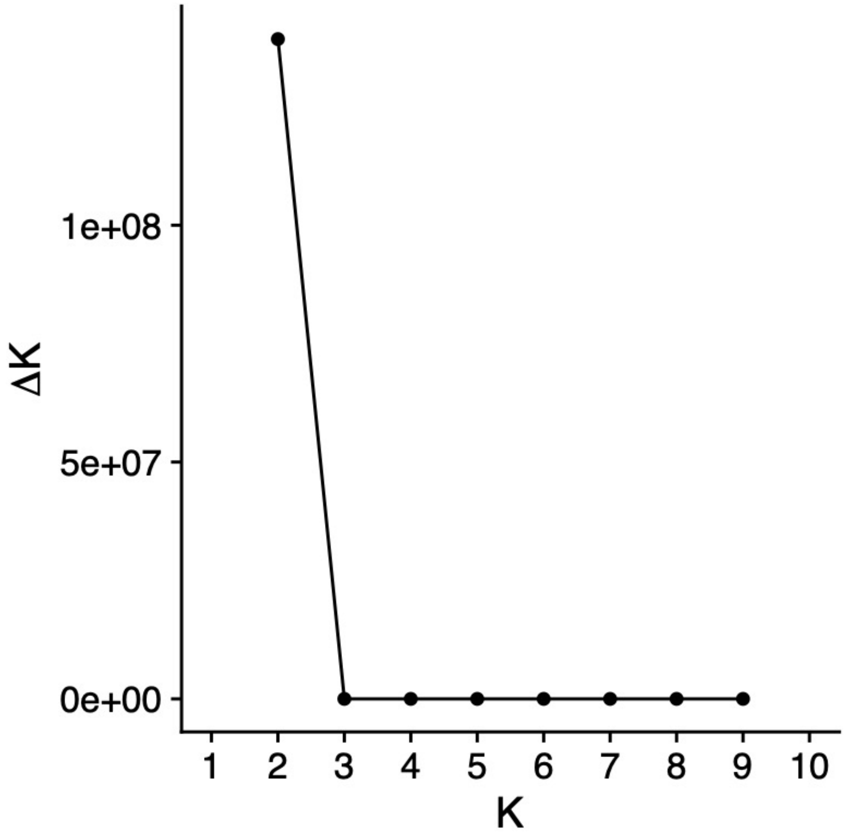

Figure 2.S4 Delta K statistic

Mean delta K for 10 ADMIXTURE runs per K for K = 1-10.

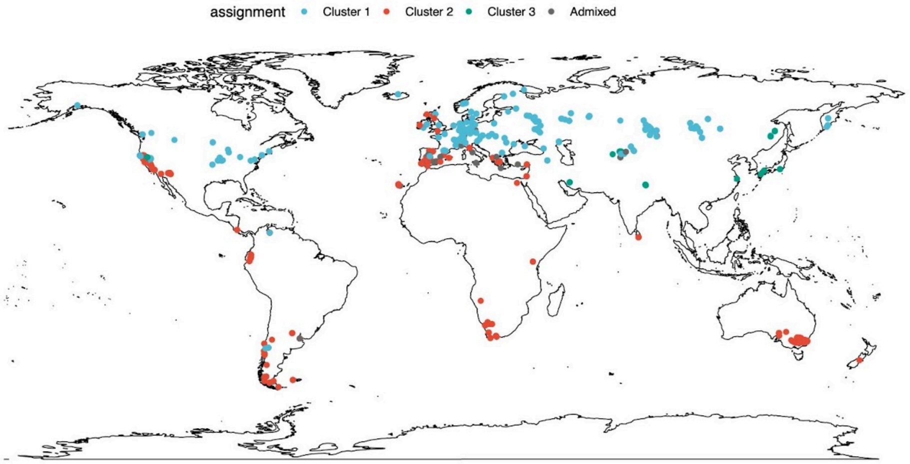

Figure 2.S5 ADMIXTURE group assignments for K = 3

Samples are plotted according to their collection sites.

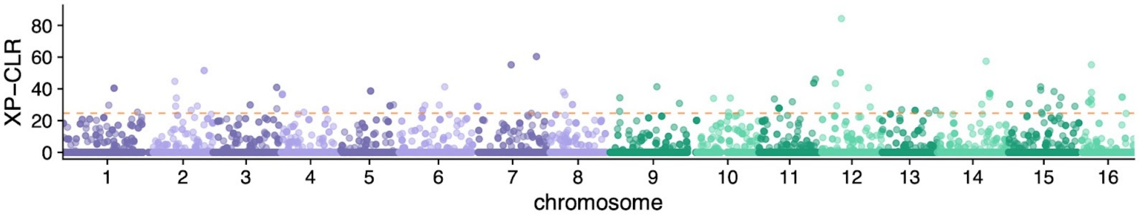

Figure 2.S6 XP-CLR scan for subpopulation Cluster 1 vs. Cluster 2

XP-CLR calculated in 100KB non-overlapping windows containing 2 or more SNPs. Points above the dotted orange line are in the top 1% of observations.

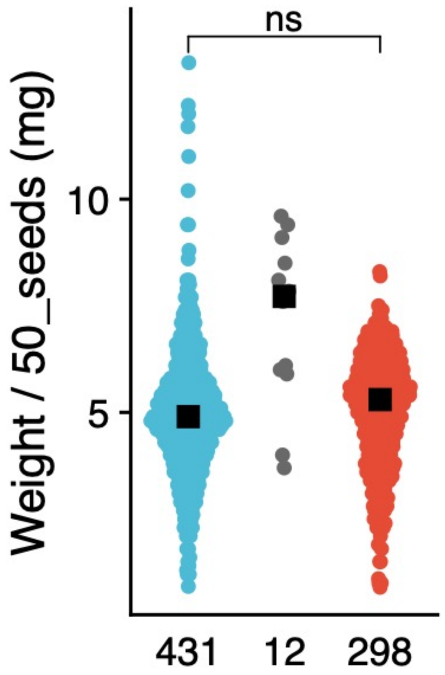

Figure 2.S7 Distribution of common garden-measured seed weight by subpopulation

Values under the X axis indicate the number of observations per group. Black square indicates median value for members within a group.

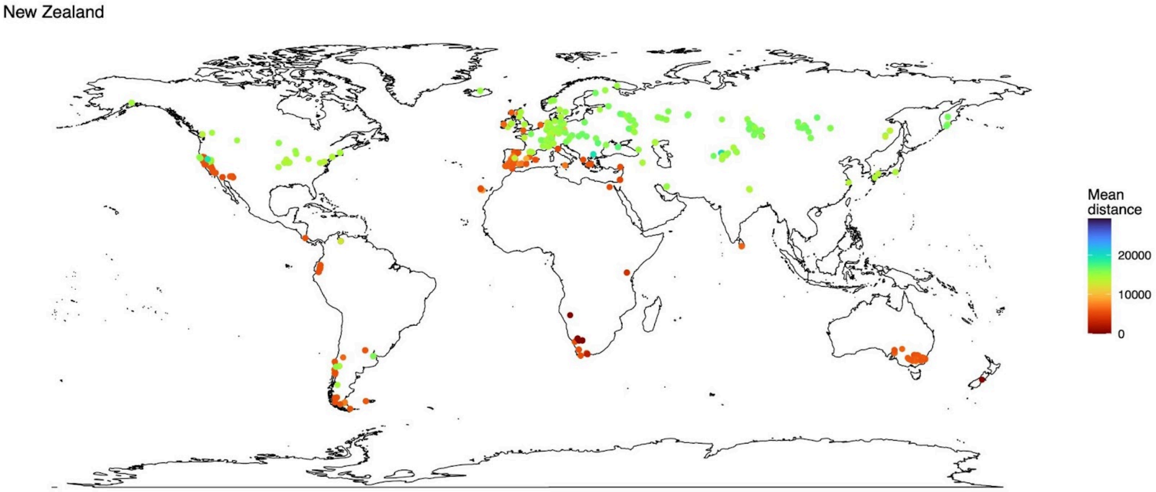

Figure 2.S8 Mean genetic distance from samples collected in New Zealand

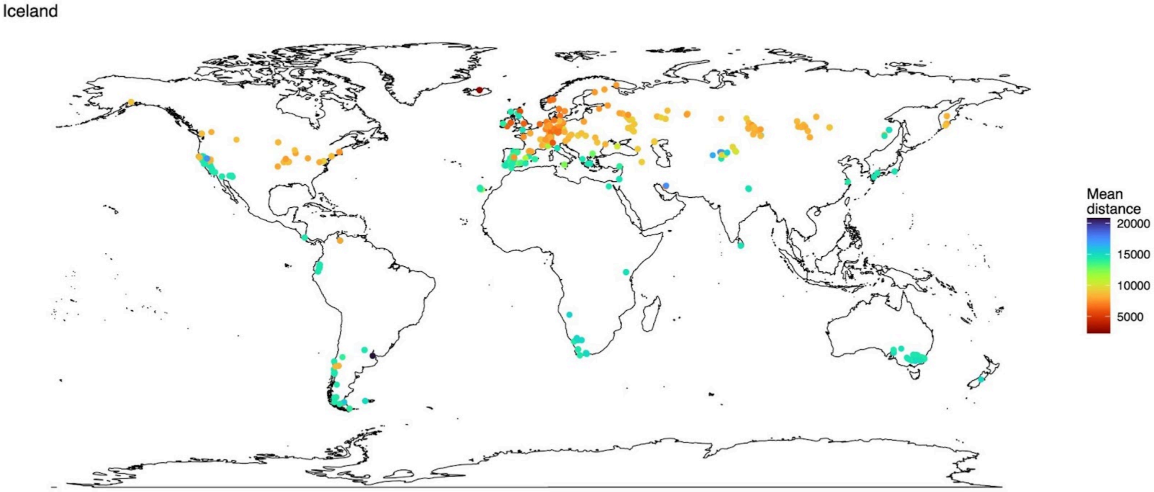

Figure 2.S9 Mean genetic distance from samples collected in Iceland

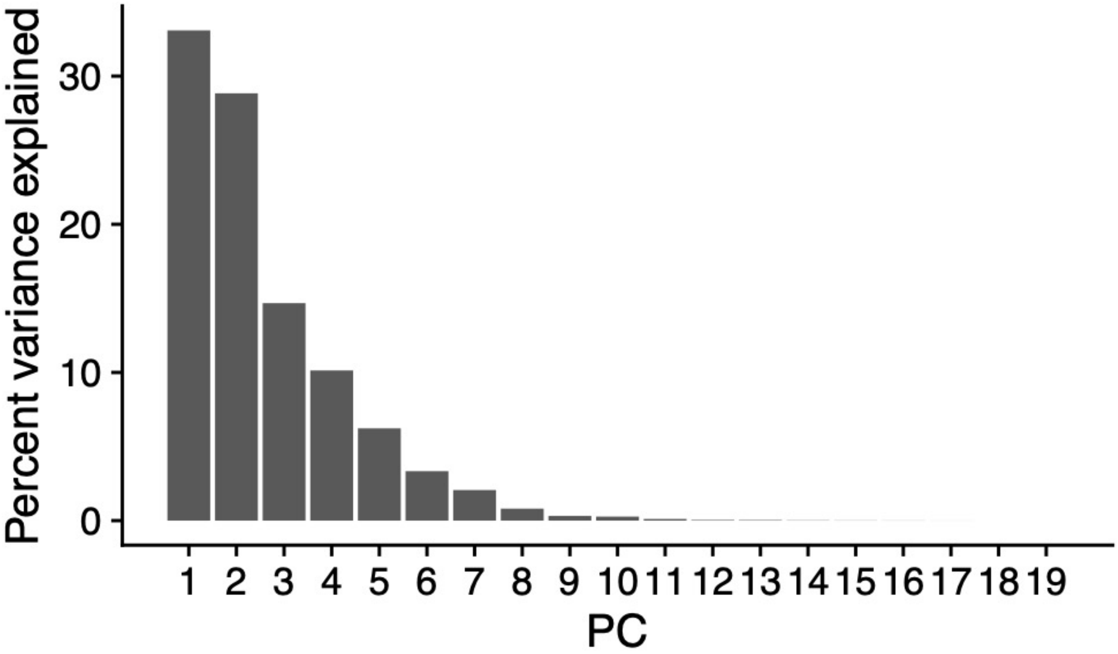

Figure 2.S10 Percent variance explained per principal component in PCA of bioclimatic variables

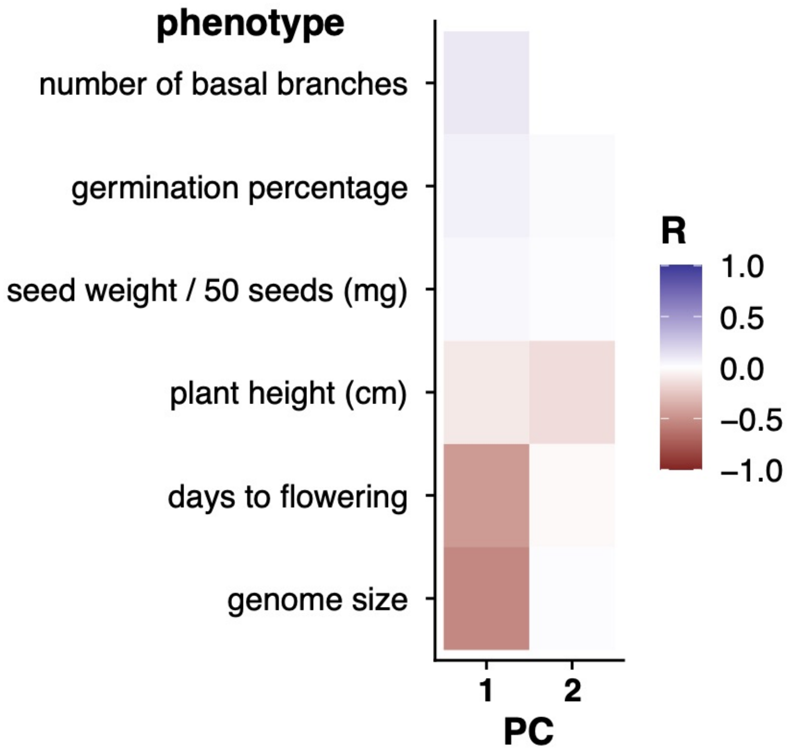

Figure 2.S11 Correlations between bioclimatic principal components and common garden measured phenotypes

Table 2.1 Genome assembly statistics

Genome	**Length**	**Scaffolds**	**N50**	**Complete BUSCOs**
C. bursa-pastoris	278339433	77	17543583	99.4%
C. rubella	158571049	129	17600677	99.0%
C. orientalis	136180346	32	16341214	99.0%

Table 2.S1 Accession information for genome assemblies

Species	Accession	Lat.	Long.	Elev.	Loc.	Ref.
Capsella bursa-pastoris	721-48	35.50	-119.28	106	Shafter, CA USA	Wesse et al. *Ecol. Evol.* 2021
Capsella orientalis	2007-03	47.23	85.72	1920	Xinjiang, China	Koenig et al. *eLife*. 2019
Capsella rubella	879	35.29	24.42	258	Nikiforos Fokas, Greece	Koenig et al. *eLife.* 2019

Lat. = Latitude, Long. = Longitude, Elev. = Elevation, Loc. = Locality, Ref= Reference.

Table 2.S2 BUSCO statistics

Genome	Complete	Complete and Single Copy	Duplicated	Fragmented	Missing
Cbp2-2	4567	242	4325	5	24
Cbp_Kasianov	4438	451	3987	57	101
Cr145	4552	4469	83	9	35
Cr_Slotte	4549	4477	72	9	38
Co39	4548	4466	82	5	43

Table 2.S3 Enriched GO terms for genes with copy number increase in subgenomes

GO.ID	Term	Annotated	Significant	Expected	P value	Enrichment
GO:0033169	histone H3-K9 demethylation	8	4	0.49	0073	3.14
GO:0080028	nitrile biosynthetic process	4	3	0.25	0081	3.09
GO:0034605	cellular response to heat	49	10	3	0086	3.07
GO:0010117	photoprotection	14	5	0.86	0095	3.02
GO:0010380	regulation of chlorophyll biosynthetic process	15	5	0.92	0136	2.87
GO:0010224	response to UV-B	53	10	3.25	0187	2.73
GO:0060321	acceptance of pollen	10	4	0.61	0198	2.70
GO:0035616	histone H2B conserved C-terminal lysine deubiquitination	2	2	0.12	0356	2.45
GO:1900186	negative regulation of clathrin-dependent endocytosis	2	2	0.12	0356	2.45
GO:0006606	protein import into nucleus	37	7	2.27	0444	2.35
GO:0042545	cell wall modification	109	10	6.68	0621	2.21
GO:0010030	positive regulation of seed germination	21	5	1.29	0682	2.17
GO:0071483	cellular response to blue light	21	5	1.29	0682	2.17
GO:0019762	glucosinolate catabolic process	15	4	0.92	0.01011	2
GO:0010045	response to nickel cation	3	2	0.18	0.01024	1.99
GO:0007076	mitotic chromosome condensation	3	2	0.18	0.01024	1.99
GO:0019676	ammonia assimilation cycle	3	2	0.18	0.01024	1.99
GO:0010372	positive regulation of gibberellin biosynthetic process	3	2	0.18	0.01024	1.99
GO:0034058	endosomal vesicle fusion	3	2	0.18	0.01024	1.99
GO:1990547	mitochondrial phosphate ion transmembrane transport	3	2	0.18	0.01024	1.99
GO:0019761	glucosinolate biosynthetic process	39	7	2.39	0.01224	1.91
GO:0006096	glycolytic process	33	6	2.02	0.01228	1.91
GO:0080156	mitochondrial mRNA modification	24	5	1.47	0.01229	1.91
GO:0046686	response to cadmium ion	53	8	3.25	0.01264	1.90
GO:0016126	sterol biosynthetic process	26	6	1.59	0.01456	1.84

GO:0010143	cutin biosynthetic process	25	5	1.53	0.01600	1.80
GO:0000966	RNA 5'-end processing	18	4	1.1	0.01967	1.71
GO:0010032	meiotic chromosome condensation	4	2	0.25	0.01968	1.71
GO:0034720	histone H3-K4 demethylation	4	2	0.25	0.01968	1.71
GO:0042276	error-prone translesion synthesis	4	2	0.25	0.01968	1.71
GO:0009553	embryo sac development	103	10	6.32	0.02282	1.64
GO:0080027	response to herbivore	19	4	1.17	0.02376	1.62
GO:0019375	galactolipid biosynthetic process	11	3	0.67	0.02434	1.61
GO:0009751	response to salicylic acid	134	13	8.22	0.02677	1.57
GO:0017148	negative regulation of translation	54	5	3.31	0.02845	1.55
GO:0045490	pectin catabolic process	62	8	3.8	0.03025	1.52
GO:0006893	Golgi to plasma membrane transport	12	3	0.74	0.03105	1.51
GO:0019346	transsulfuration	5	2	0.31	0.03151	1.50
GO:0030643	cellular phosphate ion homeostasis	5	2	0.31	0.03151	1.50
GO:0015846	polyamine transport	5	2	0.31	0.03151	1.50
GO:0019432	triglyceride biosynthetic process	21	4	1.29	0.03340	1.48
GO:0009407	toxin catabolic process	31	5	1.9	0.03489	1.46
GO:0006397	mRNA processing	226	12	13.86	0.03802	1.42
GO:0009306	protein secretion	13	3	0.8	0.03861	1.41
GO:0072318	clathrin coat disassembly	6	2	0.37	0.04541	1.34
GO:0006265	DNA topological change	6	2	0.37	0.04541	1.34

Table 2.S4 Enriched GO terms for genes lost in both subgenomes

GO.ID	Term	Annotated	Significant	Expected	P value	Enrichment
GO:0006949	syncytium formation	10	6	1.13	0024	3.62
GO:0045490	pectin catabolic process	62	17	6.99	0025	3.60
GO:0009299	mRNA transcription	14	7	1.58	0031	3.51
GO:0071456	cellular response to hypoxia	160	33	18.03	0034	3.47
GO:0006468	protein phosphorylation	722	111	81.35	0042	3.38
GO:0006499	N-terminal protein myristoylation	33	11	3.72	0050	3.30
GO:0009554	megasporogenesis	5	4	0.56	0064	3.19
GO:0033384	geranyl diphosphate biosynthetic process	5	4	0.56	0064	3.19
GO:0033386	geranylgeranyl diphosphate biosynthetic process	5	4	0.56	0064	3.19
GO:0090698	post-embryonic plant morphogenesis	150	21	16.9	0065	3.19
GO:0006950	response to stress	2280	257	256.89	0073	3.14
GO:0019748	secondary metabolic process	248	35	27.94	0085	3.07
GO:0030198	extracellular matrix organization	16	5	1.8	0129	2.89
GO:0030574	collagen catabolic process	3	3	0.34	0129	2.89
GO:0080170	hydrogen peroxide transmembrane transport	3	3	0.34	0129	2.89
GO:0006065	UDP-glucuronate biosynthetic process	3	3	0.34	0129	2.89
GO:0018105	peptidyl-serine phosphorylation	79	18	8.9	0178	2.75
GO:0009625	response to insect	28	9	3.15	0214	2.67
GO:0006412	translation	406	52	45.74	0221	2.66
GO:0051259	protein complex oligomerization	39	9	4.39	0240	2.62
GO:0030050	vesicle transport along actin filament	10	5	1.13	0241	2.62
GO:0006817	phosphate ion transport	27	7	3.04	0349	2.46
GO:0009769	photosynthesis, light harvesting in photosystem II	7	4	0.79	0376	2.42
GO:0071249	cellular response to nitrate	7	4	0.79	0376	2.42

GO:0045337	farnesyl diphosphate biosynthetic process	7	4	0.79	0376	2.42
GO:1990069	stomatal opening	13	4	1.46	0476	2.32
GO:0010376	stomatal complex formation	4	3	0.45	0476	2.32
GO:0010438	cellular response to sulfur starvation	4	3	0.45	0476	2.32
GO:0007043	cell-cell junction assembly	4	3	0.45	0476	2.32
GO:0006024	glycosaminoglycan biosynthetic process	4	3	0.45	0476	2.32
GO:0072334	UDP-galactose transmembrane transport	4	3	0.45	0476	2.32
GO:0051555	flavonol biosynthetic process	11	5	1.24	0686	2.16
GO:0034063	stress granule assembly	8	4	0.9	0687	2.16
GO:0030388	fructose 1,6-bisphosphate metabolic process	8	4	0.9	0687	2.16
GO:0002239	response to oomycetes	81	18	9.13	0701	2.15
GO:0032502	developmental process	2333	223	262.86	0773	2.11
GO:0009826	unidimensional cell growth	244	40	27.49	0776	2.11
GO:0051923	sulfation	13	5	1.46	0931	2.03
GO:0046686	response to cadmium ion	53	13	5.97	0.01068	1.97
GO:0060548	negative regulation of cell death	20	6	2.25	0.01090	1.96
GO:0000056	ribosomal small subunit export from nucleus	5	3	0.56	0.01092	1.96
GO:0010466	negative regulation of peptidase activity	5	3	0.56	0.01092	1.96
GO:0010235	guard mother cell cytokinesis	5	3	0.56	0.01092	1.96
GO:2000785	regulation of autophagosome assembly	5	3	0.56	0.01092	1.96
GO:0098754	detoxification	106	20	11.94	0.01116	1.95
GO:0007010	cytoskeleton organization	188	28	21.18	0.01119	1.95
GO:0030104	water homeostasis	12	6	1.35	0.01126	1.95
GO:0033962	P-body assembly	9	4	1.01	0.01131	1.95
GO:0009812	flavonoid metabolic process	65	10	7.32	0.01187	1.93
GO:0052386	cell wall thickening	19	4	2.14	0.01188	1.93

GO:0090602	sieve element enucleation	2	2	0.23	0.01189	1.92
GO:0070207	protein homotrimerization	2	2	0.23	0.01189	1.92
GO:0000050	urea cycle	2	2	0.23	0.01189	1.92
GO:0034635	glutathione transport	2	2	0.23	0.01189	1.92
GO:0070863	positive regulation of protein exit from endoplasmic reticulum	2	2	0.23	0.01189	1.92
GO:0045793	positive regulation of cell size	2	2	0.23	0.01189	1.92
GO:0071327	cellular response to trehalose stimulus	2	2	0.23	0.01189	1.92
GO:0000349	generation of catalytic spliceosome for first transesterification step	2	2	0.23	0.01189	1.92
GO:0010202	response to low fluence red light stimulus	2	2	0.23	0.01189	1.92
GO:0016031	tRNA import into mitochondrion	2	2	0.23	0.01189	1.92
GO:2000083	negative regulation of L-ascorbic acid biosynthetic process	2	2	0.23	0.01189	1.92
GO:0033389	putrescine biosynthetic process from arginine, using agmatinase	2	2	0.23	0.01189	1.92
GO:0080153	negative regulation of reductive pentose-phosphate cycle	2	2	0.23	0.01189	1.92
GO:0050482	arachidonic acid secretion	2	2	0.23	0.01189	1.92
GO:0006892	post-Golgi vesicle-mediated transport	29	4	3.27	0.01190	1.92
GO:0006888	endoplasmic reticulum to Golgi vesicle-mediated transport	64	13	7.21	0.01259	1.90
GO:0080092	regulation of pollen tube growth	30	8	3.38	0.01280	1.89
GO:0010497	plasmodesmata-mediated intercellular transport	14	5	1.58	0.01319	1.88
GO:0009742	brassinosteroid mediated signaling pathway	50	11	5.63	0.01703	1.77
GO:0016131	brassinosteroid metabolic process	30	5	3.38	0.01728	1.76
GO:0009920	cell plate formation involved in plant-type cell wall biogenesis	6	3	0.68	0.02009	1.70
GO:0010119	regulation of stomatal movement	78	15	8.79	0.02079	1.68

GO:0009768	photosynthesis, light harvesting in photosystem I	21	6	2.37	0.02139	1.67
GO:0000028	ribosomal small subunit assembly	27	7	3.04	0.02264	1.65
GO:0030307	positive regulation of cell growth	11	4	1.24	0.02479	1.61
GO:1900425	negative regulation of defense response to bacterium	11	4	1.24	0.02479	1.61
GO:0010942	positive regulation of cell death	30	6	3.38	0.03099	1.51
GO:0010114	response to red light	50	10	5.63	0.03159	1.50
GO:1901002	positive regulation of response to salt stress	7	3	0.79	0.03233	1.49
GO:0000266	mitochondrial fission	7	3	0.79	0.03233	1.49
GO:0035067	negative regulation of histone acetylation	7	3	0.79	0.03233	1.49
GO:0006535	cysteine biosynthetic process from serine	7	3	0.79	0.03233	1.49
GO:0098532	histone H3-K27 trimethylation	7	3	0.79	0.03233	1.49
GO:0042344	indole glucosinolate catabolic process	3	2	0.34	0.03307	1.48
GO:0010434	bract formation	3	2	0.34	0.03307	1.48
GO:0006370	7-methylguanosine mRNA capping	3	2	0.34	0.03307	1.48
GO:0046621	negative regulation of organ growth	3	2	0.34	0.03307	1.48
GO:0006435	threonyl-tRNA aminoacylation	3	2	0.34	0.03307	1.48
GO:0010254	nectary development	3	2	0.34	0.03307	1.48
GO:0050891	multicellular organismal water homeostasis	3	2	0.34	0.03307	1.48
GO:0071497	cellular response to freezing	3	2	0.34	0.03307	1.48
GO:0071457	cellular response to ozone	3	2	0.34	0.03307	1.48
GO:1901333	positive regulation of lateral root development	3	2	0.34	0.03307	1.48
GO:1901183	positive regulation of camalexin biosynthetic process	3	2	0.34	0.03307	1.48
GO:0009584	detection of visible light	3	2	0.34	0.03307	1.48
GO:0010618	aerenchyma formation	3	2	0.34	0.03307	1.48

GO:1903428	positive regulation of reactive oxygen species biosynthetic process	3	2	0.34	0.03307	1.48
GO:0006651	diacylglycerol biosynthetic process	3	2	0.34	0.03307	1.48
GO:0098869	cellular oxidant detoxification	21	7	2.37	0.03389	1.47
GO:0019762	glucosinolate catabolic process	15	6	1.69	0.03392	1.47
GO:0055085	transmembrane transport	565	76	63.66	0.03530	1.45
GO:0002229	defense response to oomycetes	62	12	6.99	0.03615	1.44
GO:0006885	regulation of pH	42	16	4.73	0.03830	1.42
GO:0006812	cation transport	238	27	26.82	0.04030	1.39
GO:0015749	monosaccharide transmembrane transport	19	6	2.14	0.04490	1.35
GO:0006508	proteolysis	540	60	60.84	0.04531	1.34
GO:0009058	biosynthetic process	3456	342	389.39	0.04548	1.34
GO:0009864	induced systemic resistance, jasmonic acid mediated signaling pathway	8	3	0.9	0.04761	1.32
GO:0009061	anaerobic respiration	8	3	0.9	0.04761	1.32
GO:0080142	regulation of salicylic acid biosynthetic process	8	3	0.9	0.04761	1.32
GO:0007015	actin filament organization	63	14	7.1	0.04798	1.32

Table 2.S5 Enriched GO terms for genes in top 1% of XP-CLR windows

GO.ID	Term	Annotated	Significant	Expected	P value	Enrichment
GO:0006649	phospholipid transfer to membrane	4	2	0.09	025	2.60
GO:0001709	cell fate determination	15	3	0.32	034	2.47
GO:0048467	gynoecium development	137	5	2.96	034	2.47
GO:0010048	vernalization response	16	3	0.35	041	2.39
GO:0051782	negative regulation of cell division	16	3	0.35	041	2.39
GO:0046686	response to cadmium ion	76	6	1.64	050	2.30
GO:0080113	regulation of seed growth	19	3	0.41	068	2.17
GO:0001678	cellular glucose homeostasis	28	3	0.6	0.0111	1.95
GO:1902065	response to L-glutamate	8	2	0.17	0.0111	1.95
GO:0010155	regulation of proton transport	8	2	0.17	0.0111	1.95
GO:0044030	regulation of DNA methylation	23	3	0.5	0.0116	1.94
GO:0010030	positive regulation of seed germination	43	4	0.93	0.0120	1.92
GO:0032366	intracellular sterol transport	11	3	0.24	0.0141	1.85
GO:1990961	xenobiotic detoxification by transmembrane export across the plasma membrane	47	4	1.01	0.0163	1.79
GO:0042147	retrograde transport, endosome to Golgi	26	3	0.56	0.0163	1.79
GO:0106167	extracellular ATP signaling	10	2	0.22	0.0174	1.76
GO:0009414	response to water deprivation	548	20	11.83	0.0175	1.76
GO:0009904	chloroplast accumulation movement	28	3	0.6	0.0199	1.70
GO:0071280	cellular response to copper ion	1	1	0.02	0.0208	1.68
GO:1905885	positive regulation of triglyceride transport	1	1	0.02	0.0208	1.68
GO:0051726	regulation of cell cycle	312	11	6.74	0.0226	1.65
GO:0006260	DNA replication	232	8	5.01	0.0247	1.61
GO:0048509	regulation of meristem development	76	4	1.64	0.0248	1.61
GO:0009903	chloroplast avoidance movement	32	3	0.69	0.0284	1.55
GO:0043248	proteasome assembly	13	2	0.28	0.0289	1.54
GO:0006367	transcription initiation from RNA polymerase II promoter	47	4	1.01	0.0306	1.51

GO:0006355	regulation of transcription, DNA-templated	2659	65	57.42	0.0321	1.49
GO:0090627	plant epidermal cell differentiation	202	6	4.36	0.0333	1.48
GO:0009263	deoxyribonucleotide biosynthetic process	14	2	0.3	0.0333	1.48
GO:0010231	maintenance of seed dormancy	14	2	0.3	0.0333	1.48
GO:0005992	trehalose biosynthetic process	14	2	0.3	0.0333	1.48
GO:0010016	shoot system morphogenesis	274	10	5.92	0.0376	1.42
GO:0045814	negative regulation of gene expression, epigenetic	112	5	2.42	0.0378	1.42
GO:0010105	negative regulation of ethylene-activated signaling pathway	36	3	0.78	0.0385	1.41
GO:0032409	regulation of transporter activity	15	2	0.32	0.0411	1.39
GO:0035437	maintenance of protein localization in endoplasmic reticulum	23	2	0.5	0.0411	1.39
GO:0009259	ribonucleotide metabolic process	264	7	5.7	0.0411	1.39
GO:0010362	negative regulation of anion channel activity by blue light	2	1	0.04	0.0412	1.39
GO:0032963	collagen metabolic process	2	1	0.04	0.0412	1.39
GO:0060250	germ-line stem-cell niche homeostasis	2	1	0.04	0.0412	1.39
GO:1903175	fatty alcohol biosynthetic process	2	1	0.04	0.0412	1.39
GO:0001935	endothelial cell proliferation	2	1	0.04	0.0412	1.39
GO:0009440	cyanate catabolic process	2	1	0.04	0.0412	1.39
GO:0006799	polyphosphate biosynthetic process	2	1	0.04	0.0412	1.39
GO:0043619	regulation of transcription from RNA polymerase II promoter in response to oxidative stress	2	1	0.04	0.0412	1.39
GO:2000011	regulation of adaxial/abaxial pattern formation	2	1	0.04	0.0412	1.39
GO:0003376	sphingosine-1-phosphate receptor signaling pathway	2	1	0.04	0.0412	1.39
GO:0070935	3'-UTR-mediated mRNA stabilization	2	1	0.04	0.0412	1.39
GO:0080166	stomium development	2	1	0.04	0.0412	1.39
GO:0000025	maltose catabolic process	2	1	0.04	0.0412	1.39

GO:0032367	intracellular cholesterol transport	2	1	0.04	0.0412	1.39
GO:0043971	histone H3-K18 acetylation	2	1	0.04	0.0412	1.39
GO:0043972	histone H3-K23 acetylation	2	1	0.04	0.0412	1.39
GO:0006679	glucosylceramide biosynthetic process	2	1	0.04	0.0412	1.39
GO:1902184	negative regulation of shoot apical meristem development	2	1	0.04	0.0412	1.39
GO:0080038	positive regulation of cytokinin-activated signaling pathway	2	1	0.04	0.0412	1.39
GO:0033611	oxalate catabolic process	2	1	0.04	0.0412	1.39
GO:2000121	regulation of removal of superoxide radicals	2	1	0.04	0.0412	1.39
GO:0022622	root system development	798	17	17.23	0.0412	1.39
GO:0032456	endocytic recycling	16	2	0.35	0.0427	1.37
GO:0006470	protein dephosphorylation	175	8	3.78	0.0435	1.36
GO:0010043	response to zinc ion	65	4	1.4	0.0464	1.33
GO:0019432	triglyceride biosynthetic process	39	3	0.84	0.0471	1.33
GO:0071482	cellular response to light stimulus	152	6	3.28	0.0476	1.32
GO:1901527	abscisic acid-activated signaling pathway involved in stomatal movement	17	2	0.37	0.0478	1.32
GO:0035999	tetrahydrofolate interconversion	17	2	0.37	0.0478	1.32

Table 2.S6 Associated regions in GWA of bioclimatic principal components

GWAS	**TAG SNP**	**MINOR**	**MAJOR**	**MAF**	**CHR**	**START**	**END**
PC1,PC2	SCF_1:7039593	T	C	0.015	SCF_1	6077964	7716083
PC1	SCF_1:7144158	A	T	0.013	SCF_1	6819285	7555373
PC2	SCF_1:14011783	A	G	0.021	SCF_1	13026365	14883355
PC2	SCF_1:14790423	T	G	0.014	SCF_1	13962260	15663286
PC2	SCF_1:14883355	C	A	0.013	SCF_1	13962260	15148351
PC2	SCF_1:14045670	T	C	0.022	SCF_1	14045670	14045670
PC1	SCF_1:18618433	T	C	0.012	SCF_1	18204353	18618433
PC1,PC2	SCF_2:1119844	T	C	0.018	SCF_2	444076	2117995
PC2	SCF_2:1664854	T	A	0.023	SCF_2	789075	2117995
PC1,PC2	SCF_2:2857512	A	C	0.018	SCF_2	1973504	3651901
PC2	SCF_2:2994784	T	C	0.037	SCF_2	2994784	2994784
PC2	SCF_2:4054003	G	T	0.015	SCF_2	3314952	4549289
PC1	SCF_2:5519431	G	T	0.016	SCF_2	4549289	6483875
PC2	SCF_2:10288969	G	A	0.016	SCF_2	9485133	11073390
PC2	SCF_2:12951311	C	A	0.02	SCF_2	12424489	13307585
PC2	SCF_2:15129299	A	C	0.018	SCF_2	14575544	15287853
PC2	SCF_3:2507815	G	A	0.04	SCF_3	2507815	3034425
PC1,PC2	SCF_3:3034422	T	C	0.015	SCF_3	3034422	3034422
PC1	SCF_3:6411205	T	C	0.015	SCF_3	5685283	7148161
PC2	SCF_3:9000256	T	C	0.023	SCF_3	8283377	9710355
PC2	SCF_3:10608132	A	C	0.016	SCF_3	9710355	11511883
PC2	SCF_3:12751259	T	G	0.021	SCF_3	11815509	13674016
PC2	SCF_3:14317573	C	T	0.014	SCF_3	13488397	15268613
PC1,PC2	SCF_3:15069712	A	T	0.015	SCF_3	14097825	15268613
PC1,PC2	SCF_4:1376250	A	G	0.013	SCF_4	642035	2315264
PC2	SCF_4:4861844	A	T	0.021	SCF_4	3890109	5845465
PC2	SCF_4:5772779	G	C	0.023	SCF_4	4828311	6370227
PC2	SCF_4:6013338	G	C	0.046	SCF_4	5029903	6761508
PC1,PC2	SCF_4:6055822	A	G	0.016	SCF_4	5090220	7016896
PC1,PC2	SCF_4:7016908	C	T	0.015	SCF_4	7016896	7838456
PC2	SCF_4:12829315	T	A	0.018	SCF_4	12829315	13213220

PC2	SCF_4:14627896	T	C	0.013	SCF_4	14627896	15279950
PC2	SCF_5:1872258	T	C	0.023	SCF_5	875833	2747409
PC1,PC2	SCF_5:3239297	T	C	0.018	SCF_5	2329915	4009954
PC2	SCF_5:4350639	A	G	0.02	SCF_5	3375137	5318916
PC2	SCF_5:4416626	C	T	0.018	SCF_5	3587799	5376030
PC1	SCF_5:5206412	G	C	0.014	SCF_5	4350639	5426257
PC1	SCF_5:11763552	C	T	0.016	SCF_5	10913098	12020181
PC1,PC2	SCF_5:14660182	C	G	0.016	SCF_5	13949575	14710244
PC1,PC2	SCF_6:4381560	T	C	0.014	SCF_6	4381560	4764998
PC1,PC2	SCF_6:6882133	A	G	0.018	SCF_6	6141279	7614217
PC2	SCF_6:11349002	T	A	0.025	SCF_6	10740351	12223346
PC1	SCF_6:14260693	A	G	0.014	SCF_6	13392367	14854201
PC2	SCF_6:18200703	C	A	0.013	SCF_6	17280538	18433280
PC2	SCF_7:898164	G	T	0.015	SCF_7	20973	1566625
PC2	SCF_7:1510267	G	T	0.025	SCF_7	898164	2455908
PC1,PC2	SCF_7:8624829	C	T	0.019	SCF_7	8361846	9490219
PC2	SCF_7:9634551	G	A	0.02	SCF_7	8675271	10377860
PC1	SCF_7:11910153	T	C	0.011	SCF_7	11910153	11910153
PC2	SCF_7:13469299	T	G	0.025	SCF_7	12502244	14451177
PC2	SCF_7:15647532	T	G	0.021	SCF_7	14871939	16370428
PC2	SCF_7:17430089	T	C	0.013	SCF_7	16663676	17430089
PC2	SCF_8:1335699	G	A	0.029	SCF_8	1131443	2319056
PC1	SCF_8:1218586	G	T	0.015	SCF_8	1218586	1682775
PC2	SCF_8:1335648	G	A	0.039	SCF_8	1335648	2319056
PC1	SCF_8:5319852	G	T	0.325	SCF_8	4449562	6319163
PC1,PC2	SCF_8:12345623	C	A	0.013	SCF_8	12345623	12345859
PC1	SCF_8:14406674	G	A	0.021	SCF_8	14004581	14406674
PC1,PC2	SCF_9:3258112	T	A	0.015	SCF_9	2697344	4166269
PC2	SCF_9:4136298	A	C	0.021	SCF_9	3185949	4539175
PC1,PC2	SCF_9:8559318	T	C	0.016	SCF_9	8098526	8774597
PC1	SCF_9:12616150	G	T	0.02	SCF_9	12092917	13551937
PC2	SCF_9:17932614	A	T	0.017	SCF_9	17583765	18813917
PC2	SCF_9:18363098	A	G	0.025	SCF_9	17583765	19350762
PC1	SCF_10:67661	C	T	0.024	SCF_10	26448	450518

PC1,PC2	SCF_10:3762185	T	G	0.016	SCF_10	3685863	4759307
PC2	SCF_10:4759307	C	T	0.026	SCF_10	3762185	5610388
PC2	SCF_10:7757419	A	G	0.013	SCF_10	7715521	7757419
PC2	SCF_10:10027706	A	C	0.016	SCF_10	9580116	10027706
PC2	SCF_10:12513938	A	G	0.014	SCF_10	11651740	12758941
PC2	SCF_10:14903653	T	A	0.017	SCF_10	13972609	15546755
PC2	SCF_11:479229	A	G	0.013	SCF_11	103323	479229
PC2	SCF_11:4710955	A	T	0.022	SCF_11	3823918	5665274
PC2	SCF_11:7800670	T	C	0.019	SCF_11	7800670	8163613
PC1	SCF_11:11388607	T	C	0.016	SCF_11	10787976	12364149
PC2	SCF_11:11845501	A	G	0.018	SCF_11	10860241	12829969
PC2	SCF_11:11598985	A	C	0.045	SCF_11	11209438	12467985
PC1	SCF_11:11611623	A	T	0.013	SCF_11	11352273	11845501
PC2	SCF_12:6499845	C	T	0.021	SCF_12	5506154	7381157
PC2	SCF_12:8327248	C	A	0.02	SCF_12	7381157	9274787
PC1,PC2	SCF_13:3985893	C	G	0.014	SCF_13	3100520	4982931
PC2	SCF_13:4605607	A	T	0.021	SCF_13	3836346	5537067
PC2	SCF_13:4669546	A	G	0.021	SCF_13	3836346	5625853
PC1,PC2	SCF_13:4030824	A	G	0.014	SCF_13	4030824	4183417
PC2	SCF_13:10087880	C	T	0.016	SCF_13	9564621	11007512
PC2	SCF_13:10603817	A	G	0.037	SCF_13	10567681	10603817
PC2	SCF_13:11838713	G	A	0.027	SCF_13	11007512	12643667
PC1,PC2	SCF_14:1265250	T	G	0.017	SCF_14	902558	1265250
PC2	SCF_14:2405578	G	A	0.013	SCF_14	1580585	2798140
PC1	SCF_14:1682108	C	G	0.015	SCF_14	1682108	1682108
PC2	SCF_14:5392790	A	C	0.026	SCF_14	4836286	5889837
PC2	SCF_14:10138825	T	C	0.023	SCF_14	9239268	10564516
PC2	SCF_14:12673456	T	C	0.015	SCF_14	12673456	12869402
PC2	SCF_14:15094029	A	G	0.018	SCF_14	14362390	15696510
PC1	SCF_14:15282471	C	T	0.014	SCF_14	14413065	15589890
PC1,PC2	SCF_14:15377114	A	T	0.017	SCF_14	14413065	15696510
PC1	SCF_14:15183887	G	A	0.014	SCF_14	15094029	15377114
PC2	SCF_14:16904837	C	T	0.021	SCF_14	16749779	16904837
PC2	SCF_15:9373267	A	T	0.024	SCF_15	8644062	10069490

PC1,PC2	SCF_15:9770381	G	A	0.02	SCF_15	9373267	10712646
PC1,PC2	SCF_15:9812857	G	C	0.013	SCF_15	9373267	10712646
PC1	SCF_15:12966236	G	A	0.329	SCF_15	12002382	13906209
PC2	SCF_15:12654902	T	C	0.025	SCF_15	12247595	13145658
PC1	SCF_15:13246362	T	C	0.016	SCF_15	12545630	14014937
PC2	SCF_16:2473083	A	C	0.012	SCF_16	2473058	2473083
PC2	SCF_16:3532249	A	T	0.014	SCF_16	3532249	3532249
PC1,PC2	SCF_16:4559492	A	T	0.014	SCF_16	4442664	4830251
PC2	SCF_16:4830251	C	A	0.021	SCF_16	4442664	5790331
PC2	SCF_16:7279514	G	A	0.019	SCF_16	6427447	7542166
PC1	SCF_16:8085704	C	A	0.026	SCF_16	7959635	8085704
PC2	SCF_16:10960436	A	G	0.024	SCF_16	10265290	11496533

Table 2.S7 Enriched GO terms for closest genes to significant SNPs for PC 1 GWA

GO.ID	**Term**	**Annotated**	**Significant**	**Expected**	**P value**	**Enrichment**
GO:0040014	regulation of multicellular organism growth	2	1	0	017	2.77
GO:0031117	positive regulation of microtubule depolymerization	2	1	0	017	2.77
GO:1901537	positive regulation of DNA demethylation	3	1	0	025	2.60
GO:0061936	fusion of sperm to egg plasma membrane involved in double fertilization forming a zygote and endosperm	4	1	0	033	2.48
GO:0048768	root hair cell tip growth	20	1	0.02	0.0166	1.78
GO:0000466	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	20	1	0.02	0.0166	1.78
GO:0009819	drought recovery	22	1	0.02	0.0183	1.74
GO:0080111	DNA demethylation	30	2	0.03	0.0198	1.70
GO:0000463	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	24	1	0.02	0.0199	1.70
GO:0010268	brassinosteroid homeostasis	31	1	0.03	0.0257	1.59
GO:0010229	inflorescence development	36	1	0.03	0.0298	1.53
GO:0048235	pollen sperm cell differentiation	38	1	0.03	0.0314	1.50
GO:0016132	brassinosteroid biosynthetic process	40	1	0.03	0.0330	1.48
GO:0090333	regulation of stomatal closure	44	1	0.04	0.0363	1.44
GO:0010252	auxin homeostasis	51	1	0.04	0.0419	1.38
GO:2000058	regulation of ubiquitin-dependent protein catabolic process	60	1	0.05	0.0491	1.31

Table 2.S8 Enriched GO terms for closest genes to significant SNPs for PC 2 GWA

GO.ID	**Term**	**Annotated**	**Significant**	**Expected**	**P value**	**Enrichment**
GO:0010268	brassinosteroid homeostasis	31	2	0.08	026	2.59
GO:0016132	brassinosteroid biosynthetic process	40	2	0.1	043	2.37
GO:0009911	positive regulation of flower development	45	2	0.11	054	2.27
GO:1901537	positive regulation of DNA demethylation	3	1	0.01	073	2.14
GO:0048657	anther wall tapetum cell differentiation	4	1	0.01	097	2.01
GO:0098721	uracil import across plasma membrane	4	1	0.01	097	2.01
GO:0061936	fusion of sperm to egg plasma membrane involved in double fertilization forming a zygote and endosperm	4	1	0.01	097	2.01
GO:0098710	guanine import across plasma membrane	4	1	0.01	097	2.01
GO:0035344	hypoxanthine transport	4	1	0.01	097	2.01
GO:0098702	adenine import across plasma membrane	4	1	0.01	097	2.01
GO:1901684	arsenate ion transmembrane transport	4	1	0.01	097	2.01
GO:0090153	regulation of sphingolipid biosynthetic process	5	1	0.01	0.0121	1.92
GO:0070072	vacuolar proton-transporting V-type ATPase complex assembly	6	1	0.02	0.0145	1.84
GO:0001732	formation of cytoplasmic translation initiation complex	6	1	0.02	0.0145	1.84
GO:0033540	fatty acid beta-oxidation using acyl-CoA oxidase	6	1	0.02	0.0145	1.84
GO:0042542	response to hydrogen peroxide	80	2	0.2	0.0163	1.79
GO:0009644	response to high light intensity	81	2	0.21	0.0167	1.78

GO:1902975	mitotic DNA replication initiation	7	1	0.02	0.0169	1.77
GO:0002188	translation reinitiation	7	1	0.02	0.0169	1.77
GO:0019745	pentacyclic triterpenoid biosynthetic process	8	1	0.02	0.0193	1.71
GO:0016125	sterol metabolic process	94	2	0.24	0.0221	1.66
GO:0098719	sodium ion import across plasma membrane	10	1	0.03	0.0241	1.62
GO:0000727	double-strand break repair via break-induced replication	12	1	0.03	0.0288	1.54
GO:1902183	regulation of shoot apical meristem development	15	1	0.04	0.0359	1.44
GO:0010158	abaxial cell fate specification	16	1	0.04	0.0383	1.42
GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	17	1	0.04	0.0406	1.39
GO:0048564	photosystem I assembly	17	1	0.04	0.0406	1.39
GO:0031053	primary miRNA processing	18	1	0.05	0.0429	1.37
GO:0009555	pollen development	472	5	1.21	0.0438	1.36
GO:0002183	cytoplasmic translational initiation	30	2	0.08	0.0446	1.35
GO:0000394	RNA splicing, via endonucleolytic cleavage and ligation	19	1	0.05	0.0453	1.34
GO:0018107	peptidyl-threonine phosphorylation	20	1	0.05	0.0476	1.32
GO:0070475	rRNA base methylation	20	1	0.05	0.0476	1.32
GO:0006526	arginine biosynthetic process	20	1	0.05	0.0476	1.32
GO:0000466	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	20	1	0.05	0.0476	1.32
GO:0006271	DNA strand elongation involved in DNA replication	21	1	0.05	0.0499	1.30
GO:0009828	plant-type cell wall loosening	21	1	0.05	0.0499	1.30
GO:0001676	long-chain fatty acid metabolic process	21	1	0.05	0.0499	1.30

Table 2.S9 Putative candidate genes from GWA of bioclimatic principal components

TAG SNP	CAND.	NOTE
SCF_1:7039593	g1562	intergenic, next gene upstream is g1562, homolog of AT1G19220, ARF19
SCF_1:7144158	g1582	intergenic, next gene upstream is g1582, homolog of AT1G19530, RGAT1, pollen dev
SCF_1:14883355	g2897	in g2897, homolog of AT1G42470, pollen development
SCF_2:1119844	g4033	in g4033, homolog of AT1G62420, DUF overexpression represses root hair growth
SCF_2:10288969	g5011	in g5011, homolog of AT1G68670, Pi uptake
SCF_4:1376250	g9349	in g9349, homolog of AT2G23030, osmotic stress response
SCF_7:8624829	g19402	intergenic, gene upstream is g19402, homolog of AT3G13640, RLI1, RNA silencing suppressor
SCF_9:8559318	g25003	in g25003, homolog of AT1G20870, pos reg of DNA demethylation, HSP20-like chaperones superfamily
SCF_11:11388607	g31576	intergenic, next gene upstream is g31576, homolog of AT3G06430, PPR2, gametogenesis
SCF_11:11845501	g31615	intergenic, next gene upstream is g31615, homolog of AT2G13540, ABH1, floral regulators
SCF_13:4669546	g35452	intergenic, next gene downstream is g35452, homolog of AT3G32980, PRX32 osmotic stress
SCF_14:15282471	g39826	intergenic, next gene downstream is g39826, homolog of AT4G11720, pollen sperm cell diff
SCF_14:15377114	g39842	in g39842, homolog of AT4G11890, AA and osmotic stress signal transduction
SCF_14:15183887	g39808	tag is 653 bp downstream of g39808, homolog of AT4G11560, RVR1, flowering

CAND = Candidate locus from Cbp

Chapter 3: Population structure and genome-wide association mapping in a cowpea (*Vigna unguiculata* (L.). Walp.) core collection

Abstract

Understanding the relationship between genotypic variation and phenotypic variation is essential to crop breeding efforts. Here, we describe the diversity and population structure of 2,021 accessions constituting a core subset of the world's largest cowpea collection held at the International Institute of Tropical Agriculture (IITA). We find that population structure in cowpea is delineated by geography, with two major population groups defined by West and Southeast Africa, respectively. We further demonstrate the utility of this core collection for genome-wide association studies by mapping the genetic basis of seed pattern and color phenotypes. Our work identifies previously unknown candidate loci for both the red and blue seed coat colors. Overall, our work represents a mapping resource for the community and contributes insight into the genetic basis of complex traits in cowpea.

Introduction

Germplasm collections are critical repositories of biodiversity that serve to bolster crop improvement and ensure food security in a rapidly changing climate [1,23]. To prevent widespread yield losses in the future it is essential that we accelerate the process of linking genotype to phenotype to predict crop performance in the field. A core set of genotyped selections spanning the crop's phenotypic and genetic diversity is a powerful tool to identify the genetic architecture underlying agronomically relevant traits. The core collection methodology has been utilized in many crops such as rice[4], barley[5], and soybean[6].

Cowpea is an annual legume that was domesticated in Sub-Saharan Africa at least 5,000 years ago[7]. It is notable for being drought tolerant and is successful in both arid and semi-arid environments[8]. The crop is cultivated around the world, with the majority of contemporary production in West Africa (7.6 million tonnes in 2020, 8.9 million tonnes produced worldwide[9]), where it is primarily produced for food, fodder, and as a cash crop[8]. While many parts of the plant are edible[10], the cowpea grain is most commonly consumed due to its high protein content (average of 25% protein by dry weight)[11].

Despite being an important legume crop, the genetic resources available for cowpea are still being developed. Previous efforts to study genetic variation in cowpea have focused on minicore subsets of global cowpea variation[12,13] or regional collections of cowpea germplasm[14–17]. Numerous QTL mapping populations have been developed to link phenotype to genotype[18–21] in this species and the various collections have been used previously for genome-wide association mapping[13,22–24].

In this work, we describe the genetic diversity and population structure of a core collection of cowpea held at the International Institute of Tropical Agriculture (IITA), a CGIAR research center in Ibadan, Nigeria. The IITA Cowpea Collection is the largest collection of cowpea, currently consisting of 16,460 accessions (including 12,000 traditional cultivars/landraces) collected from 91 countries (March 2022[25]). The core collection, which is the focus of this study, consists of 2,082 accessions that were selected to represent the diversity of geography and agrobotanical traits present in the collection[26]. There is also a 376 accession mini-core subset that is contained within the core collection that has been studied previously[12].

Results

Genetic diversity of the IITA Core Cowpea Collection

We genotyped 2,021 accessions from the IITA Core Cowpea Collection[26] for 51,128 SNP markers with the Illumina Cowpea iSelect Consortium Array[27]. Filtering sites and samples for missing data and excess heterozygosity left 1,991 samples. The distribution of pairwise hamming distances between these samples was left skewed, suggesting that some near-identical varieties were present in the core material. We defined 400 near identical lines based on genetic distance (median group size = 2, max group size = 15). After removing nearly identical lines we were left with 1,722 samples genotyped for 48,004 markers for subsequent analysis. These 1,722 accessions represent 83% (N=2082, March 2022) of the accessions present in the Core Cowpea Collection and included 324/376 (86%) of the IITA Mini-Core Cowpea Collection[12]. The set of filtered accessions consists of 1,392 landraces/traditional cultivars (hereafter landraces), 171 breeding and research lines, 32 weedy accessions, and 15 wild accessions collected from 84 countries (Table 3.S1).

We examined genetic variation in the Core Collection by calculating folded allele frequency spectrums separated by germplasm class. Compared to weedy and wild germplasm, landraces and breeding material had an enrichment for very rare alleles (MAF <= 0.05), which could reflect the strong artificial selection on these accessions (Figure 3.1A). We also observed that landraces, weedy, and wild accessions are enriched for more common alleles (MAF > 0.05) compared to breeding lines. We interpret this result to mean that there is more segregating variation in landraces compared to breeding lines, but cannot make conclusive statements about variation in weedy and wild lines due to small sample sizes and ascertainment bias from the array. As expected for a highly self compatible species, the majority of sites had very low observed compared to expected heterozygosity (Bartlett test of homogeneity of variances, K-squared = 225096.90, df = 1, p-value = 0) (Figure 3.1B) and the sample inbreeding coefficients were high with a median value of 0.99 (Figure 3.1C). Mating system appears to be unrelated to domestication in cowpea as the inbreeding coefficient was not significantly different between wild and cultivated accessions (Welch's t-test p = 0.4581). The distribution of pairwise genetic distance was non-normal with distinct local maxima, suggesting the presence of population structure within the Core Collection . The median Hamming distance per sample ranged from 13888.70 to 42170.30 (Figure 3.1D).

Selection during domestication

Compared to wild accessions, domesticated cowpea have been selected for annual lifecycle, early flowering, determinate growth pattern, increased pod and seed size, reduced pod shattering, and diversity of seed color[20]. To identify regions of the genome that have undergone selection during domestication, we calculated the XP-CLR statistic[28] in windows for wild versus breeding accessions. The top 1% of 20 KB windows were distributed across all 11 chromosomes, suggesting the loci under selection during domestication are distributed across the genome and not localized to just a few loci

(Figure 3.S1). A gene ontology (GO) enrichment analysis of genes within the top 1% of windows revealed an enrichment for numerous GO terms related to domestication traits and plant development such as GO:0008356 asymmetric cell division, GO:2000028 regulation of photoperiodism, flowering, GO:0009956, radical pattern formation, GO:0048366 leaf development, and GO:0009813 flavonoid biosynthetic process (Figure 3.S2).

Population structure

We analyzed population structure in the Core Collection by applying ADMIXTURE[29,30] to 4,245 markers in approximate linkage equilibrium. The maximum ΔK value was observed at K = 2 (Figure 3.2A), suggesting that population structure within the Core Collection is best modeled using 2 subpopulations. We assigned 1,228 samples to Cluster 1, 1,360 samples to Cluster 2, and considered 856 samples to be admixed (< 70% of ancestry originating from a cluster). Breeding lines and landraces were nearly evenly distributed between clusters while weedy and wild accessions were more common in Cluster 2 compared to Cluster 1 (Table 3.S1). The clusters are strongly differentiated genetically (Fst = 0.292) and defined by geography with Cluster 1 ancestry attributed to Southeast Africa and Cluster 2 ancestry attributed to West Africa (Figure 3.2B, Figure 3.S3). Samples that were recently introduced outside of Africa have ancestry originating from both clusters.

Modeling population structure with 3 subpopulations reclassifies 372 Cluster 2 and 246 admixed samples to a new Cluster 3. Cluster 3 is defined by samples from North Africa collected in proximity to the Nile River Delta (Figure 3.2B, Figure 3.S6). The climate near these Nile River samples is arid (Köppen climate classification: BWh/BWk) compared to the wet tropical climates inhabited by samples in Clusters 1 and 2. Additionally, nearly all of the SNPs previously assigned to Cluster 2 ancestry in samples recently introduced outside of Africa were reassigned to Cluster 3 when considering three subpopulations. This result suggests that samples assigned to Cluster 2 are probably locally adapted to tropical climates while samples assigned to Cluster 3 are locally adapted to arid climates.

Considering K = 4 yields a fourth subpopulation cluster that describes samples with a high degree of admixture when modeled with fewer subpopulations. Samples assigned to Cluster 4 are primarily found in a region of West Africa with a Tropical savanna climate (Köppen climate classification: Aw/As) and are intermixed with samples assigned to both Clusters 1 and 2 (Figure 3.2B, Figure 3.S7).

A principal component analysis (PCA) of our genotype dataset was largely consistent with our ADMIXTURE results. The first 10 PCs explain 27% of the variance between samples with nearly half of the variance (12.8%) explained by the first 2 PCs alone (Figure 3.2C). The distribution of samples along PCs 1 and 2 is continuous, suggesting few differences between adjacent samples. The subpopulation clusters determined by the ADMIXTURE analysis are non-overlapping on PCs 1 and 2, corroborating the subpopulation assignments.

Taken together, our results indicate that population structure in African cowpea is strongly linked to geography with the major division being between West and Southeast Africa.

Phenotypic distributions of subpopulations

The IITA Cowpea Characterization and Cowpea Evaluation datasets consist of 15 quantitative and 28 qualitative phenotypes[25,26]. To facilitate analysis of these datasets, we combined redundant phenotypes and separated qualitative phenotypes by state, encoding them as either discrete or binary variables. We classified the resulting 71 phenotypes into 11 categories: seed pigmentation, disease susceptibility, seed morphology, plant architecture, inflorescence morphology, pod pigmentation, pod morphology, leaf morphology, flower pigmentation, plant pigmentation, and maturity (Table 3.S2-S3).

Population structure in cowpea is strongly linked to differentiation in phenotype. We observed statistically significant differences in the distributions of 17 / 34 quantitative phenotypes (Table 3.S4) and in the frequency of 17 / 37 of the qualitative phenotypes (Table 3.S5) between the two clusters (Figure 3.3A). The West African cluster flowered earlier, was more branched, and produced larger lateral organs than the Southeast African cluster (Mann Whitney Wilcoxon test, multiple-testing corrected p-value < 0.05, Figure 3.3B-I). We also observed statistically significant differences in the distributions of 9 quantitative phenotypes with discrete values (Figure 3.S8), but caution that the differences in the distributions of these traits are difficult to interpret given the ordinal nature of these data.

For the binary-encoded qualitative traits, we examined the differences in trait frequency between Clusters. We identified 2 seed pigmentation traits, gray seed coat color and eye pattern A61, and one disease susceptibility trait that were not observed in admixed accessions. A total of 4 seed pigmentation traits, including speckled pigmentation pattern, and 2 disease susceptibility traits were not observed in Cluster 1 accessions. Eye pattern A81 and susceptibility to wet stem rot were the only traits absent from Cluster 2. The frequency of traits missing from one group tended to be at low frequency in the remaining groups (range 0.19% - 7.8%, median 0.6%). Of the 17 traits with statistically significant differential frequency between Cluster 1 and Cluster 2, 9 traits had a difference in frequency greater than 10% (Figure 3.3J). There were also 5 traits with frequency difference greater than 10% between Admixed samples and Cluster 1, and Admixed samples and Cluster 2, respectively (Figure 3.3K-L).

The genetic architecture of pigmentation patterning

Seed coat pigmentation pattern and color are very diverse in cowpea and are important consumer-preference traits targeted by breeding programs[8]. The genetic basis of seed color and pattern in cowpea has been studied for over 100 years[31–33]. Seed coat pigmentation pattern is thought to be genetically determined by a three locus system corresponding to the color factor (C locus), Watson factor (W locus) and Holstein factor (H locus)[34,35]. Candidate loci for the three seed coat pigmentation pattern factors have been reported previously based on QTL mapping and consist of a MYC transcription factor with a basic-helix-loop-helix (bHLH) domain (C locus), a WD40 repeat (WDR) superfamily gene (W locus), and an E3-ubiquitin ligase (H locus), respectively[18]. Flavonoid biosynthesis is thought to be regulated by complexes of MYB-bHLH-WDR genes[36] and a model where the W locus gene forms a complex with the C locus gene and an R2-R3 MYB to form a transcriptional activation complex (that can be repressed by the H locus) for flavonoid biosynthesis has been proposed for cowpea[18].

To demonstrate the power of the Core Collection we used the wide spectrum of seed coat pigmentation patterns to map the genetic basis of seed pigmentation traits. We identified two regions of the genome that were associated with numerous seed coat pigmentation patterns (Figure 3.4A-E). The locus on Vu09 was associated with all five pigmentation patterns, spans 1.38 Mbp (Vu09:30035583-30035583) and contains 116 genes (Figure 3.4F). The small eye, large eye, and Holstein pigmentation patterns were associated with the minor A allele at 2_01960, while the Watson and self colored pigmentation patterns were associated with the major G allele. We confirmed that *Vigun09g139900*, a WD-repeat gene identified by[18] as a candidate gene for the W locus, is present in the region between the tag SNP (2_01960) and a linked upstream significant SNP. Furthermore, the candidate gene is surrounded by other significant variants that are not linked with the tag SNP, suggesting that there may be more than one haplotype segregating in this region associated with the pigmentation pattern phenotypes.

The locus on Vu10 was associated with the small eye, Watson and self colored pigmentation patterns (Figure 3.4A-E). The locus is small, spanning 12 KB (Vu10:38454820-38467161) and overlaps with *Vigun10g165400*, an R2-R3 MYB transcription factor (Figure 3.4G). The minor C allele at 2_31919 was associated with the Watson and small eye patterns, while the major T allele was associated with the self colored pattern.

We also mapped an additional locus on Vu10 that was associated with the Holstein pigmentation pattern only (Figure 3.4C). The locus spans 189 KB (Vu10:41100865-41290623), contains 23 genes, and has numerous downstream SNPs in very high linkage (Figure 3.4H). We identified *Vigun10g199800*, a polyketide cyclase/dehydrase, as a candidate gene for this locus.

Notably, we did not map the C (color) locus on Vu07 in any of the coat pattern phenotypes except for the hilum ring and eye absent patterns (Figure 3.S9). The speckled coat pattern mapped to many loci across the genome and did not yield any clear candidates (Figure 3.S10).

The genetic architecture underlying cowpea seed color

In contrast to pigmentation patterning, seed coat color is less well understood in cowpea. There appears to be at least 4 loci that underlie the genetic basis of seed color in cowpea[33]. A R2-R3 MYB transcription factor has been identified as a candidate locus controlling black seed coat and purple pod tip[37], but to date the genetic basis of most seed color traits in cowpea remains obscure.

We identified four regions of the genome that were associated with seed coat color phenotypes. The region on Vu03 is associated with both the red and tan colors (Figure 3.5A-B), spans 274 KB (Vu03:10933603-11208404) and contains 25 genes (Figure 3.5F). The minor T allele at 2_20787 is associated with red seed color, while the major G allele is associated with tan color. The tag SNP is within *Vigun03g118700*, an anthocyanin reductase and thus a compelling candidate. However, the next gene downstream, *Vigun03g118800*, is also an anthocyanin reductase and thus should also be considered to be a strong candidate at this locus. Although our analysis does not have the power to discriminate between these two strong candidate genes, *Vigun03g118700* is expressed at an extremely high level in early seed development while *Vigun03g118800* is expressed at a low level across tissues and developmental timepoints[38] (Figure 3.S11). Black and tan seed color shared a strong peak on Vu05 (Vu05:3104538-3225877) spanning 121 KB and 13 genes (Figure 3.5B-C). This peak was also observed at the top hit for pattern of pigmentation on green pod. In this region we confirmed the candidate gene *Vigun05g039500*, a R2-R3 MYB transcription factor, that was previously identified as associated with black seed coat and pod tip[37]. The minor C allele at 2_19309 was associated with the black seed coat phenotype while the major T allele was associated with the tan seed coat phenotype.

We identified a 155 KB region on Vu06 (Vu06:13491073-13645944) that was associated with the blue seed coat and spans 4 genes (Figure 3.5D). The top SNP (2_22603) is in *Vigun06g031000*, a flavin amine oxidase gene (Figure 3.5G). The minor G allele is associated with having a blue seed coat. White seed color mapped to the Vu10 locus described previously (Figure 3.4G). There were no significant SNPs for the mapping of brown seed coat color.

Mapping of additional phenotypes

In addition to dissecting the genetic basis of pigment color in cowpea, we mapped the genetic basis of 71 distinct phenotypes. Despite the fact that many of these traits were collected across trials and years, we identified 748 significant SNPs across 42 phenotypes. The number of significant SNPs per analysis ranged from 1 to 106, with a median of 8. A total of 698 of the significant SNPs were associated with variation in only one phenotype, while 50 SNPs were associated with more than one phenotype. We found numerous interesting peaks for other traits. Pigmentation of vegatative tissues had a significant SNP (2_33257, Vu07:10637029) within the gene *Vigun07078100*, an integral membrane TerC family protein that is a homolog of *AT5G12130* (*PROTEIN-PIGMENT DEFECTIVE 149*, *Arabidopsis thaliana).* A significant SNP for trait pattern of pigmentation on flower (2_05822, Vu07:25947911) is adjacent to *Vigun07g148800*, an E3 ubiquitin-protein ligase. The trait incidence of rust had two loci with clear candidate regions, a significant SNP in a 12-oxophytodienoate reductase (*Vigun02g192500*) involved in the Jasmonic acid biosynthesis pathway and a very strong peak on Vu12 spanning 90KB (2156441-2246970) spanning numerous TIR-NBS-LRR disease resistance genes. Finally, hastate terminal leaf shape had a significant SNP in *Vigun09g156900* (*SCARECROW-LIKE PROTEIN 1*). A full list of significant regions across all association mapping analyses is available in Table 3.S6.

Discussion

Throughout the 20th century, considerable efforts were directed towards establishing rich germplasm collections for many crops with the goal of supporting breeding programs, enabling research, and ensuring food security[2]. Given that the size of many existing germplasm collections are large and at least partially redundant across the spectrums of genotypic and phenotypic diversity present in a species, it is not economically feasible to evaluate an entire collection for a trait or locus of interest. To circumvent this, core collections that represent the genotypic and phenotypic diversity present in a germplasm collection using a subset of collected lines have been established and have been used extensively for germplasm evaluation[39,40]. In this study, we used microarray-based genotyping to characterize the patterns of genetic variation in a core collection of cowpea held at IITA and demonstrated that this collection has the potential for successful genome-wide association mapping.

One surprising finding from this work is that there is a substantial number of samples in the Core Collection that are genetically identical to one or more other samples. This finding is indicative of the fact that the initial selection of lines was based on variation across geography and phenotype and did not utilize genetic markers[26]. The genetic redundancy in this collection is probably due to human-dispersal of identical lines across geopolitical boundaries which were then sampled after dispersal in an attempt to select lines representative of the geopolitical regions present in the collection. We speculate that patterns of genetic redundancy are also present in other core collections and highlight here the advantage of using modern genotyping to detect identical lines.

The analysis of population structure revealed that the germplasm held in the IITA Cowpea Collection is broadly genetically differentiated into two clusters, with one cluster representing accessions endemic to West Africa and the other representing accessions endemic to Southeast Africa. The segregation of the germplasm into these two groups is consistent with previous analysis of population structure of 105 IITA breeding lines and 41 landraces, which yielded the same conclusion as the present study[27]. However, additional analyses of population structure in other subsets of the world cowpea germplasm have found additional subpopulation clusters. Population structure analyses of the IITA minicore (included in the IITA core collection) and UCR minicore (233 overlapping accessions with the IITA core collection) both yielded two subpopulation clusters within West Africa and separate clusters of samples from North Africa[12,13]. The division of samples from West Africa into two separate subpopulations and North Africa as a separate subpopulation was also found in our analysis when considering K > 2 subpopulations. Consistent with the hypothesis that West Africa is the center of diversity for cowpea[13], the samples present in cluster 4 when modeling 4 subpopulations appear admixed (i.e. between the other clusters) in the PCA (Figure 3.2). While we hold the view that the pattern of genetic differentiation in global cowpea germplasm is broadly defined by West vs. Southeast Africa, we admit that the method we used for determining the number of subpopulations is imperfect and likely biased towards adopting K = 2 subpopulations[41].

The IITA Core Collection represents the largest panel that has been used for genome-wide association mapping in cowpea. Although we were able to identify many regions of the genome that were significantly associated with variation of many diverse phenotypes, we were largely unsuccessful in mapping variation in continuous traits. For example, we were unable to identify loci associated with variation in flowering time, despite this trait being highly heritable and successfully mapped previously in this species using smaller association mapping panels[22]. Although there are many factors that influence the power to identify significant loci using GWAS (reviewed[42]), our lack of success in mapping the genetic basis of continuously distributed quantitative traits is likely due to our inability to control for the contribution of environmental variance to phenotypic variance. Unfortunately, the continuously distributed phenotypes represent reference trait values used for breeding purposes and were collected across many environments, years and sites without record. We anticipate that the genetic basis of a continuously distributed phenotype would be able to be elucidated using the Core Collection panel if the full cohort was phenotyped in a single experiment.

However, we were successful in mapping traits that do not have environmental variance such as seed coat pigmentation patterns and color. Our mapping results confirmed the candidate genes previously proposed for the C locus on Vu07 (*Vigun07g110700*), the W locus on Vu09 (*Vigun09g139900*)[18], and the locus on Vu05 for black seed coat color and purple pod tip (*Vigun05g039500*)[37]. However, we were unable to map the candidate gene previously proposed for the H locus on Vu10 (*Vigun10g16390*). Instead, we identified two candidate loci that could represent either the H factor or genes that interact with the H factor. The first locus was identified in the small eye, Watson, and self colored mapping studies and consists of a ~12 KB region spanning the R2-R3 MYB *Vigun10g165400*. It has been speculated previously that this R2-R3 MYB gene might interact with the H locus candidate gene proposed by[18]. The second locus was identified in the association mapping for the Holstein coat pattern, where we are proposing *Vigun10g199800*, a polyketide cyclase/ dehydrase, as a candidate since polyketides are precursors in anthocyanin biosynthesis[43]. Further study is needed to evaluate the merit of the proposed candidate genes for the H locus. In particular, it is of interest to determine whether the Holstein pattern is regulated by one gene or two closely linked genes as has been speculated for quite some time[32]. It is also possible that the Holstein pattern is subject to allelic heterogeneity, which could explain our inability to map the H locus candidate gene derived from QTL mapping studies.

In addition to lending support to previously established candidate loci regulating seed pigmentation pattern and color in cowpea, we were able to propose candidates for both the red and blue seed coat colors based on our association mapping results. Our results suggest a model in which Tan seed coat color is caused by a combination of alleles at both the R and B color loci that are different from the alleles that cause the red and black seed coat phenotypes. The candidate locus for the blue seed coat phenotype, *Vigun06g031000*, a flavin amine oxidase gene, is a potential modifier of anthocyanin. Molecular characterization of these novel proposed loci is required to confirm the activity of the candidate loci.

This work represents the largest survey of the cowpea world germplasm collection that has been studied. Using this resource, we were able to yield new insights into the genetic basis of seed pigmentation traits and propose numerous candidate genes for molecular characterization.

Materials and Methods

Genotyping and variant filtering

Accessions were genotyped using the Cowpea iSelect Consortium Array which assays 51,128 SNPs as described in[27].

SNPs with greater than 95% of missing calls across samples were filtered first, followed by filtering of samples with greater than 50% missing calls or more than 20% heterozygous calls across sites. Near identical lines were identified by calculating pairwise Hamming distance between samples with plink 1.9[44], applying hierarchical clustering to the distance matrix, and defining clusters of accessions using a static tree cut at height of 500. We randomly selected one sample from each cluster to retain for subsequent analysis.

From the filtered SNP set, we also produced a set of SNPs in approximate linkage equilibrium by first subsetting to SNPs with minor allele frequency greater than or equal to 0.01 with no more than 5% missing calls. The filtered SNPs were then pruned pairwise in 50 SNP windows with a step size of 10 and an R^2 threshold of 0.20. All SNP filtering and pruning was done using plink 1.9[44]. The pruned SNP set was used for the calculation of inbreeding coefficients and for all population structure analyses.

Genetic diversity statistics

Allele frequencies, sample inbreeding coefficients, and pairwise genetic distances were calculated using plink v.1.9[44]. Expected and observed heterozygosity per site were calculated with the adegenet v. 2.1.5 R package[45].

Selection tests

XP-CLR statistic[28] was calculated in 20 KB genomic windows containing 2 or more SNPs using xpclr 1.1.2[46]. Gene ontology enrichment analysis was performed for genes within the top 1% of windows with topGO[47] using the “weight01” algorithm to prune the directed acrylic graph and Fisher’s Exact Test to test for enrichment (all other parameters were default). GO terms with $p < 0.05$ were considered to be significantly enriched.

Population structure

Population structure was analyzed using ADMIXTURE 1.3.0[29,30] for K = 1 to 10 with 10 replicates per K. The most likely K value was determined using the Evanno method[48].

ADMIXTURE runs were post-processed and visualized using the pophelper 2.3.1 R package[49]. Samples were assigned to the group contributing 70% or more of the sample's estimated ancestry fraction. All other samples were considered to be admixed.

Principal component analysis on allele frequencies was done using the adegenet v. 2.1.5[45] R package. The mean allele frequency at a locus was substituted for missing genotype calls.

Phenotypic analyses

Phenotypic data were downloaded from the International Institute of Tropical Agriculture (IITA) website[25] and consisted of 15 quantitative and 23 qualitative traits. The data were collected as part of the IITA cowpea breeding program across multiple field trials spanning many years and thus represent reference values used for breeding. For the analysis, seed color pigmentation traits were defined according to the majority color of the seed and similar traits were combined as described in Table 3.S2. Qualitative traits were coded into binary "case/control" variables using the fastDummies 1.6.3 R package[50] or considered to be discrete numerical variables. Differentiation in phenotype distribution between population structure clusters was tested using Mann Whitney Wilcoxon tests for quantitative phenotypes and Fisher's Exact test for qualitative phenotypes in R[51]. Two-sided tests were used for all analyses and a Bonferroni adjusted threshold was used to determine significance at $\alpha = 0.05$.

Genome-wide association mapping

Univariate mixed linear models were fit with GEMMA 0.98.4[52]. The models included a centered relatedness matrix to correct for spurious associations due to population structure. Only sites with minor allele frequency greater than 0.01 and missing in fewer than 5% of samples were tested in this analysis. Continuous quantitative phenotypes were log-transformed prior to analysis. Bonferroni correction was used to correct p-values for multiple testing and significance was assessed at $\alpha = 0.05$. Linked significant SNPs ($R^2 > 0.20$) within 1 Mbp were considered to define a single peak and the SNP with the lowest p-value per peak was assigned to be the “tag SNP.” Candidate genes were identified by examining the overlaps between significant peaks and loci described in the *Vigna unguiculata* v.1.2 genome annotation[53].

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Figures and Tables

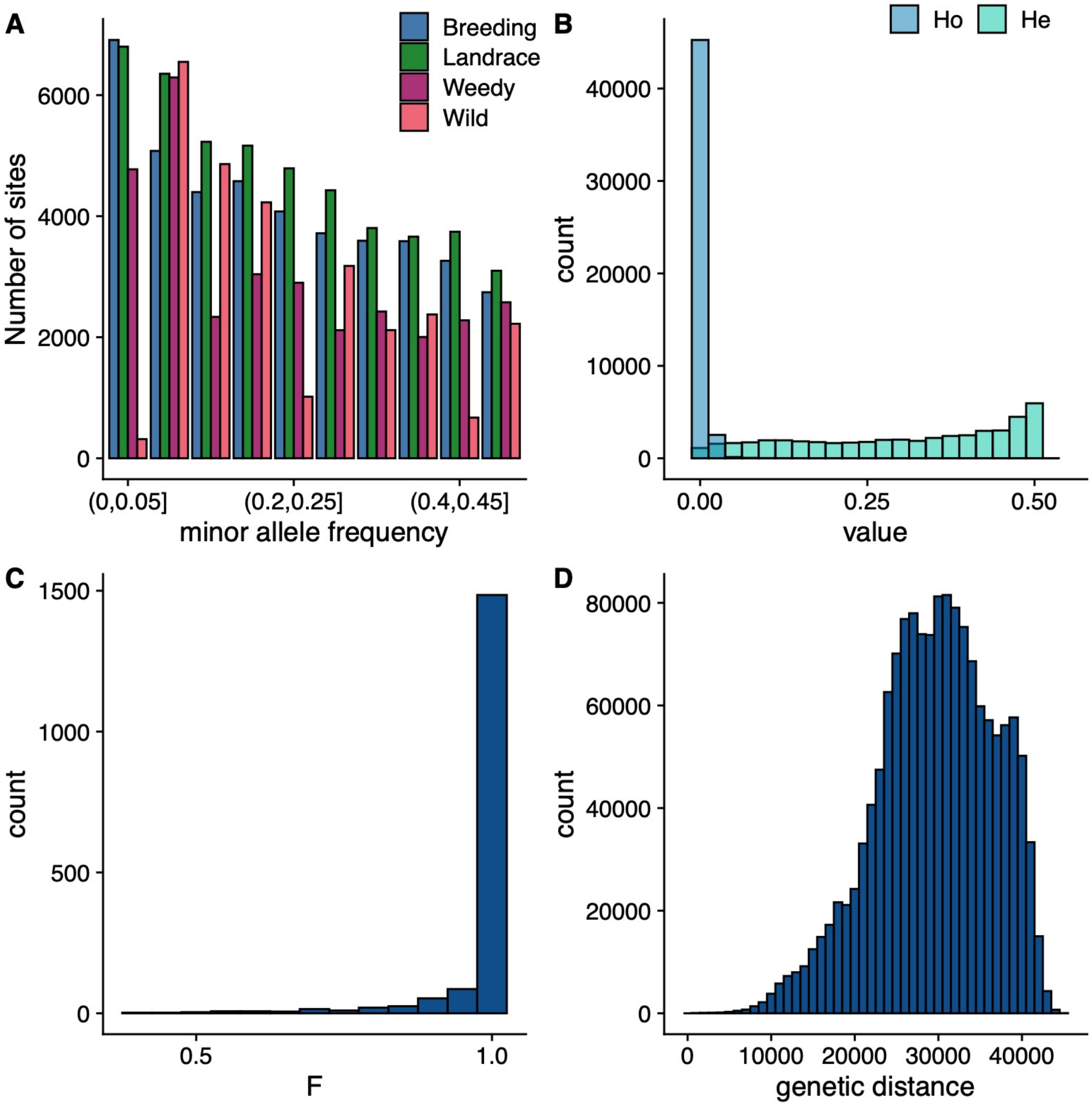

Figure 3.1 Genetic diversity of the IITA Core Cowpea Collection

A) Folded allele frequency spectrum by accession biological status in 0.05 frequency bins. B) Distributions of expected and observed heterozygosity across sites. One value of Ho > 0.50 is omitted and a binwidth of 0.025 was used. C) Inbreeding coefficient estimates per sample in binwidth of 0.05. D) Distribution of pairwise genetic distance per sample in allele counts in binwidth of 1000.

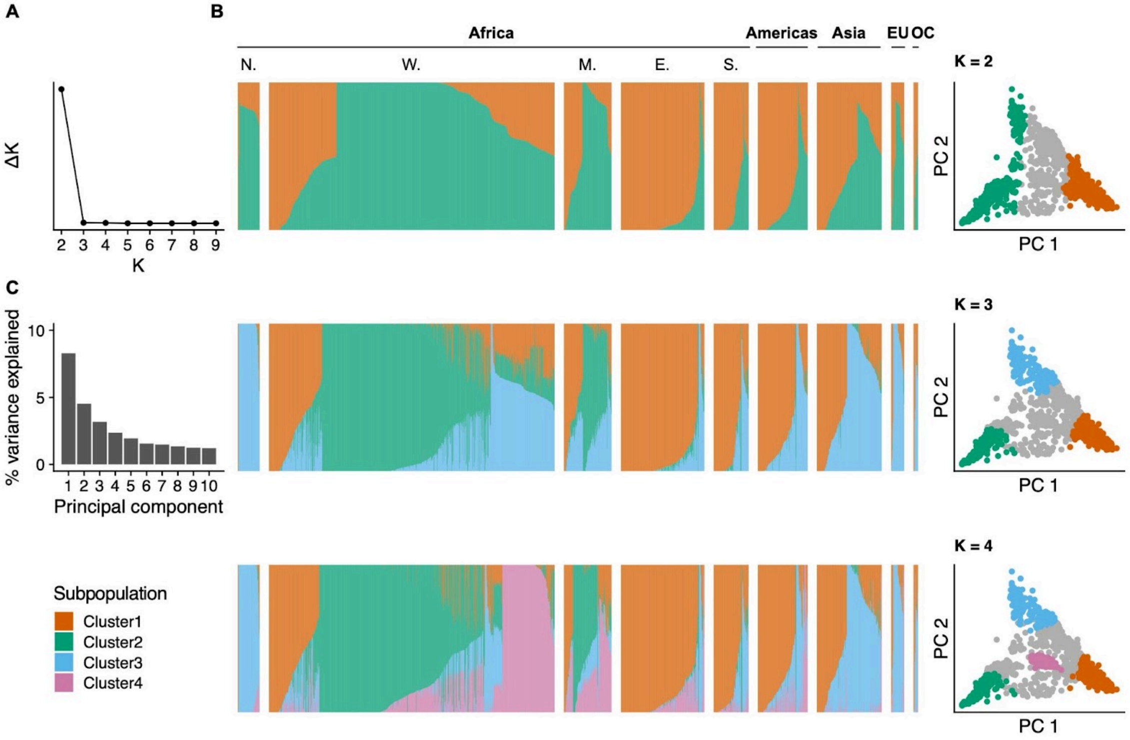

Figure 3.2 Population structure analyses

A) Delta K (second order rate of change of mean log likelihood / standard deviation of log likelihood) for 10 ADMIXTURE runs modeling 1 to 10 inferred subpopulations. B) Proportion of ancestry per individual and principal component analysis of genotype frequencies for K = 2, K = 3, and K = 4 subpopulation clusters. Regional groups: EU-Europe, OC-Oceania. Subregions of Africa: N-Northern, W-Western, M-Middle, E-Eastern, S-Southern. C) Percent variance explained across the first 10 principal components.

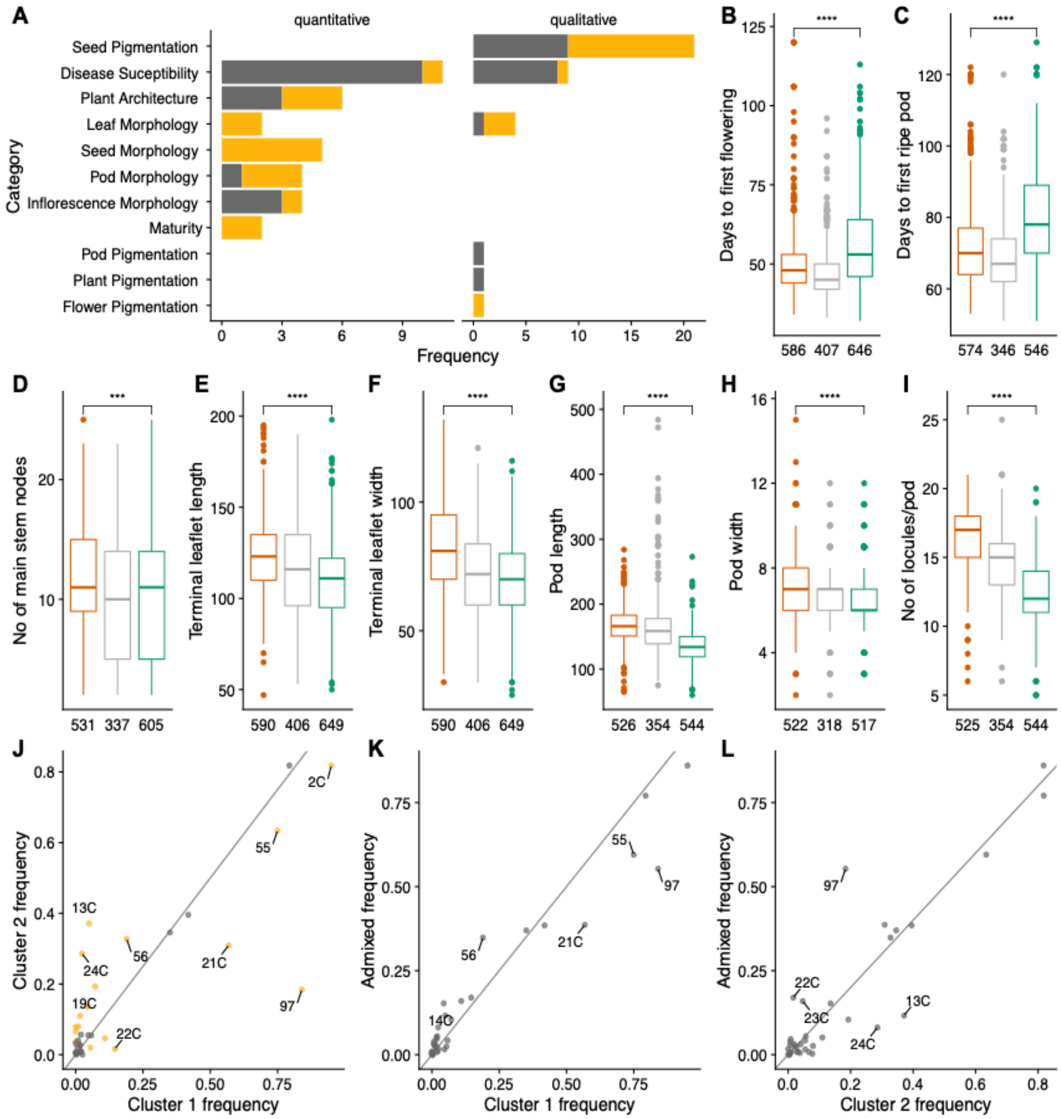

Figure 3.3 Phenotypic distribution between population subclusters

A) Assignment of phenotypes by type into 11 categories. Bars are filled according to the number of statistical tests (Wilcox-Mann-Whitney for quantitative, Fisher's Exact Test for qualitative) with p-value below significance (goldenrod) or insignificant (dark grey). B-I) Tukey's boxplots for quantitative phenotypes with significant differences between clusters. Middle group is Admixed and numbers below boxplots indicate the N per group. Colors match key from Figure 2. J) Frequencies of qualitative traits in Clusters 1 and 2. Goldenrod points are phenotypes with statistically significant differential frequency. K) Frequencies of qualitative traits in Cluster 1 and Admixed samples. L) Frequencies of qualitative traits in Cluster 2 and Admixed samples. In J-K, phenotypes with a frequency difference > 10% are labeled by phenotype ID (Table 3.S2).

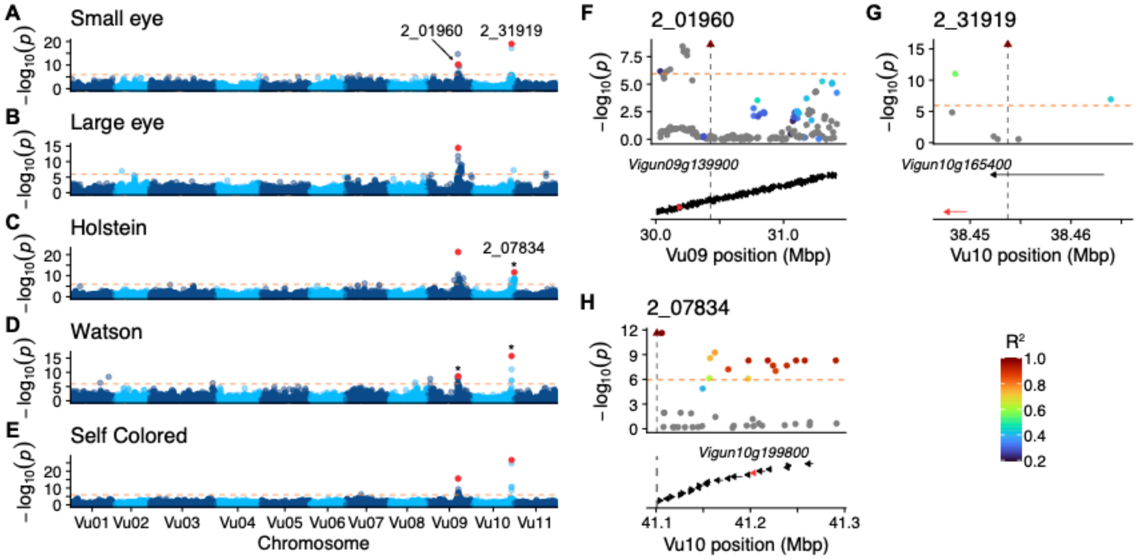

Figure 3.4 The genetic basis of seed coat pigmentation pattern

A-E) Manhattan plots from genome-wide association mapping of seed coat pigmentation pattern phenotypes. Orange line indicates Bonferroni corrected significance threshold. Tag SNPs are highlighted in red and labeled. Tag SNP 2_07834 is unique to Holstein, highlighted SNP on Vu10 in Watson and Self Colored correspond to 2_31919. F-H) Local linkage equilibrium for tag SNPs (triangle) for peaks indicated by * in A-E. Candidate genes are indicated in red and labeled.

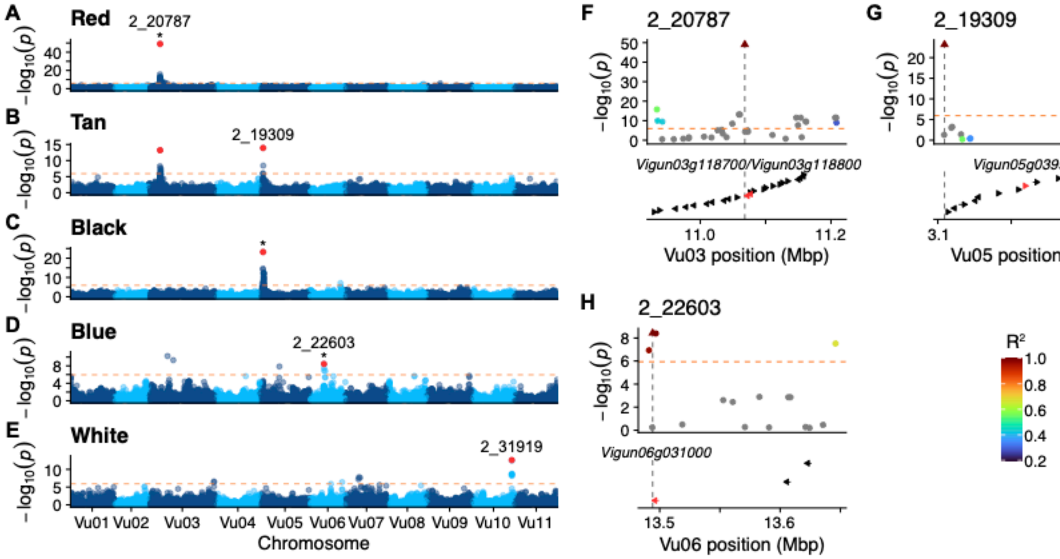

Figure 3.5 The genetic basis of seed coat color

A-E) Manhattan plots from genome-wide association mapping of seed color phenotypes. Orange line indicates Bonferroni corrected significance threshold. Tag SNPs are highlighted in red and labeled. F-H) Local linkage equilibrium for tag SNPs (triangle) for peaks indicated by * in A-E. Candidate genes are indicated in red and labeled.

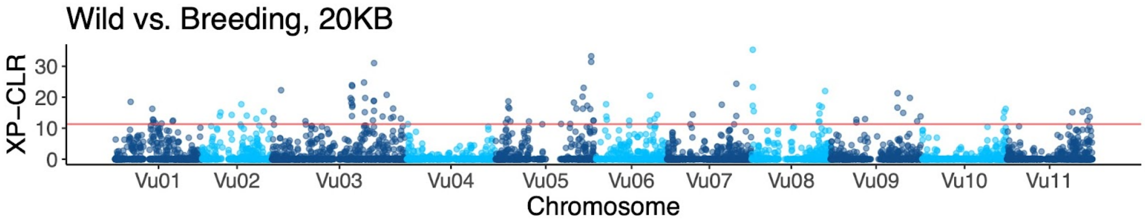

Figure 3.S1 Selection scan to identify regions of the genome under selection during domestication.

Each point indicates XP-CLR statistic for a 20KB non-overlapping window.

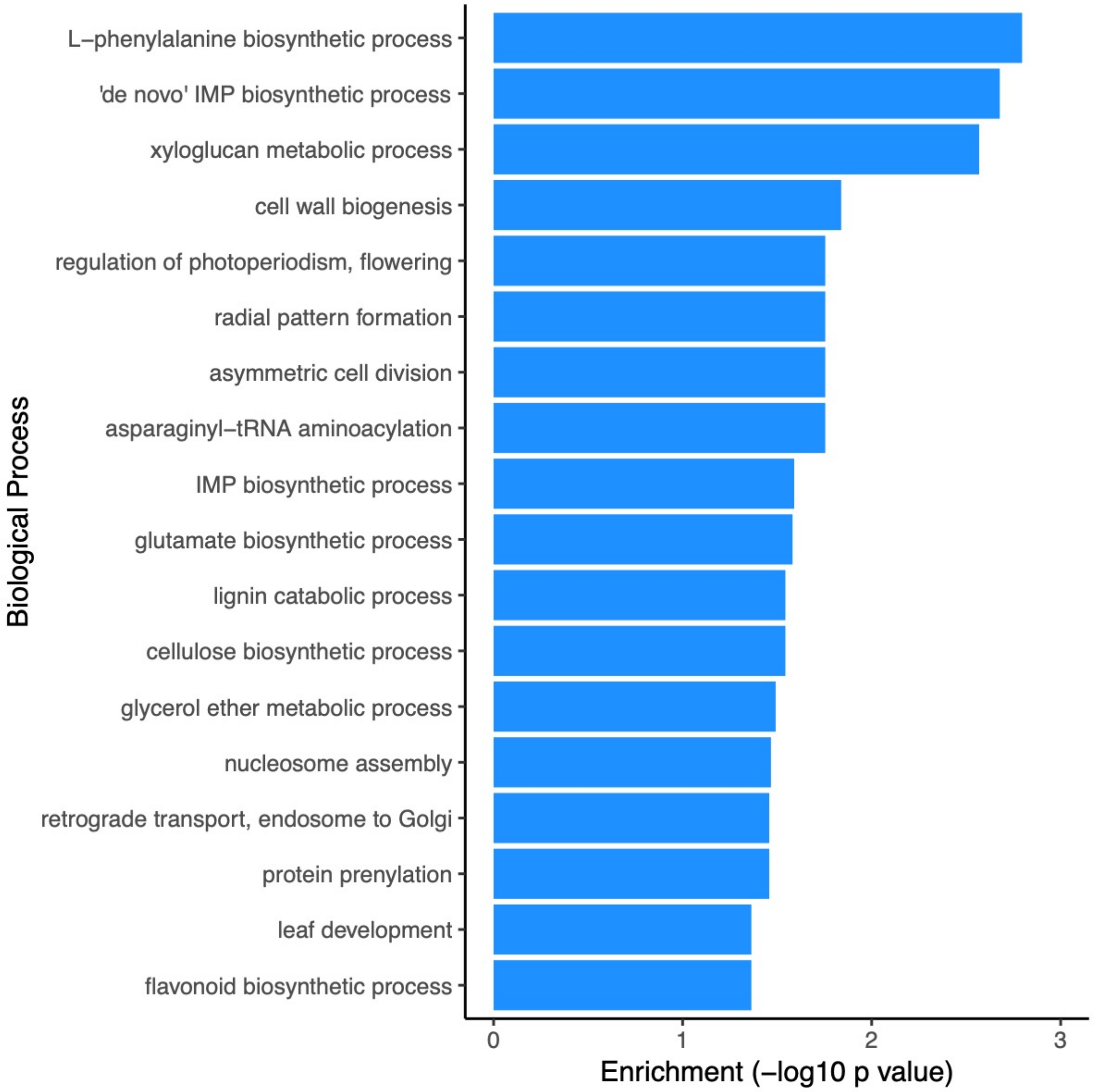

Figure 3.S2 Enriched gene ontology terms in top 1% of 20 KB windows under selection during domestication.

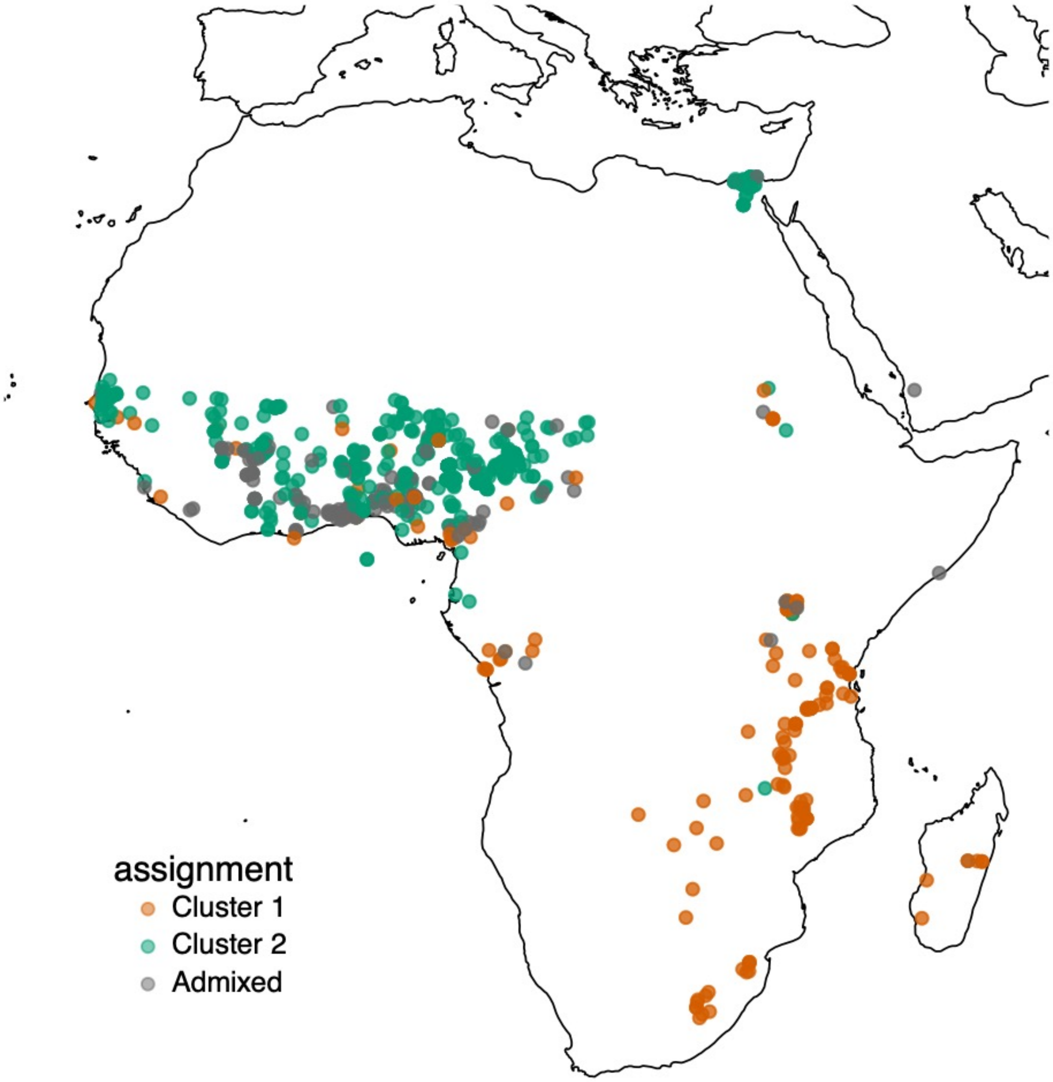

Figure 3.S3 Admixture of samples for K = 2.

Samples are plotted according to their collection site and pie charts indicate the proportion of ancestry attributed to each clusters. Only samples identified as traditional cultivars/landraces, weedy, or wild and collected in Africa are shown.

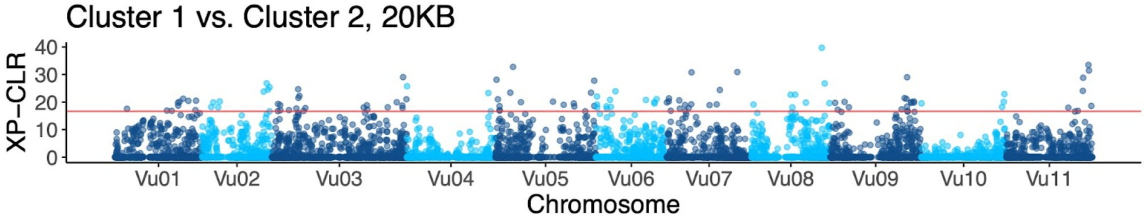

Figure 3.S4 Selection scan to identify regions of the genome under selection during population differentiation.

Each point indicates XP-CLR statistic for a 20KB non-overlapping window.

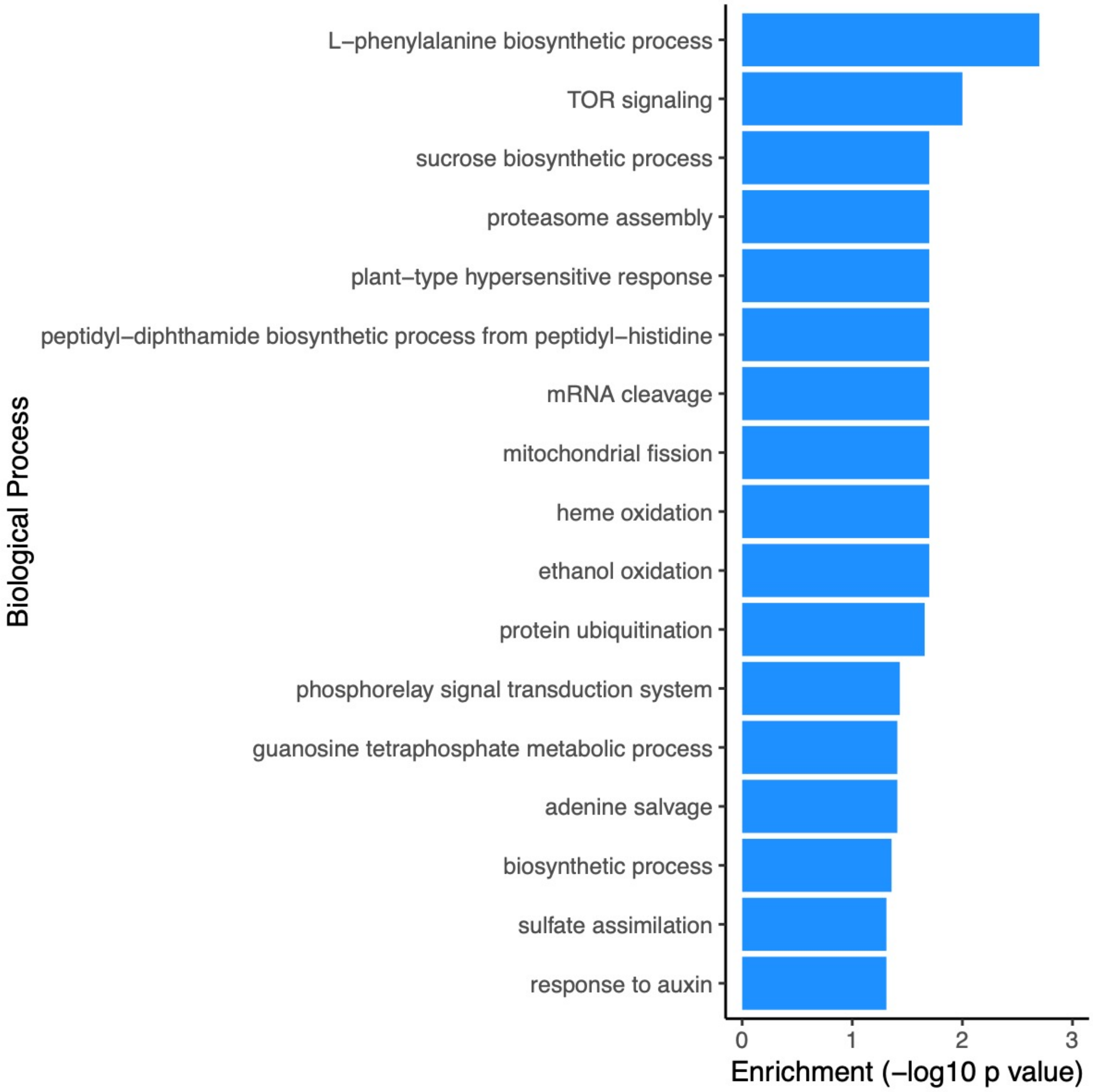

Figure 3.S5 Enriched gene ontology terms in top 1% of 20 KB windows under selection during population differentiation.

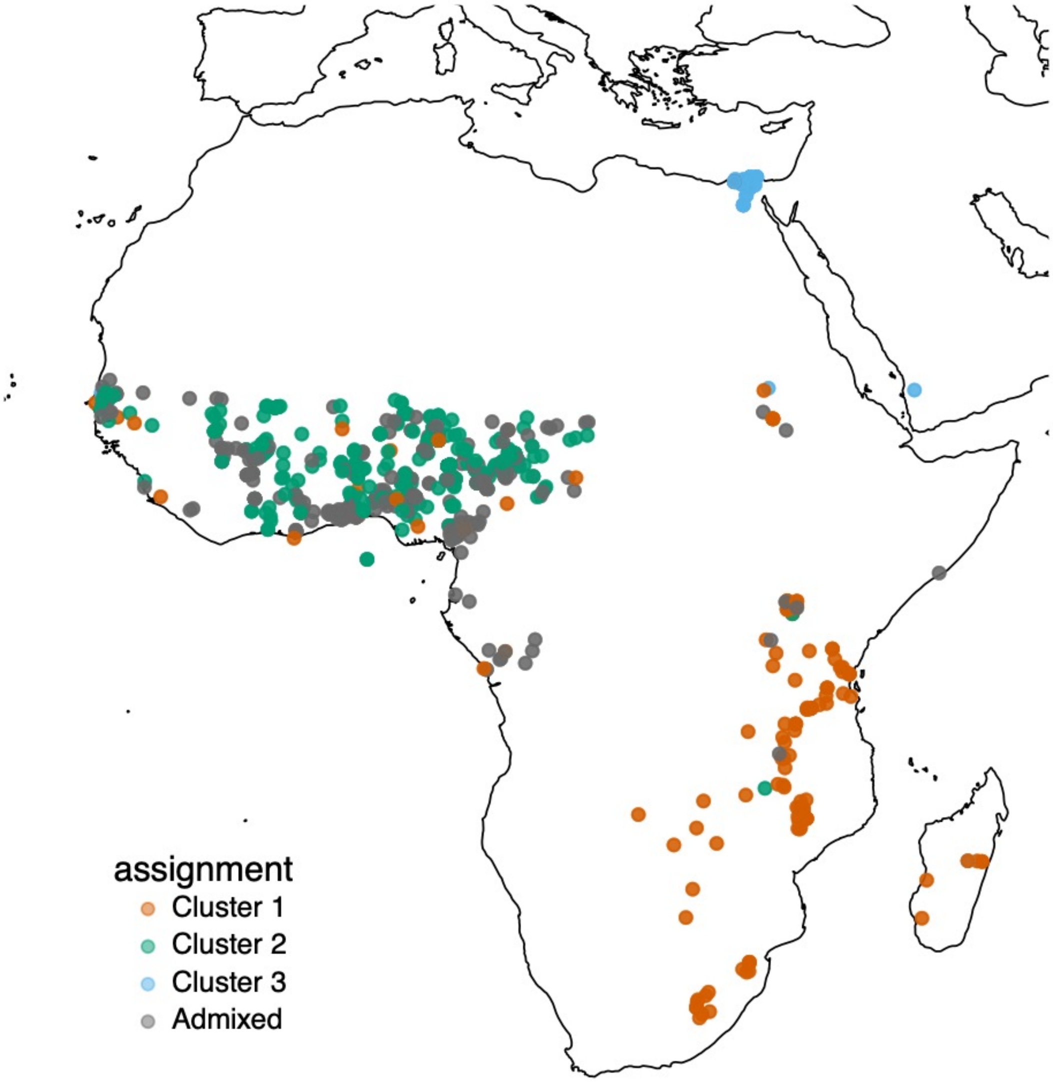

Figure 3.S6 Admixture of samples for K = 3.

Samples are plotted according to their collection site and pie charts indicate the proportion of ancestry attributed to each clusters. Only samples identified as traditional cultivars/landraces, weedy, or wild and collected in Africa are shown.

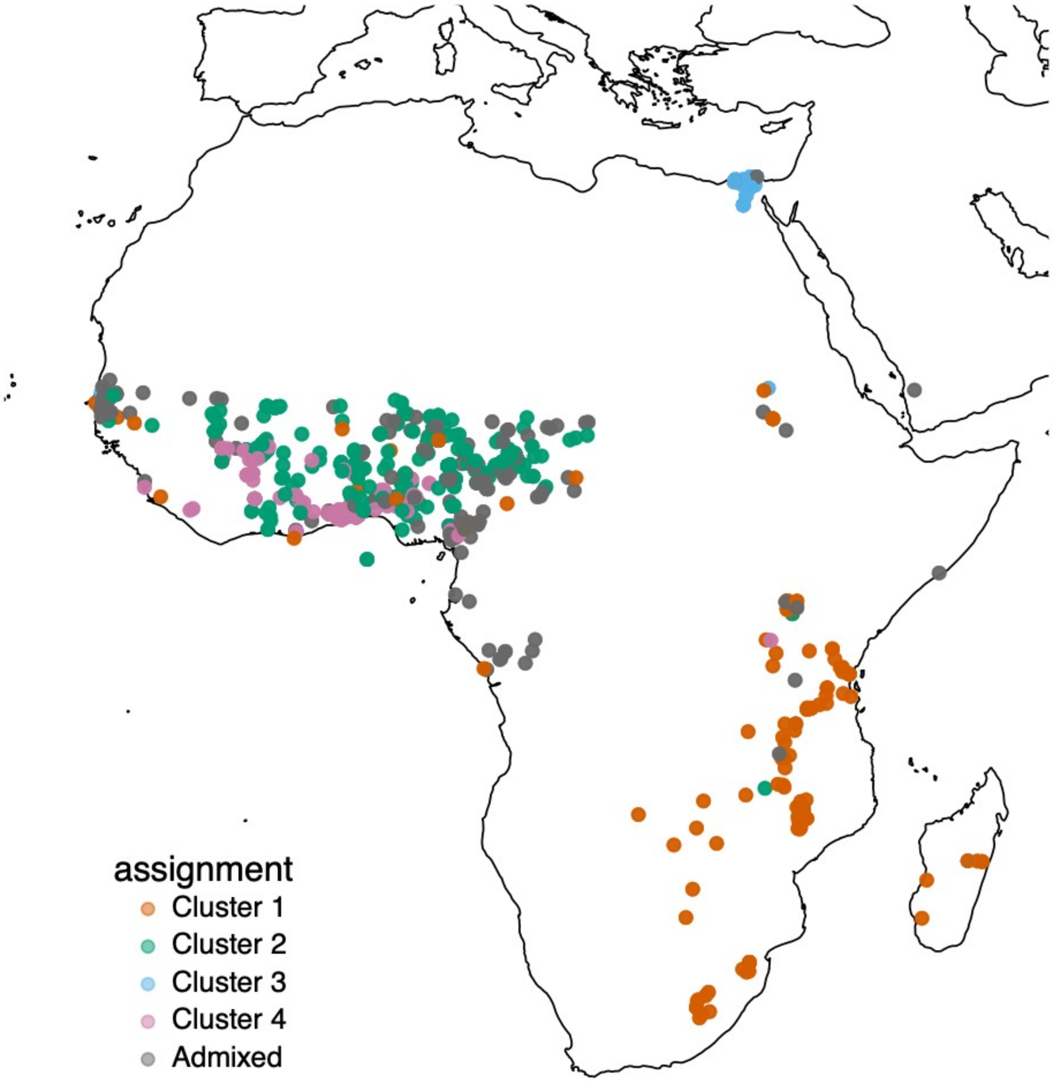

Figure 3.S7 Admixture of samples for K = 4.

Samples are plotted according to their collection site and pie charts indicate the proportion of ancestry attributed to each clusters. Only samples identified as traditional cultivars/landraces, weedy, or wild and collected in Africa are shown.

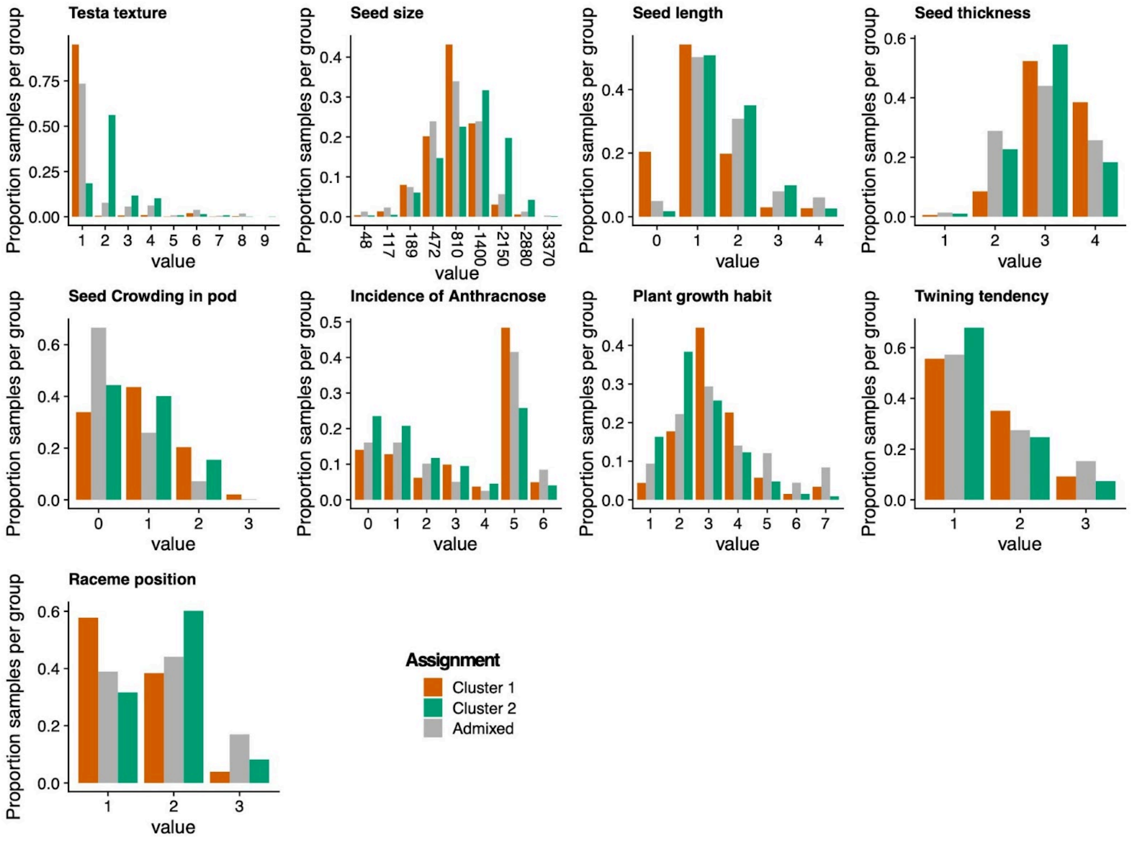

Figure 3.S8 Distributions of discrete phenotypes that vary between Cluster 1 and Cluster 2.

All phenotypes shown had a statistically significant difference between the two population clusters (Mann Whitney Wilcoxon adjusted p-value < 0.05).

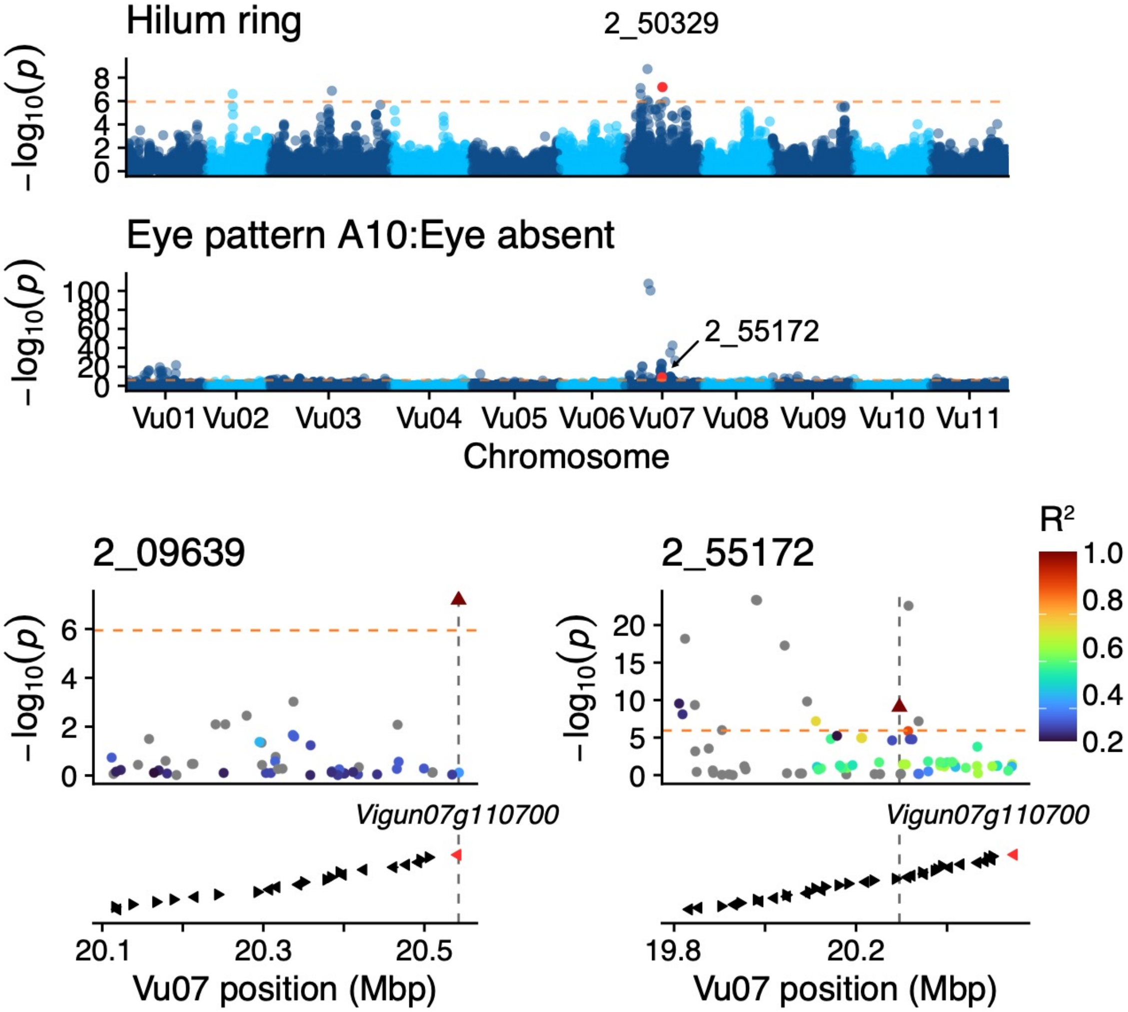

Figure 3.S9 Genome-wide association mapping manhattan plots and focal loci for additional eye pattern phenotypes.

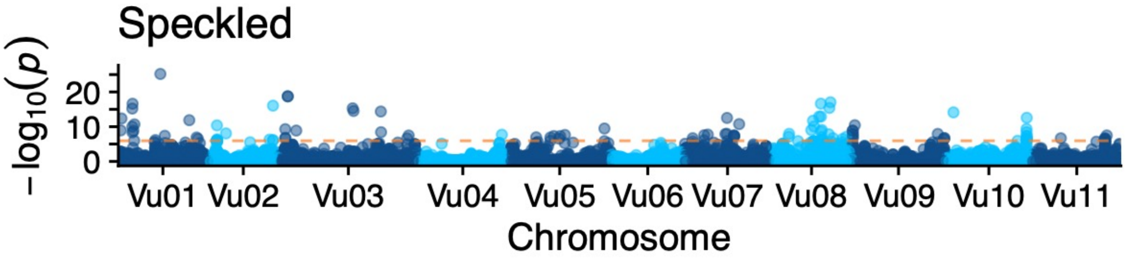

Figure 3.S10 Genome-wide association mapping manhattan plot for Speckled coat pattern.

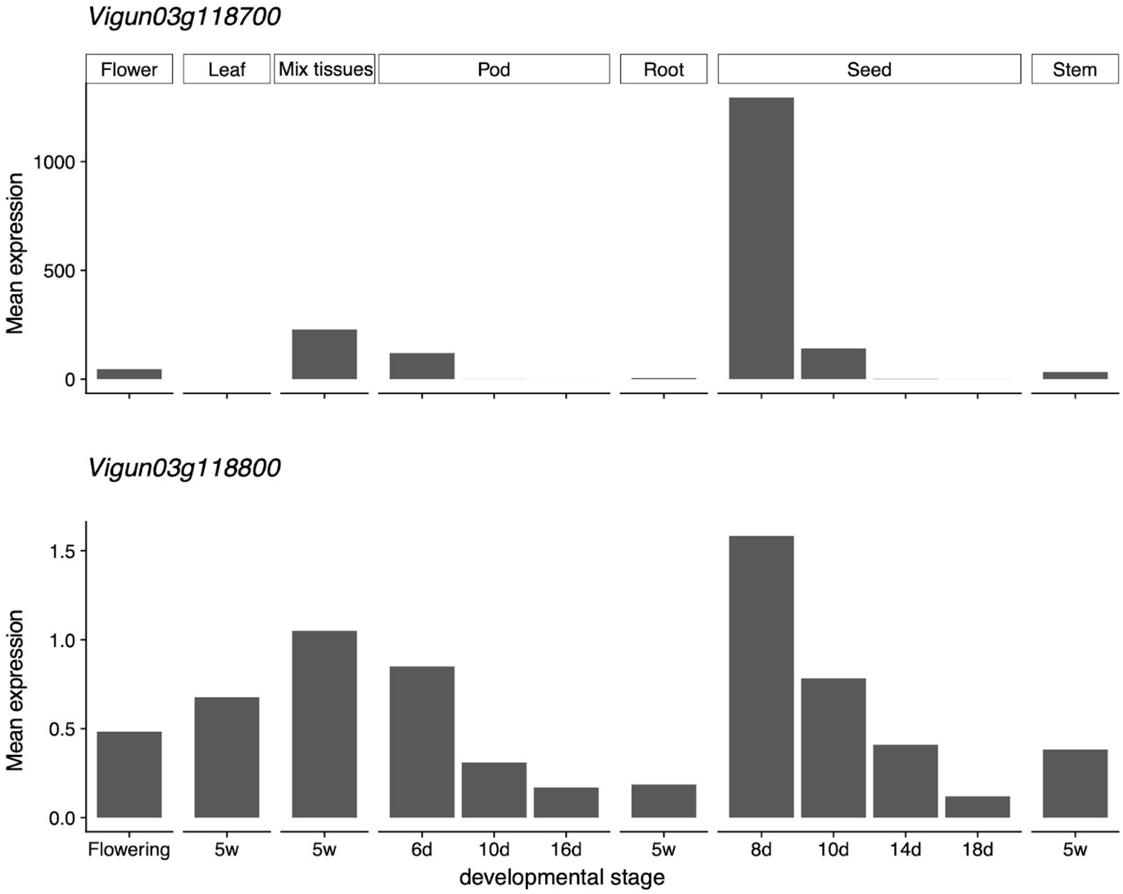

Figure 3.S11 Expression of 2 candidate genes for Tan and Red seed coat color across developmental stages and tissues.

Table 3.S1 List of samples

ID	Country	Lat.	Long.	Elev.	Bio. status	Geno. filter	Near identical	K2 assign.	Clus1 anc.	Clus2 anc.	In GWAS
TVu-1	Nigeria	NA	NA	NA	BRM	PASS	TVu-11485	Admixed	0.36	0.64	TRUE
TVu-4	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8	Nigeria	NA	NA	NA	LR	PASS	NA	Admixed	0.50	0.50	TRUE
TVu-18	Nigeria	NA	NA	NA	BRM	FILTER	TVu-10206, TVu-109, TVu-14891, TVu-16343, TVu-16408, TVu-1975, TVu-1996, TVu-1999, TVu-36, TVu-374, TVu-745	NA	NA	NA	FALSE
TVu-21	Philippines	NA	NA	NA	NA	PASS	NA	Admixed	0.52	0.48	TRUE
TVu-30	United States of America	NA	NA	NA	BRM	PASS	TVu-1564, TVu-2222, TVu-4607, TVu-6869	Clus. 1	1	0	TRUE
TVu-34	Uganda	11.25	4.97	1,276	BRM	PASS	NA	Clus. 1	1	0	TRUE
TVu-36	South Africa	NA	NA	NA	BRM	FILTER	TVu-10206, TVu-109, TVu-14891, TVu-16343,	NA	NA	NA	FALSE

							TVu-16408, TVu-18, TVu-1975, TVu-1996, TVu-1999, TVu-374, TVu-745				
TVu-42	Nigeria	7.47	4.57	286	LR	PASS	NA	Clus. 1	0.91	0.09	TRUE
TVu-43	Nigeria	7.47	4.57	286	LR	FILTER	TVu-647, TVu-984, TVu-985	NA	NA	NA	FALSE
TVu-45	Nigeria	7.47	4.57	286	BRM	FILTER	TVu-14759, TVu-7069	NA	NA	NA	FALSE
TVu-50	Nigeria	7.47	4.57	286	BRM	FILTER	TVu-1045, TVu-1838, TVu-1977, TVu-205, TVu-418	NA	NA	NA	FALSE
TVu-53	Nigeria	7.47	4.57	286	LR	PASS	NA	Clus. 2	0.16	0.84	TRUE
TVu-58	Nigeria	7.47	4.57	286	BRM	PASS	NA	Clus. 1	1	0	TRUE
TVu-59	Nigeria	7.47	4.57	286	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-62	Nigeria	7.47	4.57	286	BRM	PASS	NA	Clus. 1	0.84	0.16	TRUE
TVu-64	Nigeria	7.47	4.57	286	BRM	PASS	NA	Admixed	0.43	0.57	TRUE
TVu-66	Nigeria	7.47	4.57	286	BRM	PASS	NA	Admixed	0.45	0.55	TRUE
TVu-79	Tanzania	NA	NA	NA	NA	PASS	NA	Clus. 1	1	0	TRUE
TVu-83	South Africa	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.92	0.08	TRUE
TVu-84	South Africa	NA	NA	NA	LR	PASS	NA	Clus. 1	0.99	0.01	TRUE
TVu-86	Tanzania	NA	NA	NA	NA	PASS	NA	Clus. 1	1	0	TRUE
TVu-96	South Africa	NA	NA	NA	NA	PASS	NA	Admixed	0.68	0.32	TRUE
TVu-109	Tanzania	NA	NA	NA	NA	FILTER	TVu-10206, TVu-	NA	NA	NA	FALSE

							14891, TVu-16343, TVu-16408, TVu-18, TVu-1975, TVu-1996, TVu-1999, TVu-36, TVu-374, TVu-745				
TVu-113	Uganda	NA	NA	NA	NA	PASS	NA	Clus. 1	1	0	TRUE
TVu-117	Uganda	NA	NA	NA	NA	PASS	NA	Clus. 1	0.75	0.25	TRUE
TVu-123	Botswana	NA	NA	NA	LR	PASS	TVu-14484	Clus. 1	1	0	TRUE
TVu-132	Uganda	NA	NA	NA	NA	PASS	NA	Clus. 1	0.79	0.21	TRUE
TVu-134	Uganda	NA	NA	NA	NA	PASS	NA	Clus. 1	0.72	0.28	TRUE
TVu-144	Tanzania	NA	NA	NA	NA	PASS	NA	Clus. 1	1	0	TRUE
TVu-145	Kenya	NA	NA	NA	LR	PASS	NA	Clus. 1	0.92	0.08	TRUE
TVu-157	Nigeria	NA	NA	NA	NA	FILTER	TVu-158, TVu-201	NA	NA	NA	FALSE
TVu-158	Nigeria	NA	NA	NA	NA	FILTER	TVu-157, TVu-201	NA	NA	NA	FALSE
TVu-161	United States of America	NA	NA	NA	BRM	PASS	TVu-14795, TVu-14939	Clus. 2	0.19	0.81	TRUE
TVu-172	Nigeria	NA	NA	NA	NA	PASS	NA	Clus. 2	0	1	TRUE
TVu-176	United States of America	NA	NA	NA	NA	PASS	NA	Admixed	0.40	0.60	TRUE
TVu-186	United States of America	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.79	0.21	TRUE
TVu-191	United States of America	NA	NA	NA	BRM	PASS	TVu-1258, TVu-1593, TVu-233, TVu-726,	Clus. 1	1	0	TRUE

							TVu-739, TVu-853				
TVu-200	United States of America	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.93	0.07	TRUE
TVu-201	United States of America	NA	NA	NA	BRM	PASS	TVu-157, TVu-158	Clus. 1	1	0	TRUE
TVu-202	United States of America	NA	NA	NA	BRM	FILTER	TVu-15685, TVu-238, TVu-243, TVu-697, TVu-990	NA	NA	NA	FALSE
TVu-205	United States of America	NA	NA	NA	BRM	FILTER	TVu-1045, TVu-1838, TVu-1977, TVu-418, TVu-50	NA	NA	NA	FALSE
TVu-222	United States of America	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.88	0.12	TRUE
TVu-231	United States of America	NA	NA	NA	BRM	PASS	NA	Admixed	0.48	0.52	TRUE
TVu-232	United States of America	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.95	0.05	TRUE
TVu-233	United States of America	NA	NA	NA	BRM	FILTER	TVu-1258, TVu-1593, TVu-191, TVu-726, TVu-739, TVu-853	NA	NA	NA	FALSE
TVu-238	South Africa	NA	NA	NA	BRM	PASS	TVu-15685, TVu-202, TVu-243, TVu-697, TVu-990	Clus. 1	1	0	TRUE

TVu-243	United States of America	NA	NA	NA	BRM	FILTER	TVu-15685, TVu-202, TVu-238, TVu-697, TVu-990	NA	NA	NA	FALSE
TVu-254	Nigeria	NA	NA	NA	BRM	PASS	NA	Clus. 2	0	1	TRUE
TVu-261	United States of America	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.88	0.12	TRUE
TVu-263	United States of America	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.84	0.16	TRUE
TVu-264	United States of America	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.82	0.18	TRUE
TVu-266	United States of America	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.99	0.01	TRUE
TVu-274	South Africa	NA	NA	NA	BRM	FILTER	TVu-12597, TVu-6365	NA	NA	NA	FALSE
TVu-280	United States of America	NA	NA	NA	BRM	PASS	NA	Clus. 1	1	0	TRUE
TVu-297	United States of America	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.99	0.01	TRUE
TVu-301	Nigeria	NA	NA	NA	NA	PASS	TVu-316	Clus. 1	0.89	0.11	TRUE
TVu-305	United States of America	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.90	0.10	TRUE
TVu-308	Nigeria	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.96	0.04	TRUE
TVu-310	United States of America	NA	NA	NA	BRM	PASS	NA	Clus. 1	1	0	TRUE
TVu-315	United States of America	NA	NA	NA	BRM	PASS	TVu-14967, TVu-15866, TVu-387, TVu-763	Clus. 1	0.98	0.02	TRUE
TVu-316	Hungary	NA	NA	NA	NA	FILTER	TVu-301	NA	NA	NA	FALSE

TVu-317	United States of America	NA	NA	NA	NA	PASS	NA	Clus. 1	0.94	0.06	TRUE
TVu-320	Nigeria	NA	NA	NA	BRM	PASS	NA	Clus. 2	0.17	0.83	TRUE
TVu-332	United States of America	NA	NA	NA	BRM	FILTER	TVu-14434, TVu-1985, TVu-1986, TVu-470, TVu-492, TVu-493	NA	NA	NA	FALSE
TVu-335	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-336	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-337	United States of America	NA	NA	NA	LR	FILTER	TVu-566, TVu-6493	NA	NA	NA	FALSE
TVu-345	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 1	0.91	0.09	TRUE
TVu-347	Kenya	NA	NA	NA	LR	FILTER	TVu-14905, TVu-565	NA	NA	NA	FALSE
TVu-359	Nigeria	NA	NA	NA	NA	PASS	NA	Clus. 2	0	1	TRUE
TVu-374	United States of America	NA	NA	NA	NA	PASS	TVu-10206, TVu-109, TVu-14891, TVu-16343, TVu-16408, TVu-18, TVu-1975, TVu-1996, TVu-1999, TVu-36, TVu-745	Clus. 1	1	0	TRUE
TVu-382	Hungary	NA	NA	NA	NA	PASS	TVu-6356	Admixed	0.51	0.49	TRUE

TVu-384	United States of America	NA	NA	NA	NA	PASS	NA	Clus. 1	0.88	0.12	TRUE
TVu-387	United States of America	NA	NA	NA	BRM	FILTER	TVu-14967, TVu-15866, TVu-315, TVu-763	NA	NA	NA	FALSE
TVu-393	United States of America	NA	NA	NA	BRM	PASS	TVu-5126	Clus. 1	1	0	TRUE
TVu-401	United States of America	NA	NA	NA	LR	PASS	NA	Admixed	0.33	0.67	TRUE
TVu-408	United States of America	NA	NA	NA	NA	FILTER	TVu-3246	NA	NA	NA	FALSE
TVu-409	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-415	United States of America	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.71	0.29	TRUE
TVu-418	United States of America	NA	NA	NA	NA	FILTER	TVu-1045, TVu-1838, TVu-1977, TVu-205, TVu-50	NA	NA	NA	FALSE
TVu-422	United States of America	NA	NA	NA	NA	PASS	NA	Clus. 1	0.86	0.14	TRUE
TVu-430	United States of America	NA	NA	NA	LR	PASS	NA	Clus. 1	0.83	0.17	TRUE
TVu-433	Kenya	NA	NA	NA	BRM	PASS	TVu-1980, TVu-1982, TVu-746	Clus. 1	1	0	TRUE
TVu-440	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-443	United States of America	NA	NA	NA	NA	FILTER	TVu-3670, TVu-3699, TVu-3874, TVu-5465, TVu-5623	NA	NA	NA	FALSE

TVu-445	United States of America	NA	NA	NA	BRM	PASS	NA	Clus. 1	1	0	TRUE
TVu-449	Nigeria	NA	NA	NA	LR	PASS	NA	Admixed	0.52	0.48	TRUE
TVu-450	Nigeria	12	8.52	473	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-456	United States of America	NA	NA	NA	NA	PASS	NA	Clus. 1	1	0	TRUE
TVu-459	United States of America	NA	NA	NA	BRM	PASS	NA	Clus. 1	1	0	TRUE
TVu-467	Mauritania	NA	NA	NA	BRM	PASS	NA	Clus. 1	1	0	TRUE
TVu-468	Mauritania	NA	NA	NA	BRM	PASS	NA	Clus. 1	1	0	TRUE
TVu-470	United States of America	NA	NA	NA	NA	FILTER	TVu-14434, TVu-1985, TVu-1986, TVu-332, TVu-492, TVu-493	NA	NA	NA	FALSE
TVu-471	United States of America	NA	NA	NA	NA	PASS	NA	Clus. 1	0.93	0.07	TRUE
TVu-472	United States of America	NA	NA	NA	NA	PASS	NA	Clus. 1	1	0	TRUE
TVu-483	United States of America	NA	NA	NA	BRM	PASS	NA	Clus. 1	1	0	TRUE
TVu-486	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-488	United States of America	NA	NA	NA	NA	PASS	NA	Clus. 1	0.91	0.09	TRUE
TVu-492	Nigeria	NA	NA	NA	NA	FILTER	TVu-14434, TVu-1985, TVu-1986, TVu-332, TVu-470, TVu-493	NA	NA	NA	FALSE
TVu-493	United States of America	NA	NA	NA	NA	FILTER	TVu-14434,	NA	NA	NA	FALSE

							TVu-1985, TVu-1986, TVu-332, TVu-470, TVu-492				
TVu-497	United States of America	NA	NA	NA	NA	PASS	NA	Admixed	0.57	0.43	TRUE
TVu-506	Nigeria	NA	NA	NA	NA	PASS	NA	Clus. 2	0	1	TRUE
TVu-523	United States of America	NA	NA	NA	NA	PASS	NA	Clus. 1	0.77	0.23	TRUE
TVu-527	Nigeria	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.79	0.21	TRUE
TVu-535	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 2	0.15	0.85	TRUE
TVu-537	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-565	United States of America	NA	NA	NA	BRM	PASS	TVu-14905, TVu-347	Clus. 1	1	0	TRUE
TVu-566	United States of America	NA	NA	NA	BRM	FILTER	TVu-337, TVu-6493	NA	NA	NA	FALSE
TVu-578	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-603	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-612	Nigeria	NA	NA	NA	NA	PASS	NA	Admixed	0.49	0.51	TRUE
TVu-618	Nigeria	NA	NA	NA	LR	PASS	TVu-625	Clus. 2	0	1	TRUE
TVu-625	Nigeria	NA	NA	NA	NA	FILTER	TVu-618	NA	NA	NA	FALSE
TVu-645	Hungary	NA	NA	NA	LR	PASS	NA	Clus. 1	0.98	0.02	TRUE
TVu-647	Nigeria	NA	NA	NA	NA	FILTER	TVu-43, TVu-984, TVu-985	NA	NA	NA	FALSE
TVu-662	Nigeria	NA	NA	NA	NA	PASS	NA	Clus. 1	0.91	0.09	TRUE
TVu-689	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-697	United States of America	NA	NA	NA	NA	FILTER	TVu-15685, TVu-202, TVu-238,	NA	NA	NA	FALSE

							TVu-243, TVu-990				
TVu-712	Nigeria	NA	NA	NA	NA	PASS	NA	Clus. 2	0	1	TRUE
TVu-726	Nigeria	NA	NA	NA	NA	FILTER	TVu-1258, TVu-1593, TVu-191, TVu-233, TVu-739, TVu-853	NA	NA	NA	FALSE
TVu-739	United States of America	NA	NA	NA	BRM	FILTER	TVu-1258, TVu-1593, TVu-191, TVu-233, TVu-726, TVu-853	NA	NA	NA	FALSE
TVu-745	Nigeria	NA	NA	NA	BRM	FILTER	TVu-10206, TVu-109, TVu-14891, TVu-16343, TVu-16408, TVu-18, TVu-1975, TVu-1996, TVu-1999, TVu-36, TVu-374	NA	NA	NA	FALSE
TVu-746	Nigeria	NA	NA	NA	NA	FILTER	TVu-1980, TVu-1982, TVu-433	NA	NA	NA	FALSE
TVu-763	Nigeria	NA	NA	NA	LR	FILTER	TVu-14967,	NA	NA	NA	FALSE

							TVu-15866, TVu-315, TVu-387				
TVu-773	Nigeria	12	8.52	484	LR	PASS	NA	Clus. 1	0.98	0.02	TRUE
TVu-790	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 2	0.03	0.97	TRUE
TVu-816	Nigeria	8.48	8.52	289	LR	PASS	NA	Clus. 2	0.07	0.93	TRUE
TVu-841	Nigeria	12	8.52	484	LR	PASS	NA	Clus. 2	0.27	0.73	TRUE
TVu-845	Nigeria	NA	NA	NA	LR	PASS	NA	Admixed	0.69	0.31	TRUE
TVu-850	Nigeria	NA	NA	NA	NA	PASS	NA	Clus. 2	0	1	TRUE
TVu-853	Nigeria	12.52	7.73	598	LR	FILTER	TVu-1258, TVu-1593, TVu-191, TVu-233, TVu-726, TVu-739	NA	NA	NA	FALSE
TVu-857	Nigeria	NA	NA	NA	NA	FILTER	NA	NA	NA	NA	FALSE
TVu-866	Nigeria	NA	NA	NA	NA	PASS	NA	Admixed	0.50	0.50	TRUE
TVu-870	Nigeria	NA	NA	NA	NA	PASS	NA	Clus. 2	0	1	TRUE
TVu-875	Nigeria	12	8.52	484	NA	PASS	NA	Admixed	0.52	0.48	TRUE
TVu-889	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 2	0.14	0.86	TRUE
TVu-911	South Africa	NA	NA	NA	LR	PASS	NA	Clus. 1	0.95	0.05	TRUE
TVu-912	Israel	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-928	Ghana	NA	NA	NA	LR	PASS	NA	Clus. 1	0.74	0.26	TRUE
TVu-945	Nigeria	12	8.52	484	NA	PASS	NA	Clus. 2	0.15	0.85	TRUE
TVu-946	Nigeria	12	8.52	484	NA	PASS	NA	Admixed	0.57	0.43	TRUE
TVu-947	Nigeria	12	8.52	484	NA	PASS	NA	Clus. 1	1	0	TRUE
TVu-964	Nigeria	NA	NA	NA	NA	PASS	NA	Clus. 2	0	1	TRUE
TVu-968	Nigeria	7.80	6.74	54	LR	PASS	NA	Clus. 2	0.02	0.98	TRUE
TVu-969	Nigeria	7.80	6.74	54	LR	PASS	NA	Admixed	0.51	0.49	TRUE
TVu-971	Nigeria	7.80	6.74	54	LR	PASS	NA	Admixed	0.50	0.50	TRUE
TVu-972	Nigeria	7.80	6.74	54	LR	PASS	NA	Clus. 1	0.76	0.24	TRUE
TVu-980	Nigeria	12	8.52	473	LR	PASS	NA	Clus. 2	0	1	TRUE

TVu-984	Nigeria	12	8.52	473	NA	PASS	TVu-43, TVu-647, TVu-985	Clus. 1	1	0	TRUE
TVu-985	Hungary	NA	NA	NA	NA	FILTER	TVu-43, TVu-647, TVu-984	NA	NA	NA	FALSE
TVu-990	South Africa	NA	NA	NA	BRM	FILTER	TVu-15685, TVu-202, TVu-238, TVu-243, TVu-697	NA	NA	NA	FALSE
TVu-997	Ghana	4.80	-2.13	NA	LR	PASS	NA	Clus. 1	0.96	0.04	TRUE
TVu-999	Ghana	NA	NA	NA	LR	PASS	NA	Admixed	0.61	0.39	TRUE
TVu-1000	Ghana	NA	NA	NA	NA	FILTER	TVu-11977, TVu-1452, TVu-14602	NA	NA	NA	FALSE
TVu-1004	United States of America	NA	NA	NA	NA	PASS	NA	Clus. 1	0.85	0.15	TRUE
TVu-1008	United States of America	NA	NA	NA	BRM	PASS	NA	Admixed	0.41	0.59	TRUE
TVu-1016	United States of America	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.95	0.05	TRUE
TVu-1027	United States of America	NA	NA	NA	BRM	PASS	NA	Clus. 2	0.23	0.77	TRUE
TVu-1030	United States of America	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.72	0.28	TRUE
TVu-1032	United States of America	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.76	0.24	TRUE
TVu-1036	United States of America	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.92	0.08	TRUE
TVu-1037	United States of America	NA	NA	NA	NA	PASS	NA	Clus. 1	0.84	0.16	TRUE

TVu-1043	United States of America	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.97	0.03	TRUE
TVu-1045	United States of America	NA	NA	NA	BRM	FILTER	TVu-1838, TVu-1977, TVu-205, TVu-418, TVu-50	NA	NA	NA	FALSE
TVu-1059	United States of America	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.98	0.02	TRUE
TVu-1081	United States of America	NA	NA	NA	BRM	FILTER	NA	NA	NA	NA	FALSE
TVu-1084	Ghana	NA	NA	NA	LR	PASS	NA	Admixed	0.47	0.53	TRUE
TVu-1124	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-1152	United States of America	NA	NA	NA	NA	PASS	NA	Clus. 2	0.22	0.78	TRUE
TVu-1163	South Africa	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-1171	South Africa	NA	NA	NA	BRM	PASS	NA	Clus. 1	1	0	TRUE
TVu-1172	Nigeria	NA	NA	NA	NA	PASS	NA	Admixed	0.43	0.57	TRUE
TVu-1176	Uganda	NA	NA	NA	NA	PASS	NA	Clus. 1	1	0	TRUE
TVu-1184	Uganda	NA	NA	NA	NA	PASS	NA	Clus. 1	1	0	TRUE
TVu-1185	Uganda	NA	NA	NA	NA	PASS	NA	Clus. 1	0.97	0.03	TRUE
TVu-1192	Tanzania	NA	NA	NA	NA	PASS	NA	Clus. 1	0.99	0.01	TRUE
TVu-1201	Australia	NA	NA	NA	NA	PASS	NA	Clus. 1	1	0	TRUE
TVu-1204	Botswana	NA	NA	NA	NA	PASS	NA	Clus. 1	0.74	0.26	TRUE
TVu-1206	Botswana	NA	NA	NA	NA	PASS	NA	Clus. 1	1	0	TRUE
TVu-1207	Guyana	NA	NA	NA	LR	FILTER	TVu-1330, TVu-4642, TVu-8453	NA	NA	NA	FALSE
TVu-1208	Guyana	NA	NA	NA	LR	PASS	NA	Clus. 2	0.05	0.95	TRUE
TVu-1236	South Africa	NA	NA	NA	BRM	PASS	NA	Admixed	0.41	0.59	TRUE
TVu-1241	South Africa	NA	NA	NA	NA	PASS	NA	Clus. 1	0.72	0.28	TRUE
TVu-1251	United States of America	NA	NA	NA	NA	PASS	NA	Clus. 1	0.97	0.03	TRUE

TVu-1258	United States of America	NA	NA	NA	NA	FILTER	TVu-1593, TVu-191, TVu-233, TVu-726, TVu-739, TVu-853	NA	NA	NA	FALSE
TVu-1261	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 1	0.96	0.04	TRUE
TVu-1271	Uganda	NA	NA	NA	LR	PASS	NA	Clus. 1	0.97	0.03	TRUE
TVu-1274	Tanzania	NA	NA	NA	NA	PASS	TVu-1644	Clus. 1	1	0	TRUE
TVu-1275	Tanzania	NA	NA	NA	NA	PASS	NA	Clus. 1	1	0	TRUE
TVu-1279	Tanzania	NA	NA	NA	NA	PASS	NA	Clus. 1	1	0	TRUE
TVu-1280	Tanzania	NA	NA	NA	NA	FILTER	TVu-10442	NA	NA	NA	FALSE
TVu-1283	Uganda	NA	NA	NA	LR	PASS	NA	Clus. 1	0.98	0.02	TRUE
TVu-1330	Uganda	NA	NA	NA	BRM	FILTER	TVu-1207, TVu-4642, TVu-8453	NA	NA	NA	FALSE
TVu-1331	Uganda	NA	NA	NA	BRM	PASS	NA	Clus. 1	1	0	TRUE
TVu-1332	Uganda	NA	NA	NA	BRM	PASS	NA	Clus. 1	1	0	TRUE
TVu-1346	Uganda	NA	NA	NA	BRM	PASS	NA	Clus. 2	0.29	0.71	TRUE
TVu-1351	Uganda	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.96	0.04	TRUE
TVu-1362	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 1	0.82	0.18	TRUE
TVu-1366	Uganda	NA	NA	NA	LR	PASS	NA	Admixed	0.58	0.42	TRUE
TVu-1387	Nicaragua	NA	NA	NA	NA	PASS	NA	Clus. 1	1	0	TRUE
TVu-1395	Uganda	NA	NA	NA	NA	PASS	NA	Clus. 1	1	0	TRUE
TVu-1404	India	NA	NA	NA	NA	FILTER	TVu-1433, TVu-1461, TVu-2207, TVu-3565	NA	NA	NA	FALSE
TVu-1412	Colombia	NA	NA	NA	NA	FILTER	TVu-10111, TVu-1536, TVu-1549, TVu-1707, TVu-2300	NA	NA	NA	FALSE

TVu-1416	Uruguay	NA	NA	NA	NA	PASS	NA	Clus. 1	0.99	0.01	TRUE
TVu-1418	Republic of the Congo	NA	NA	NA	NA	PASS	NA	Admixed	0.68	0.32	TRUE
TVu-1433	India	NA	NA	NA	NA	FILTER	TVu-1404, TVu-1461, TVu-2207, TVu-3565	NA	NA	NA	FALSE
TVu-1434	India	NA	NA	NA	NA	PASS	NA	Clus. 1	1	0	TRUE
TVu-1449	Nigeria	NA	NA	NA	NA	PASS	NA	Clus. 1	0.71	0.29	TRUE
TVu-1452	Australia	NA	NA	NA	NA	PASS	TVu-1000, TVu-11977, TVu-14602	Clus. 1	1	0	TRUE
TVu-1461	India	NA	NA	NA	NA	PASS	TVu-1404, TVu-1433, TVu-2207, TVu-3565	Clus. 1	1	0	TRUE
TVu-1477	Mali	NA	NA	NA	NA	PASS	NA	Clus. 1	0.80	0.20	TRUE
TVu-1494	United States of America	NA	NA	NA	NA	PASS	NA	Clus. 1	0.93	0.07	TRUE
TVu-1496	Indonesia	NA	NA	NA	LR	PASS	NA	Admixed	0.58	0.42	TRUE
TVu-1497	Indonesia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.75	0.25	TRUE
TVu-1508	Nigeria	7.47	4.57	286	BRM	PASS	NA	Clus. 2	0.26	0.74	TRUE
TVu-1523	India	NA	NA	NA	NA	PASS	NA	Clus. 2	0.13	0.87	TRUE
TVu-1528	Turkey	NA	NA	NA	NA	PASS	NA	Clus. 1	0.96	0.04	TRUE
TVu-1536	Turkey	NA	NA	NA	NA	PASS	TVu-10111, TVu-1412, TVu-1549, TVu-1707, TVu-2300	Clus. 1	1	0	TRUE
TVu-1540	Turkey	NA	NA	NA	NA	PASS	NA	Clus. 2	0.14	0.86	TRUE
TVu-1543	India	NA	NA	NA	LR	PASS	NA	Clus. 2	0.20	0.80	TRUE
TVu-1544	Lebanon	NA	NA	NA	NA	PASS	NA	Clus. 2	0.28	0.72	TRUE

TVu-1549	Ghana	NA	NA	NA	NA	FILTER	TVu-10111, TVu-1412, TVu-1536, TVu-1707, TVu-2300	NA	NA	NA	FALSE
TVu-1551	Nigeria	NA	NA	NA	NA	PASS	NA	Admixed	0.46	0.54	TRUE
TVu-1556	Nigeria	NA	NA	NA	NA	FILTER	TVu-1656, TVu-2252	NA	NA	NA	FALSE
TVu-1562	United States of America	NA	NA	NA	BRM	FILTER	TVu-1771, TVu-3898	NA	NA	NA	FALSE
TVu-1563	United States of America	NA	NA	NA	BRM	PASS	NA	Admixed	0.66	0.34	TRUE
TVu-1564	United States of America	NA	NA	NA	BRM	FILTER	TVu-2222, TVu-30, TVu-4607, TVu-6869	NA	NA	NA	FALSE
TVu-1569	Puerto Rico	NA	NA	NA	NA	PASS	NA	Clus. 2	0.22	0.78	TRUE
TVu-1572	Iran	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.87	0.13	TRUE
TVu-1576	Guatemala	NA	NA	NA	NA	PASS	TVu-1578	Clus. 1	0.81	0.19	TRUE
TVu-1578	Guatemala	NA	NA	NA	NA	FILTER	TVu-1576	NA	NA	NA	FALSE
TVu-1579	Iran	NA	NA	NA	NA	PASS	NA	Clus. 2	0.18	0.82	TRUE
TVu-1583	Nigeria	NA	NA	NA	NA	PASS	NA	Clus. 1	1	0	TRUE
TVu-1586	Nigeria	NA	NA	NA	NA	PASS	NA	Admixed	0.43	0.57	TRUE
TVu-1591	Puerto Rico	NA	NA	NA	LR	PASS	TVu-1637	Clus. 1	1	0	TRUE
TVu-1593	Nigeria	NA	NA	NA	LR	FILTER	TVu-1258, TVu-191, TVu-233, TVu-726, TVu-739, TVu-853	NA	NA	NA	FALSE
TVu-1609	United States of America	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.94	0.06	TRUE

TVu-1616	United States of America	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.88	0.12	TRUE
TVu-1637	Puerto Rico	NA	NA	NA	LR	FILTER	TVu-1591	NA	NA	NA	FALSE
TVu-1639	Kenya	NA	NA	NA	LR	PASS	NA	Clus. 1	0.97	0.03	TRUE
TVu-1641	South Africa	NA	NA	NA	LR	PASS	NA	Clus. 1	0.76	0.24	TRUE
TVu-1644	South Africa	NA	NA	NA	BRM	FILTER	TVu-1274	NA	NA	NA	FALSE
TVu-1651	Puerto Rico	NA	NA	NA	LR	PASS	NA	Clus. 2	0.20	0.80	TRUE
TVu-1656	Puerto Rico	NA	NA	NA	LR	FILTER	TVu-1556, TVu-2252	NA	NA	NA	FALSE
TVu-1680	Turkey	NA	NA	NA	LR	PASS	NA	Clus. 2	0.15	0.85	TRUE
TVu-1695	Honduras	NA	NA	NA	LR	PASS	NA	Admixed	0.50	0.50	TRUE
TVu-1702	Spain	NA	NA	NA	LR	PASS	NA	Clus. 2	0.11	0.89	TRUE
TVu-1706	Pakistan	NA	NA	NA	LR	PASS	NA	Clus. 1	0.94	0.06	TRUE
TVu-1707	Israel	NA	NA	NA	LR	FILTER	TVu-10111, TVu-1412, TVu-1536, TVu-1549, TVu-2300	NA	NA	NA	FALSE
TVu-1710	United States of America	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.71	0.29	TRUE
TVu-1715	United States of America	NA	NA	NA	BRM	PASS	NA	Admixed	0.60	0.40	TRUE
TVu-1727	United States of America	NA	NA	NA	BRM	PASS	TVu-2500	Admixed	0.63	0.37	TRUE
TVu-1732	Mexico	NA	NA	NA	BRM	PASS	NA	Admixed	0.35	0.65	TRUE
TVu-1738	Nigeria	NA	NA	NA	LR	FILTER	TVu-1739, TVu-3903	NA	NA	NA	FALSE
TVu-1739	United States of America	NA	NA	NA	BRM	FILTER	TVu-1738, TVu-3903	NA	NA	NA	FALSE
TVu-1744	India	NA	NA	NA	BRM	FILTER	TVu-3625, TVu-9393	NA	NA	NA	FALSE
TVu-1761	United States of America	NA	NA	NA	BRM	PASS	NA	Admixed	0.62	0.38	TRUE

TVu-1771	United Kingdom	NA	NA	NA	LR	FILTER	TVu-1562, TVu-3898	NA	NA	NA	FALSE
TVu-1775	Paraguay	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-1779	Mexico	NA	NA	NA	LR	PASS	NA	Clus. 1	0.93	0.07	TRUE
TVu-1780	Japan	NA	NA	NA	LR	PASS	NA	Clus. 1	0.91	0.09	TRUE
TVu-1782	Guatemala	NA	NA	NA	LR	PASS	NA	Clus. 1	0.91	0.09	TRUE
TVu-1799	Mexico	NA	NA	NA	LR	PASS	NA	Clus. 1	0.93	0.07	TRUE
TVu-1801	Kenya	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-1807	Puerto Rico	NA	NA	NA	LR	PASS	NA	Clus. 1	0.95	0.05	TRUE
TVu-1811	Puerto Rico	NA	NA	NA	LR	PASS	NA	Clus. 2	0.15	0.85	TRUE
TVu-1828	Iran	NA	NA	NA	LR	PASS	NA	Clus. 2	0.17	0.83	TRUE
TVu-1832	Pakistan	NA	NA	NA	LR	PASS	TVu-14260, TVu-15979	Admixed	0.36	0.64	TRUE
TVu-1836	United States of America	NA	NA	NA	BRM	FILTER	TVu-14512, TVu-2274	NA	NA	NA	FALSE
TVu-1838	United States of America	NA	NA	NA	BRM	FILTER	TVu-1045, TVu-1977, TVu-205, TVu-418, TVu-50	NA	NA	NA	FALSE
TVu-1851	United States of America	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.86	0.14	TRUE
TVu-1875	India	NA	NA	NA	LR	PASS	NA	Admixed	0.67	0.33	TRUE
TVu-1877	Zaire	NA	NA	NA	LR	PASS	NA	Admixed	0.58	0.42	TRUE
TVu-1878	Guatemala	NA	NA	NA	LR	PASS	TVu-1880	Clus. 1	0.96	0.04	TRUE
TVu-1880	El Salvador	NA	NA	NA	LR	FILTER	TVu-1878	NA	NA	NA	FALSE
TVu-1886	Pakistan	NA	NA	NA	LR	PASS	NA	Clus. 2	0.22	0.78	TRUE
TVu-1888	Puerto Rico	NA	NA	NA	LR	PASS	NA	Clus. 1	0.99	0.01	TRUE
TVu-1908	South Africa	NA	NA	NA	LR	PASS	NA	Clus. 1	0.81	0.19	TRUE
TVu-1916	Iran	NA	NA	NA	LR	PASS	NA	Admixed	0.61	0.39	TRUE
TVu-1923	United States of America	NA	NA	NA	LR	PASS	NA	Admixed	0.42	0.58	TRUE

TVu-1933	South Africa	NA	NA	NA	LR	PASS	NA	Admixed	0.44	0.56	TRUE
TVu-1934	United States of America	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.77	0.23	TRUE
TVu-1940	Colombia	NA	NA	NA	LR	PASS	NA	Admixed	0.49	0.51	TRUE
TVu-1943	Paraguay	NA	NA	NA	LR	PASS	NA	Clus. 1	0.95	0.05	TRUE
TVu-1947	Nigeria	NA	NA	NA	LR	PASS	NA	Admixed	0.48	0.52	TRUE
TVu-1948	Nigeria	NA	NA	NA	LR	FILTER	TVu-1956, TVu-1962	NA	NA	NA	FALSE
TVu-1954	Iran	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-1955	Madagascar	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-1956	Nigeria	NA	NA	NA	LR	FILTER	TVu-1948, TVu-1962	NA	NA	NA	FALSE
TVu-1962	United States of America	NA	NA	NA	BRM	PASS	TVu-1948, TVu-1956	Admixed	0.48	0.52	TRUE
TVu-1973	Paraguay	NA	NA	NA	LR	PASS	TVu-12646, TVu-12937	Clus. 1	1	0	TRUE
TVu-1977	South Africa	NA	NA	NA	LR	PASS	TVu-1045, TVu-1838, TVu-205, TVu-418, TVu-50	Clus. 1	0.95	0.05	TRUE
TVu-1978	Argentina	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-1979	Argentina	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-1980	Argentina	NA	NA	NA	LR	FILTER	TVu-1982, TVu-433, TVu-746	NA	NA	NA	FALSE
TVu-1982	Hungary	NA	NA	NA	LR	FILTER	TVu-1980, TVu-433, TVu-746	NA	NA	NA	FALSE
TVu-1985	United States of America	NA	NA	NA	BRM	FILTER	TVu-14434, TVu-1986, TVu-332,	NA	NA	NA	FALSE

							TVu-470, TVu-492, TVu-493				
TVu-1986	United States of America	NA	NA	NA	BRM	PASS	TVu-14434, TVu-1985, TVu-332, TVu-470, TVu-492, TVu-493	Clus. 1	1	0	TRUE
TVu-1996	Nicaragua	NA	NA	NA	LR	FILTER	TVu-10206, TVu-109, TVu-14891, TVu-16343, TVu-16408, TVu-18, TVu-1975, TVu-1999, TVu-36, TVu-374, TVu-745	NA	NA	NA	FALSE
TVu-1999	India	NA	NA	NA	LR	FILTER	TVu-10206, TVu-109, TVu-14891, TVu-16343, TVu-16408, TVu-18,	NA	NA	NA	FALSE

							TVu-1975, TVu-1996, TVu-36, TVu-374, TVu-745				
TVu-2000	South Africa	NA	NA	NA	BRM	PASS	NA	Clus. 1	1	0	TRUE
TVu-2004	Tanzania	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-2006	Uganda	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-2009	Argentina	NA	NA	NA	LR	PASS	NA	Admixed	0.40	0.60	TRUE
TVu-2010	Afghanistan	NA	NA	NA	LR	PASS	NA	Admixed	0.43	0.57	TRUE
TVu-2027	Nigeria	11.99	8.51	508	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-2033	Nigeria	11.99	8.51	508	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-2046	United States of America	27.83	-81.72	345	NA	PASS	NA	Clus. 1	0.88	0.12	TRUE
TVu-2081	United States of America	27.83	-81.72	345	NA	PASS	NA	Clus. 1	0.73	0.27	TRUE
TVu-2085	United States of America	27.83	-81.72	345	NA	PASS	NA	Clus. 1	0.90	0.10	TRUE
TVu-2095	United States of America	27.83	-81.72	345	NA	PASS	NA	Clus. 1	0.86	0.14	TRUE
TVu-2104	United States of America	27.83	-81.72	345	NA	PASS	NA	Admixed	0.47	0.53	TRUE
TVu-2122	United States of America	27.83	-81.72	345	NA	PASS	NA	Clus. 1	0.92	0.08	TRUE
TVu-2130	United States of America	27.83	-81.72	345	NA	PASS	NA	Clus. 1	0.89	0.11	TRUE
TVu-2154	United States of America	27.83	-81.72	345	NA	PASS	NA	Admixed	0.60	0.40	TRUE
TVu-2155	United States of America	27.83	-81.72	345	NA	FILTER	NA	NA	NA	NA	FALSE
TVu-2168	Iran	NA	NA	NA	NA	PASS	NA	Admixed	0.47	0.53	TRUE
TVu-2172	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.78	0.22	TRUE
TVu-2181	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.76	0.24	TRUE
TVu-2185	India	NA	NA	NA	LR	PASS	NA	Admixed	0.35	0.65	TRUE

TVu-2207	India	NA	NA	NA	LR	FILTER	TVu-1404, TVu-1433, TVu-1461, TVu-3565	NA	NA	NA	FALSE
TVu-2222	Nigeria	7.39	3.90	252	Wild	FILTER	TVu-1564, TVu-30, TVu-4607, TVu-6869	NA	NA	NA	FALSE
TVu-2242	Nigeria	NA	NA	NA	Wild	PASS	NA	Clus. 1	0.89	0.11	TRUE
TVu-2252	United Kingdom	NA	NA	NA	LR	PASS	TVu-1556, TVu-1656	Admixed	0.37	0.63	TRUE
TVu-2267	Colombia	NA	NA	NA	LR	PASS	NA	Admixed	0.46	0.54	TRUE
TVu-2269	Colombia	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-2273	Dominican Republic	NA	NA	NA	LR	PASS	NA	Clus. 1	0.77	0.23	TRUE
TVu-2274	Dominican Republic	NA	NA	NA	LR	PASS	TVu-14512, TVu-1836	Admixed	0.48	0.52	TRUE
TVu-2276	Paraguay	NA	NA	NA	LR	PASS	NA	Clus. 1	0.93	0.07	TRUE
TVu-2280	Peru	NA	NA	NA	LR	PASS	NA	Admixed	0.44	0.56	TRUE
TVu-2299	Turkey	NA	NA	NA	LR	PASS	NA	Admixed	0.37	0.63	TRUE
TVu-2300	Turkey	NA	NA	NA	LR	FILTER	TVu-10111, TVu-1412, TVu-1536, TVu-1549, TVu-1707	NA	NA	NA	FALSE
TVu-2311	Turkey	NA	NA	NA	LR	PASS	NA	Clus. 2	0.15	0.85	TRUE
TVu-2321	Turkey	NA	NA	NA	LR	PASS	NA	Clus. 2	0.15	0.85	TRUE
TVu-2322	Turkey	NA	NA	NA	LR	PASS	NA	Admixed	0.49	0.51	TRUE
TVu-2329	United Arab Emirates	NA	NA	NA	LR	PASS	NA	Clus. 1	0.82	0.18	TRUE
TVu-2350	Zaire	NA	NA	NA	LR	PASS	NA	Admixed	0.46	0.54	TRUE
TVu-2373	Palau	NA	NA	NA	LR	PASS	NA	Admixed	0.50	0.50	TRUE

TVu-2377	Cuba	NA	NA	NA	LR	PASS	NA	Admixed	0.59	0.41	TRUE
TVu-2382	Afghanistan	NA	NA	NA	LR	PASS	NA	Admixed	0.52	0.48	TRUE
TVu-2394	South Africa	NA	NA	NA	LR	PASS	NA	Clus. 1	0.75	0.25	TRUE
TVu-2397	South Africa	NA	NA	NA	LR	PASS	NA	Admixed	0.39	0.61	TRUE
TVu-2398	Iran	NA	NA	NA	LR	PASS	NA	Clus. 2	0.22	0.78	TRUE
TVu-2407	Guatemala	NA	NA	NA	LR	PASS	NA	Clus. 1	0.89	0.11	TRUE
TVu-2417	Pakistan	NA	NA	NA	LR	PASS	NA	Admixed	0.35	0.65	TRUE
TVu-2418	United Arab Emirates	NA	NA	NA	LR	PASS	NA	Clus. 2	0.18	0.82	TRUE
TVu-2422	Spain	NA	NA	NA	LR	PASS	NA	Clus. 2	0.16	0.84	TRUE
TVu-2427	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 1	0.71	0.29	TRUE
TVu-2449	India	NA	NA	NA	LR	PASS	NA	Admixed	0.55	0.45	TRUE
TVu-2458	Israel	NA	NA	NA	LR	PASS	NA	Clus. 1	0.79	0.21	TRUE
TVu-2483	South Africa	NA	NA	NA	LR	PASS	NA	Admixed	0.53	0.47	TRUE
TVu-2500	United States of America	NA	NA	NA	BRM	FILTER	TVu-1727	NA	NA	NA	FALSE
TVu-2539	United States of America	NA	NA	NA	BRM	PASS	NA	Clus. 2	0.14	0.86	TRUE
TVu-2548	United States of America	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.88	0.12	TRUE
TVu-2606	United States of America	NA	NA	NA	BRM	PASS	NA	Admixed	0.47	0.53	TRUE
TVu-2646	Uganda	NA	NA	NA	LR	PASS	NA	Admixed	0.41	0.59	TRUE
TVu-2651	Kenya	NA	NA	NA	LR	PASS	NA	Admixed	0.61	0.39	TRUE
TVu-2653	South Africa	NA	NA	NA	LR	PASS	NA	Admixed	0.41	0.59	TRUE
TVu-2657	South Africa	NA	NA	NA	LR	PASS	TVu-6914	Clus. 1	1	0	TRUE
TVu-2680	Nigeria	NA	NA	NA	LR	PASS	NA	Admixed	0.69	0.31	TRUE
TVu-2685	India	NA	NA	NA	NA	PASS	NA	Clus. 1	1	0	TRUE
TVu-2717	India	NA	NA	NA	LR	PASS	TVu-2896	Clus. 1	1	0	TRUE
TVu-2723	India	NA	NA	NA	LR	PASS	NA	Admixed	0.38	0.62	TRUE
TVu-2728	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.92	0.08	TRUE
TVu-2736	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.71	0.29	TRUE
TVu-2750	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.90	0.10	TRUE
TVu-2755	India	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE

TVu-2757	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.85	0.15	TRUE
TVu-2769	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.74	0.26	TRUE
TVu-2785	India	NA	NA	NA	LR	PASS	NA	Admixed	0.62	0.38	TRUE
TVu-2797	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.71	0.29	TRUE
TVu-2825	India	NA	NA	NA	LR	PASS	TVu-3310	Clus. 1	1	0	TRUE
TVu-2845	India	NA	NA	NA	LR	PASS	TVu-3346	Admixed	0.34	0.66	TRUE
TVu-2846	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.82	0.18	TRUE
TVu-2847	India	NA	NA	NA	LR	PASS	NA	Admixed	0.69	0.31	TRUE
TVu-2851	India	NA	NA	NA	LR	PASS	TVu-3408	Clus. 1	0.99	0.01	TRUE
TVu-2852	India	NA	NA	NA	LR	PASS	NA	Admixed	0.57	0.43	TRUE
TVu-2861	India	NA	NA	NA	LR	PASS	NA	Clus. 2	0.21	0.79	TRUE
TVu-2864	India	NA	NA	NA	LR	PASS	NA	Clus. 2	0.24	0.76	TRUE
TVu-2870	India	NA	NA	NA	LR	PASS	NA	Admixed	0.32	0.68	TRUE
TVu-2885	India	NA	NA	NA	LR	PASS	NA	Admixed	0.61	0.39	TRUE
TVu-2886	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.70	0.30	TRUE
TVu-2887	India	NA	NA	NA	LR	FILTER	TVu-14963, TVu-14978, TVu-15589, TVu-7317, TVu-8123, TVu-8456	NA	NA	NA	FALSE
TVu-2891	India	NA	NA	NA	LR	FILTER	TVu-12968, TVu-3107	NA	NA	NA	FALSE
TVu-2896	India	NA	NA	NA	LR	FILTER	TVu-2717	NA	NA	NA	FALSE
TVu-2933	India	NA	NA	NA	LR	PASS	NA	Admixed	0.69	0.31	TRUE
TVu-2939	India	NA	NA	NA	LR	FILTER	NA	NA	NA	NA	FALSE
TVu-2962	India	NA	NA	NA	LR	PASS	NA	Clus. 2	0.22	0.78	TRUE
TVu-2964	India	NA	NA	NA	LR	PASS	NA	Admixed	0.54	0.46	TRUE
TVu-2968	India	NA	NA	NA	LR	PASS	NA	Clus. 2	0.20	0.80	TRUE
TVu-2971	India	NA	NA	NA	LR	PASS	NA	Admixed	0.48	0.52	TRUE

TVu-2978	India	NA	NA	NA	LR	PASS	NA	Admixed	0.68	0.32	TRUE
TVu-3043	India	NA	NA	NA	LR	PASS	NA	Clus. 2	0.21	0.79	TRUE
TVu-3076	India	NA	NA	NA	LR	PASS	NA	Clus. 2	0.21	0.79	TRUE
TVu-3107	India	NA	NA	NA	LR	PASS	TVu-12968, TVu-2891	Admixed	0.56	0.44	TRUE
TVu-3147	India	NA	NA	NA	LR	PASS	NA	Admixed	0.57	0.43	TRUE
TVu-3156	India	NA	NA	NA	LR	PASS	NA	Clus. 2	0.24	0.76	TRUE
TVu-3169	India	NA	NA	NA	LR	PASS	NA	Clus. 2	0.24	0.76	TRUE
TVu-3172	India	NA	NA	NA	LR	PASS	NA	Clus. 2	0.21	0.79	TRUE
TVu-3192	India	NA	NA	NA	LR	PASS	NA	Admixed	0.52	0.48	TRUE
TVu-3199	India	NA	NA	NA	LR	PASS	NA	Clus. 2	0.23	0.77	TRUE
TVu-3246	India	NA	NA	NA	LR	PASS	TVu-408	Clus. 1	0.85	0.15	TRUE
TVu-3282	India	NA	NA	NA	LR	PASS	NA	Admixed	0.57	0.43	TRUE
TVu-3310	India	NA	NA	NA	LR	FILTER	TVu-2825	NA	NA	NA	FALSE
TVu-3346	India	NA	NA	NA	LR	FILTER	TVu-2845	NA	NA	NA	FALSE
TVu-3354	India	NA	NA	NA	LR	PASS	NA	Clus. 2	0.23	0.77	TRUE
TVu-3360	India	NA	NA	NA	LR	PASS	NA	Admixed	0.66	0.34	TRUE
TVu-3364	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.77	0.23	TRUE
TVu-3389	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.83	0.17	TRUE
TVu-3391	India	NA	NA	NA	LR	PASS	NA	Admixed	0.47	0.53	TRUE
TVu-3408	India	NA	NA	NA	LR	FILTER	TVu-2851	NA	NA	NA	FALSE
TVu-3415	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.97	0.03	TRUE
TVu-3416	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.96	0.04	TRUE
TVu-3430	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.93	0.07	TRUE
TVu-3433	India	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-3435	India	NA	NA	NA	LR	PASS	NA	Admixed	0.53	0.47	TRUE
TVu-3445	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.75	0.25	TRUE
TVu-3496	India	NA	NA	NA	LR	PASS	NA	Admixed	0.43	0.57	TRUE
TVu-3511	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.88	0.12	TRUE
TVu-3521	India	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-3529	India	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-3552	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.84	0.16	TRUE

TVu-3565	India	NA	NA	NA	LR	FILTER	TVu-1404, TVu-1433, TVu-1461, TVu-2207	NA	NA	NA	FALSE
TVu-3625	India	NA	NA	NA	LR	FILTER	TVu-1744, TVu-9393	NA	NA	NA	FALSE
TVu-3629	Nigeria	NA	NA	NA	BRM	PASS	NA	Admixed	0.53	0.47	TRUE
TVu-3640	Cameroon	7.35	13.57	1,104	LR	PASS	NA	Clus. 1	0.99	0.01	TRUE
TVu-3641	France	NA	NA	NA	LR	FILTER	TVu-16449	NA	NA	NA	FALSE
TVu-3647	Angola	NA	NA	NA	LR	PASS	NA	Clus. 1	0.80	0.20	TRUE
TVu-3648	Zaire	NA	NA	NA	LR	PASS	NA	Clus. 1	0.83	0.17	TRUE
TVu-3649	Zaire	NA	NA	NA	LR	PASS	NA	Clus. 1	0.91	0.09	TRUE
TVu-3650	Zaire	NA	NA	NA	LR	PASS	NA	Clus. 1	0.70	0.30	TRUE
TVu-3652	Australia	47.33	13.33	3,797	LR	PASS	NA	Clus. 1	0.78	0.22	TRUE
TVu-3656	New Caledonia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.78	0.22	TRUE
TVu-3657	China	NA	NA	NA	LR	PASS	NA	Admixed	0.50	0.50	TRUE
TVu-3661	Zaire	NA	NA	NA	LR	PASS	NA	Clus. 1	0.84	0.16	TRUE
TVu-3662	Zaire	NA	NA	NA	LR	PASS	NA	Clus. 1	0.84	0.16	TRUE
TVu-3670	Nigeria	9.87	4.48	252	LR	FILTER	TVu-3699, TVu-3874, TVu-443, TVu-5465, TVu-5623	NA	NA	NA	FALSE
TVu-3672	Nigeria	12.20	8.48	508	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-3686	Nigeria	13.40	5.25	272	Weedy	PASS	NA	Clus. 2	0.19	0.81	TRUE
TVu-3689	Nigeria	13.47	4.71	297	Weedy	PASS	NA	Clus. 2	0.29	0.71	TRUE
TVu-3699	Nigeria	12.75	4.18	230	Weedy	FILTER	TVu-3670, TVu-3874, TVu-443, TVu-5465, TVu-5623	NA	NA	NA	FALSE
TVu-3701	Nigeria	12.50	4.18	230	Weedy	PASS	NA	Clus. 2	0.28	0.72	TRUE
TVu-3707	Nigeria	12.73	6.50	312	Weedy	PASS	NA	Clus. 2	0.28	0.72	TRUE

TVu-3709	Nigeria	12.73	6.50	312	Weedy	PASS	NA	Clus. 2	0.29	0.71	TRUE
TVu-3710	Nigeria	13	7.53	508	LR	FILTER	TVu-4982, TVu-5285, TVu-6236, TVu-7598	NA	NA	NA	FALSE
TVu-3713	Nigeria	12.93	8.10	508	Weedy	PASS	NA	Clus. 2	0.28	0.72	TRUE
TVu-3717	Nigeria	12.55	8.45	508	Weedy	PASS	NA	Admixed	0.51	0.49	TRUE
TVu-3718	Nigeria	12.47	8.47	508	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-3722	Nigeria	12	8.52	508	Weedy	PASS	NA	Clus. 2	0.07	0.93	TRUE
TVu-3724	Nigeria	10.12	9.20	615	Weedy	PASS	NA	Clus. 2	0.27	0.73	TRUE
TVu-3736	Nigeria	11.37	9.95	508	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-3739	Nigeria	11.67	10.67	372	Weedy	PASS	NA	Clus. 2	0.30	0.70	TRUE
TVu-3745	Nigeria	12.12	13.07	299	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-3752	Nigeria	12.77	13.65	290	Weedy	PASS	NA	Clus. 1	0.87	0.13	TRUE
TVu-3760	Nigeria	11.25	13.67	508	Weedy	PASS	NA	Clus. 2	0.27	0.73	TRUE
TVu-3761	Nigeria	11.08	13.63	508	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-3766	Nigeria	11.37	13.68	126	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-3773	Nigeria	11.88	12.78	297	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-3786	Nigeria	10.23	11.43	535	Weedy	PASS	NA	Clus. 2	0.29	0.71	TRUE
TVu-3787	Nigeria	10.28	10.25	508	Weedy	PASS	NA	Clus. 2	0.29	0.71	TRUE
TVu-3788	Nigeria	10.27	11.03	508	Wild	PASS	NA	Clus. 2	0	1	TRUE
TVu-3790	Nigeria	10.32	10.65	508	Weedy	PASS	NA	Clus. 2	0	1	TRUE
TVu-3791	Nigeria	10.22	10.12	615	LR	FILTER	TVu-13882, TVu-3853	NA	NA	NA	FALSE
TVu-3799	Nigeria	11.02	10.40	508	Weedy	PASS	NA	Clus. 2	0.27	0.73	TRUE
TVu-3801	Nigeria	11.23	10.57	408	Weedy	PASS	NA	Clus. 2	0	1	TRUE
TVu-3804	Nigeria	11.38	10.28	408	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-3817	Nigeria	12.37	9.73	336	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-3818	Nigeria	12.35	9.12	508	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-3820	Nigeria	12	8.52	508	Weedy	PASS	NA	Clus. 1	0.72	0.28	TRUE
TVu-3827	Nigeria	12.32	8.03	508	Weedy	PASS	NA	Clus. 2	0	1	TRUE
TVu-3830	Nigeria	12.28	7.77	573	Weedy	PASS	NA	Admixed	0.41	0.59	TRUE
TVu-3833	Nigeria	12.05	7.73	616	LR	PASS	NA	Clus. 2	0	1	TRUE

TVu-3835	Nigeria	11.83	7.67	573	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-3842	Nigeria	11.28	7.40	614	Weedy	PASS	NA	Admixed	0.46	0.54	TRUE
TVu-3843	Nigeria	11.28	7.40	614	Weedy	PASS	NA	Clus. 2	0.14	0.86	TRUE
TVu-3847	Nigeria	11.07	7.73	671	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-3850	Nigeria	11.02	7.63	671	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-3853	Nigeria	10.62	7.10	612	Weedy	PASS	TVu-13882, TVu-3791	Clus. 2	0	1	TRUE
TVu-3857	Nigeria	9.42	6	281	LR	PASS	TVu-8010	Clus. 2	0.01	0.99	TRUE
TVu-3874	Nigeria	12.65	6.63	383	LR	PASS	TVu-3670, TVu-3699, TVu-443, TVu-5465, TVu-5623	Clus. 2	0	1	TRUE
TVu-3890	Nigeria	11.88	13.27	299	LR	PASS	NA	Clus. 2	0.09	0.91	TRUE
TVu-3896	Nigeria	12.38	8.03	573	Weedy	PASS	NA	Clus. 2	0	1	TRUE
TVu-3897	Nigeria	12.72	13.57	281	Weedy	PASS	NA	Clus. 2	0.08	0.92	TRUE
TVu-3898	United Kingdom	NA	NA	NA	LR	PASS	TVu-1562, TVu-1771	Admixed	0.49	0.51	TRUE
TVu-3903	Nigeria	NA	NA	NA	LR	PASS	TVu-1738, TVu-1739	Admixed	0.51	0.49	TRUE
TVu-3906	India	NA	NA	NA	NA	PASS	NA	Clus. 1	0.98	0.02	TRUE
TVu-3914	Nigeria	12.42	10.03	336	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-3923	Nigeria	6.47	6.23	252	LR	PASS	TVu-8828	Clus. 2	0	1	TRUE
TVu-3924	Nigeria	12.61	4.88	308	LR	PASS	NA	Clus. 2	0.13	0.87	TRUE
TVu-3937	Nigeria	8.73	5.75	80	LR	FILTER	TVu-5225, TVu-5334	NA	NA	NA	FALSE
TVu-3941	Nigeria	9.88	4.52	151	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-3947	Nigeria	7.36	7.10	252	LR	PASS	NA	Admixed	0.64	0.36	TRUE
TVu-3958	Suriname	NA	NA	NA	LR	PASS	NA	Admixed	0.64	0.36	TRUE
TVu-3965	Nigeria	7.73	4.52	252	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-3969	Nigeria	7.75	4.55	252	LR	PASS	NA	Clus. 2	0.03	0.97	TRUE
TVu-3978	Nigeria	8.08	4.65	508	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-3997	Nigeria	7.93	6.30	440	LR	PASS	NA	Admixed	0.52	0.48	TRUE

TVu-4026	Nigeria	7.18	6.27	207	LR	PASS	NA	Admixed	0.52	0.48	TRUE
TVu-4030	Nigeria	7.10	6.57	207	LR	PASS	NA	Clus. 2	0.06	0.94	TRUE
TVu-4048	Nigeria	6.78	6.22	86	LR	PASS	NA	Admixed	0.50	0.50	TRUE
TVu-4057	Nigeria	5.67	7	71	LR	PASS	NA	Clus. 1	0.85	0.15	TRUE
TVu-4097	Nigeria	7.10	7.66	213	LR	PASS	NA	Clus. 2	0.07	0.93	TRUE
TVu-4107	Nigeria	7.17	9.50	114	LR	PASS	NA	Clus. 2	0.09	0.91	TRUE
TVu-4191	Nigeria	8.92	11.42	202	LR	PASS	NA	Clus. 2	0.10	0.90	TRUE
TVu-4200	Nigeria	8.92	11.42	202	LR	PASS	NA	Clus. 2	0.13	0.87	TRUE
TVu-4210	Nigeria	9.07	11.52	192	LR	PASS	NA	Clus. 2	0.12	0.88	TRUE
TVu-4213	Nigeria	9.07	11.52	192	LR	PASS	NA	Clus. 2	0.14	0.86	TRUE
TVu-4229	Nigeria	9.88	12.63	192	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-4232	Nigeria	10.03	12.67	192	LR	PASS	NA	Clus. 2	0.01	0.99	TRUE
TVu-4233	Nigeria	10.03	12.67	192	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-4243	Nigeria	10.18	12.70	575	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-4247	Nigeria	10.17	12.83	575	LR	PASS	NA	Clus. 2	0.01	0.99	TRUE
TVu-4255	Nigeria	10.25	13.13	575	LR	PASS	NA	Clus. 2	0.12	0.88	TRUE
TVu-4275	Nigeria	9.47	12.05	156	LR	PASS	NA	Clus. 2	0.15	0.85	TRUE
TVu-4285	Nigeria	9.62	11.88	156	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-4306	Nigeria	9.80	11.23	460	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-4307	Nigeria	9.80	11.23	460	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-4309	Nigeria	9.95	11.17	460	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-4312	Nigeria	9.95	11.17	460	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-4316	Nigeria	10.05	11.13	460	LR	PASS	NA	Admixed	0.69	0.31	TRUE
TVu-4328	Nigeria	9.10	9.10	1,195	LR	PASS	NA	Clus. 2	0.27	0.73	TRUE
TVu-4344	Nigeria	9.35	9.58	1,196	LR	PASS	NA	Clus. 2	0.15	0.85	TRUE
TVu-4374	Nigeria	9.17	9.78	330	LR	PASS	NA	Clus. 2	0.16	0.84	TRUE
TVu-4384	Nigeria	9.17	9.78	330	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-4395	Nigeria	8.58	6.14	67	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-4419	Nigeria	10.30	13.38	575	LR	PASS	NA	Clus. 2	0.12	0.88	TRUE
TVu-4438	Nigeria	10.30	13.38	575	LR	PASS	NA	Clus. 2	0.15	0.85	TRUE
TVu-4461	Nigeria	10.30	13.38	575	LR	PASS	NA	Clus. 2	0.03	0.97	TRUE
TVu-4481	Ghana	6.69	-1.62	270	LR	PASS	NA	Clus. 1	0.79	0.21	TRUE
TVu-4483	Ghana	6.69	-1.62	270	LR	PASS	NA	Clus. 1	0.80	0.20	TRUE

TVu-4484	Ghana	6.69	-1.62	270	LR	PASS	NA	Clus. 1	0.97	0.03	TRUE
TVu-4489	Ghana	6.72	1.60	287	LR	PASS	NA	Clus. 1	0.73	0.27	TRUE
TVu-4492	Ghana	6.68	-1.62	246	LR	PASS	NA	Admixed	0.56	0.44	TRUE
TVu-4535	Nigeria	NA	NA	NA	BRM	PASS	NA	Admixed	0.40	0.60	TRUE
TVu-4536	Nigeria	NA	NA	NA	BRM	PASS	NA	Admixed	0.36	0.64	TRUE
TVu-4537	Nigeria	NA	NA	NA	BRM	PASS	NA	Admixed	0.63	0.37	TRUE
TVu-4539	Nigeria	NA	NA	NA	BRM	PASS	TVu-4540	Admixed	0.69	0.31	TRUE
TVu-4540	Nigeria	NA	NA	NA	BRM	FILTER	TVu-4539	NA	NA	NA	FALSE
TVu-4545	Nigeria	NA	NA	NA	BRM	PASS	NA	Admixed	0.41	0.59	TRUE
TVu-4546	Nigeria	NA	NA	NA	BRM	PASS	NA	Clus. 1	1	0	TRUE
TVu-4549	Nigeria	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.72	0.28	TRUE
TVu-4557	Nigeria	NA	NA	NA	BRM	FILTER	TVu-15986	NA	NA	NA	FALSE
TVu-4558	Nigeria	NA	NA	NA	BRM	PASS	NA	Admixed	0.48	0.52	TRUE
TVu-4559	Nigeria	NA	NA	NA	BRM	PASS	NA	Clus. 2	0.27	0.73	TRUE
TVu-4562	Nigeria	NA	NA	NA	BRM	PASS	NA	Clus. 2	0.25	0.75	TRUE
TVu-4569	Nigeria	NA	NA	NA	BRM	PASS	NA	Admixed	0.48	0.52	TRUE
TVu-4574	Nigeria	NA	NA	NA	BRM	PASS	NA	Admixed	0.43	0.57	TRUE
TVu-4578	Nigeria	NA	NA	NA	Weedy	PASS	NA	Admixed	0.56	0.44	TRUE
TVu-4600	Tanzania	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-4607	Tanzania	NA	NA	NA	LR	FILTER	TVu-1564, TVu-2222, TVu-30, TVu-6869	NA	NA	NA	FALSE
TVu-4622	Tanzania	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-4624	Tanzania	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-4631	Tanzania	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-4632	Tanzania	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-4642	Tanzania	NA	NA	NA	LR	PASS	TVu-1207, TVu-1330, TVu-8453	Clus. 1	0.99	0.01	TRUE
TVu-4649	Nigeria	12.93	8.10	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-4669	Niger	13.03	8.37	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-4672	Niger	13.03	8.37	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-4676	Niger	13.03	8.37	NA	LR	PASS	NA	Clus. 2	0	1	TRUE

TVu-4696	Niger	13.03	8.37	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-4701	Niger	13.03	8.37	NA	LR	PASS	NA	Clus. 2	0.01	0.99	TRUE
TVu-4708	Niger	13.03	8.37	NA	LR	FILTER	TVu-4732, TVu-4783, TVu-4808, TVu-4815, TVu-4823, TVu-4943, TVu-4987	NA	NA	NA	FALSE
TVu-4711	Niger	13.03	8.37	NA	LR	PASS	NA	Clus. 2	0.17	0.83	TRUE
TVu-4732	Niger	12.95	8.28	NA	LR	FILTER	TVu-4708, TVu-4783, TVu-4808, TVu-4815, TVu-4823, TVu-4943, TVu-4987	NA	NA	NA	FALSE
TVu-4733	Niger	12.95	8.28	NA	LR	PASS	TVu-14906, TVu-14919	Clus. 2	0	1	TRUE
TVu-4737	Niger	12.95	8.28	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-4740	Niger	12.95	8.28	NA	LR	PASS	TVu-6944	Clus. 2	0	1	TRUE
TVu-4745	Niger	12.95	8.28	NA	Weedy	FILTER	TVu-4748, TVu-4759, TVu-4760, TVu-4761	NA	NA	NA	FALSE
TVu-4746	Niger	12.95	8.28	NA	Weedy	PASS	NA	Clus. 2	0.27	0.73	TRUE
TVu-4747	Niger	12.95	8.28	NA	Weedy	PASS	NA	Clus. 2	0.15	0.85	TRUE
TVu-4748	Niger	12.95	8.28	NA	Weedy	FILTER	TVu-4745, TVu-4759, TVu-4760, TVu-4761	NA	NA	NA	FALSE
TVu-4759	Niger	12.95	8.28	NA	Weedy	PASS	TVu-4745, TVu-4748,	Clus. 2	0.27	0.73	TRUE

							TVu-4760, TVu-4761				
TVu-4760	Niger	12.95	8.28	NA	Weedy	FILTER	TVu-4745, TVu-4748, TVu-4759, TVu-4761	NA	NA	NA	FALSE
TVu-4761	Niger	12.95	8.28	NA	Weedy	FILTER	TVu-4745, TVu-4748, TVu-4759, TVu-4760	NA	NA	NA	FALSE
TVu-4776	Niger	12.95	8.28	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-4783	Niger	12.95	8.28	NA	LR	PASS	TVu-4708, TVu-4732, TVu-4808, TVu-4815, TVu-4823, TVu-4943, TVu-4987	Clus. 2	0.06	0.94	TRUE
TVu-4806	Niger	12.55	8.45	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-4808	Niger	12.55	8.45	NA	LR	FILTER	TVu-4708, TVu-4732, TVu-4783, TVu-4815, TVu-4823, TVu-4943, TVu-4987	NA	NA	NA	FALSE
TVu-4809	Niger	12.55	8.45	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-4815	Niger	12.55	8.45	NA	LR	FILTER	TVu-4708, TVu-4732, TVu-4783, TVu-4808, TVu-4823, TVu-4943, TVu-4987	NA	NA	NA	FALSE

TVu-4823	Niger	12.55	8.45	NA	LR	FILTER	TVu-4708, TVu-4732, TVu-4783, TVu-4808, TVu-4815, TVu-4943, TVu-4987	NA	NA	NA	FALSE
TVu-4825	Niger	12.55	8.45	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-4834	Niger	12.55	8.45	NA	LR	PASS	TVu-4836	Clus. 2	0	1	TRUE
TVu-4835	Niger	12.55	8.45	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-4836	Niger	12.55	8.45	NA	LR	FILTER	TVu-4834	NA	NA	NA	FALSE
TVu-4841	Niger	12.55	8.45	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-4877	Niger	12.55	8.45	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-4886	Niger	12.55	8.45	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-4923	Niger	12.47	8.47	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-4924	Niger	12.47	8.47	NA	LR	FILTER	TVu-10065, TVu-4946, TVu-4976, TVu-4984, TVu-5020, TVu-5029, TVu-5031, TVu-5035, TVu-5040, TVu-5052, TVu-5055, TVu-5057, TVu-5247, TVu-5314	NA	NA	NA	FALSE
TVu-4926	Niger	12.47	8.47	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-4943	Niger	12.47	8.47	NA	LR	FILTER	TVu-4708, TVu-4732, TVu-4783, TVu-4808,	NA	NA	NA	FALSE

							TVu-4815, TVu-4823, TVu-4987				
TVu-4944	Niger	12.47	8.47	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-4946	Niger	12.47	8.47	NA	LR	FILTER	TVu-10065, TVu-4924, TVu-4976, TVu-4984, TVu-5020, TVu-5029, TVu-5031, TVu-5035, TVu-5040, TVu-5052, TVu-5055, TVu-5057, TVu-5247, TVu-5314	NA	NA	NA	FALSE
TVu-4960	Niger	12.47	8.47	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-4963	Niger	12.47	8.47	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-4970	Niger	12.47	8.47	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-4976	Niger	12.47	8.47	NA	LR	FILTER	TVu-10065, TVu-4924, TVu-4946, TVu-4984, TVu-5020, TVu-5029, TVu-5031, TVu-5035, TVu-5040, TVu-5052, TVu-5055, TVu-5057,	NA	NA	NA	FALSE

							TVu-5247, TVu-5314				
TVu-4982	Niger	12.47	8.47	NA	LR	FILTER	TVu-3710, TVu-5285, TVu-6236, TVu-7598	NA	NA	NA	FALSE
TVu-4984	Niger	12.47	8.47	NA	LR	FILTER	TVu-10065, TVu-4924, TVu-4946, TVu-4976, TVu-5020, TVu-5029, TVu-5031, TVu-5035, TVu-5040, TVu-5052, TVu-5055, TVu-5057, TVu-5247, TVu-5314	NA	NA	NA	FALSE
TVu-4987	Niger	12.22	8.50	NA	LR	FILTER	TVu-4708, TVu-4732, TVu-4783, TVu-4808, TVu-4815, TVu-4823, TVu-4943	NA	NA	NA	FALSE
TVu-5009	Niger	12.22	8.50	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5018	Niger	12.22	8.50	NA	LR	PASS	NA	Clus. 2	0.01	0.99	TRUE
TVu-5020	Niger	12.22	8.50	NA	LR	FILTER	TVu-10065, TVu-4924, TVu-4946, TVu-4976,	NA	NA	NA	FALSE

							TVu-4984, TVu-5029, TVu-5031, TVu-5035, TVu-5040, TVu-5052, TVu-5055, TVu-5057, TVu-5247, TVu-5314				
TVu-5029	Niger	12.22	8.50	NA	LR	FILTER	TVu-10065, TVu-4924, TVu-4946, TVu-4976, TVu-4984, TVu-5020, TVu-5031, TVu-5035, TVu-5040, TVu-5052, TVu-5055, TVu-5057, TVu-5247, TVu-5314	NA	NA	NA	FALSE
TVu-5031	Niger	12.22	8.50	NA	LR	FILTER	TVu-10065, TVu-4924, TVu-4946, TVu-4976, TVu-4984, TVu-5020, TVu-5029, TVu-5035, TVu-5040,	NA	NA	NA	FALSE

							TVu-5052, TVu-5055, TVu-5057, TVu-5247, TVu-5314				
TVu-5035	Niger	12.22	8.50	NA	LR	FILTER	TVu-10065, TVu-4924, TVu-4946, TVu-4976, TVu-4984, TVu-5020, TVu-5029, TVu-5031, TVu-5040, TVu-5052, TVu-5055, TVu-5057, TVu-5247, TVu-5314	NA	NA	NA	FALSE
TVu-5040	Niger	12.22	8.50	NA	LR	FILTER	TVu-10065, TVu-4924, TVu-4946, TVu-4976, TVu-4984, TVu-5020, TVu-5029, TVu-5031, TVu-5035, TVu-5052, TVu-5055, TVu-5057, TVu-5247, TVu-5314	NA	NA	NA	FALSE

TVu-5047	Niger	12.22	8.50	NA	LR	PASS	NA	Clus. 2	0.04	0.96	TRUE
TVu-5052	Niger	12.22	8.50	NA	LR	PASS	TVu-10065, TVu-4924, TVu-4946, TVu-4976, TVu-4984, TVu-5020, TVu-5029, TVu-5031, TVu-5035, TVu-5040, TVu-5055, TVu-5057, TVu-5247, TVu-5314	Clus. 2	0.06	0.94	TRUE
TVu-5055	Niger	12.22	8.50	NA	LR	FILTER	TVu-10065, TVu-4924, TVu-4946, TVu-4976, TVu-4984, TVu-5020, TVu-5029, TVu-5031, TVu-5035, TVu-5040, TVu-5052, TVu-5057, TVu-5247, TVu-5314	NA	NA	NA	FALSE
TVu-5057	Niger	12.22	8.50	NA	LR	FILTER	TVu-10065, TVu-4924, TVu-4946,	NA	NA	NA	FALSE

							TVu-4976, TVu-4984, TVu-5020, TVu-5029, TVu-5031, TVu-5035, TVu-5040, TVu-5052, TVu-5055, TVu-5247, TVu-5314				
TVu-5076	Niger	12.13	8.43	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5077	Niger	12.13	8.43	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5096	Niger	12.13	8.43	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5107	Niger	12.13	8.43	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5126	Brazil	NA	NA	NA	LR	FILTER	TVu-393	NA	NA	NA	FALSE
TVu-5137	Brazil	NA	NA	NA	LR	PASS	NA	Clus. 1	0.93	0.07	TRUE
TVu-5138	Brazil	NA	NA	NA	LR	PASS	NA	Clus. 1	0.93	0.07	TRUE
TVu-5146	Brazil	NA	NA	NA	LR	PASS	NA	Clus. 1	0.95	0.05	TRUE
TVu-5163	Brazil	NA	NA	NA	LR	PASS	NA	Clus. 1	0.95	0.05	TRUE
TVu-5165	Brazil	NA	NA	NA	LR	PASS	NA	Clus. 1	0.98	0.02	TRUE
TVu-5168	Brazil	NA	NA	NA	LR	FILTER	TVu-14358, TVu-7144	NA	NA	NA	FALSE
TVu-5225	Nigeria	11.85	8.50	NA	LR	FILTER	TVu-3937, TVu-5334	NA	NA	NA	FALSE
TVu-5247	Niger	NA	NA	NA	LR	FILTER	TVu-10065, TVu-4924, TVu-4946, TVu-4976, TVu-4984, TVu-5020, TVu-5029, TVu-5031,	NA	NA	NA	FALSE

							TVu-5035, TVu-5040, TVu-5052, TVu-5055, TVu-5057, TVu-5314				
TVu-5258	Niger	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5285	Niger	NA	NA	NA	LR	PASS	TVu-3710, TVu-4982, TVu-6236, TVu-7598	Clus. 2	0	1	TRUE
TVu-5307	Niger	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5314	Niger	NA	NA	NA	LR	FILTER	TVu-10065, TVu-4924, TVu-4946, TVu-4976, TVu-4984, TVu-5020, TVu-5029, TVu-5031, TVu-5035, TVu-5040, TVu-5052, TVu-5055, TVu-5057, TVu-5247	NA	NA	NA	FALSE
TVu-5331	Niger	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5334	Niger	NA	NA	NA	LR	PASS	TVu-3937, TVu-5225	Clus. 2	0	1	TRUE
TVu-5335	Niger	NA	NA	NA	LR	PASS	NA	Clus. 1	0.79	0.21	TRUE
TVu-5362	Niger	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5365	Niger	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5368	Niger	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5390	Niger	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE

TVu-5393	Niger	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5415	Niger	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5443	Niger	NA	NA	NA	LR	PASS	NA	Admixed	0.62	0.38	TRUE
TVu-5444	Niger	NA	NA	NA	LR	PASS	NA	Admixed	0.55	0.45	TRUE
TVu-5465	Niger	NA	NA	NA	LR	FILTER	TVu-3670, TVu-3699, TVu-3874, TVu-443, TVu-5623	NA	NA	NA	FALSE
TVu-5466	Niger	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5467	Niger	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5473	Niger	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5474	Niger	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5478	Niger	10.12	9.20	NA	LR	PASS	TVu-5504	Clus. 2	0	1	TRUE
TVu-5488	Niger	10.12	9.20	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5495	Niger	10.12	9.20	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5498	Niger	10.12	9.20	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5500	Niger	10.12	9.20	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5504	Niger	10.12	9.20	NA	LR	FILTER	TVu-5478	NA	NA	NA	FALSE
TVu-5519	Niger	10.12	9.20	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5524	Niger	10.12	9.20	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5540	Niger	10.12	9.20	NA	LR	PASS	NA	Clus. 2	0.04	0.96	TRUE
TVu-5550	Niger	10.12	9.20	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5557	Niger	10.12	9.20	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5562	Niger	10.12	9.20	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5573	Niger	10.12	9.20	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5584	Niger	10.12	9.20	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5597	Niger	10.12	9.20	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5609	Niger	10.12	9.20	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5623	Niger	10.12	9.20	NA	LR	FILTER	TVu-3670, TVu-3699, TVu-3874, TVu-443, TVu-5465	NA	NA	NA	FALSE

TVu-5624	Niger	10.12	9.20	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5632	Niger	10.12	9.20	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5649	Niger	10.12	9.20	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5653	Niger	10.12	9.20	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5655	Niger	10.12	9.20	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5659	Niger	10.12	9.20	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5662	Niger	10.12	9.20	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5694	Nigeria	10.12	9.20	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5721	Nigeria	10.12	9.20	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5739	Nigeria	10.12	9.20	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5757	Nigeria	10.12	9.20	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5796	Nigeria	10.20	9.37	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5799	Nigeria	10.20	9.37	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5806	Nigeria	10.20	9.37	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5828	Nigeria	10.20	9.37	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5874	Nigeria	10.20	9.37	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-5957	Nigeria	10.20	9.37	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-6192	Nigeria	10.20	9.37	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-6236	Niger	NA	NA	NA	LR	FILTER	TVu-3710, TVu-4982, TVu-5285, TVu-7598	NA	NA	NA	FALSE
TVu-6238	Niger	NA	NA	NA	LR	PASS	NA	Clus. 2	0.06	0.94	TRUE
TVu-6314	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 2	0.23	0.77	TRUE
TVu-6329	South Africa	NA	NA	NA	LR	PASS	NA	Clus. 1	0.85	0.15	TRUE
TVu-6335	Uganda	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-6345	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 1	0.73	0.27	TRUE
TVu-6351	Nigeria	NA	NA	NA	LR	PASS	NA	Admixed	0.31	0.69	TRUE
TVu-6356	United States of America	NA	NA	NA	LR	FILTER	TVu-382	NA	NA	NA	FALSE
TVu-6361	United States of America	NA	NA	NA	LR	PASS	NA	Clus. 1	0.74	0.26	TRUE

TVu-6365	United States of America	NA	NA	NA	LR	PASS	TVu-12597, TVu-274	Clus. 1	1	0	TRUE
TVu-6389	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 1	0.73	0.27	TRUE
TVu-6399	United States of America	NA	NA	NA	LR	PASS	NA	Clus. 1	0.97	0.03	TRUE
TVu-6414	Nigeria	NA	NA	NA	LR	PASS	TVu-6906	Clus. 1	1	0	TRUE
TVu-6422	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-6433	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-6439	South Africa	NA	NA	NA	LR	PASS	NA	Clus. 1	0.97	0.03	TRUE
TVu-6441	Ghana	NA	NA	NA	LR	PASS	NA	Admixed	0.59	0.41	TRUE
TVu-6451	United States of America	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.94	0.06	TRUE
TVu-6455	United States of America	NA	NA	NA	BRM	PASS	NA	Admixed	0.67	0.33	TRUE
TVu-6463	Uganda	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-6464	Uganda	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-6477	Suriname	NA	NA	NA	LR	PASS	NA	Clus. 1	0.84	0.16	TRUE
TVu-6493	South Africa	NA	NA	NA	LR	PASS	TVu-337, TVu-566	Admixed	0.56	0.44	TRUE
TVu-6499	Puerto Rico	NA	NA	NA	LR	PASS	NA	Clus. 1	0.72	0.28	TRUE
TVu-6500	Puerto Rico	NA	NA	NA	LR	FILTER	NA	NA	NA	NA	FALSE
TVu-6521	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 1	0.91	0.09	TRUE
TVu-6536	South Africa	NA	NA	NA	LR	PASS	NA	Clus. 2	0.21	0.79	TRUE
TVu-6537	Argentina	NA	NA	NA	LR	PASS	NA	Clus. 1	0.89	0.11	TRUE
TVu-6554	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.81	0.19	TRUE
TVu-6584	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.77	0.23	TRUE
TVu-6596	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.83	0.17	TRUE
TVu-6601	India	NA	NA	NA	LR	PASS	NA	Clus. 2	0.23	0.77	TRUE
TVu-6626	India	NA	NA	NA	LR	PASS	NA	Clus. 2	0.24	0.76	TRUE
TVu-6641	Liberia	NA	NA	NA	LR	PASS	NA	Admixed	0.40	0.60	TRUE
TVu-6642	Liberia	NA	NA	NA	LR	PASS	NA	Admixed	0.59	0.41	TRUE
TVu-6643	Liberia	NA	NA	NA	LR	PASS	NA	Admixed	0.58	0.42	TRUE
TVu-6644	Liberia	NA	NA	NA	LR	PASS	NA	Admixed	0.58	0.42	TRUE

TVu-6645	India	NA	NA	NA	LR	PASS	NA	Admixed	0.41	0.59	TRUE
TVu-6663	Nigeria	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.72	0.28	TRUE
TVu-6666	Nigeria	NA	NA	NA	BRM	PASS	NA	Clus. 2	0.29	0.71	TRUE
TVu-6744	Nigeria	12	8.52	484	LR	PASS	NA	Admixed	0.50	0.50	TRUE
TVu-6775	Nigeria	NA	NA	NA	LR	FILTER	TVu-10056	NA	NA	NA	FALSE
TVu-6782	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 2	0.12	0.88	TRUE
TVu-6824	Nigeria	12.77	13.65	291	Weedy	PASS	NA	Admixed	0.34	0.66	TRUE
TVu-6826	Suriname	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-6837	Turkey	NA	NA	NA	LR	PASS	NA	Clus. 1	0.99	0.01	TRUE
TVu-6838	South Africa	NA	NA	NA	LR	PASS	TVu-14290, TVu-14325, TVu-14700, TVu-14721, TVu-14886, TVu-14890, TVu-14914, TVu-15424, TVu-15968, TVu-16422, TVu-7149	Clus. 1	1	0	TRUE
TVu-6855	Nigeria	NA	NA	NA	LR	PASS	NA	Admixed	0.59	0.41	TRUE
TVu-6858	Nigeria	NA	NA	NA	LR	PASS	NA	Admixed	0.41	0.59	TRUE
TVu-6867	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 1	0.97	0.03	TRUE
TVu-6868	Tanzania	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE

TVu-6869	Tanzania	NA	NA	NA	LR	FILTER	TVu-1564, TVu-2222, TVu-30, TVu-4607	NA	NA	NA	FALSE
TVu-6874	Tanzania	NA	NA	NA	LR	PASS	NA	Clus. 1	0.95	0.05	TRUE
TVu-6906	Tanzania	NA	NA	NA	LR	FILTER	TVu-6414	NA	NA	NA	FALSE
TVu-6914	Botswana	NA	NA	NA	NA	FILTER	TVu-2657	NA	NA	NA	FALSE
TVu-6944	Niger	NA	NA	NA	LR	FILTER	TVu-4740	NA	NA	NA	FALSE
TVu-6947	Niger	NA	NA	NA	LR	PASS	NA	Clus. 2	0.03	0.97	TRUE
TVu-6956	Niger	NA	NA	NA	LR	PASS	NA	Admixed	0.37	0.63	TRUE
TVu-6959	Niger	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-6965	Niger	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-6966	Niger	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-6968	Niger	NA	NA	NA	LR	PASS	NA	Clus. 2	0.04	0.96	TRUE
TVu-6972	Niger	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-6982	Niger	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-6988	Niger	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-6994	Niger	NA	NA	NA	LR	PASS	TVu-15569, TVu-16440	Clus. 2	0	1	TRUE
TVu-7001	Niger	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7006	Niger	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7068	Indonesia	NA	NA	NA	LR	PASS	NA	Admixed	0.54	0.46	TRUE
TVu-7069	Venezuela	NA	NA	NA	LR	PASS	TVu-14759, TVu-45	Clus. 1	0.97	0.03	TRUE
TVu-7070	Venezuela	NA	NA	NA	LR	FILTER	TVu-14598	NA	NA	NA	FALSE
TVu-7074	Ghana	NA	NA	NA	LR	PASS	NA	Clus. 1	0.85	0.15	TRUE
TVu-7084	Nigeria	NA	NA	NA	LR	PASS	NA	Admixed	0.51	0.49	TRUE
TVu-7119	Nigeria	10.50	11.25	508	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7127	United States of America	21.31	-157.86	18	LR	PASS	NA	Clus. 1	0.88	0.12	TRUE

TVu-7144	Ethiopia	NA	NA	NA	LR	PASS	TVu-14358, TVu-5168	Clus. 2	0.11	0.89	TRUE
TVu-7145	Ethiopia	NA	NA	NA	LR	PASS	NA	Clus. 2	0.12	0.88	TRUE
TVu-7146	Ethiopia	NA	NA	NA	LR	PASS	NA	Clus. 2	0.21	0.79	TRUE
TVu-7147	Ethiopia	NA	NA	NA	LR	PASS	NA	Clus. 2	0.12	0.88	TRUE
TVu-7148	Ethiopia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.95	0.05	TRUE
TVu-7149	Ethiopia	NA	NA	NA	LR	FILTER	TVu-14290, TVu-14325, TVu-14700, TVu-14721, TVu-14886, TVu-14890, TVu-14914, TVu-15424, TVu-15968, TVu-16422, TVu-6838	NA	NA	NA	FALSE
TVu-7153	United States of America	NA	NA	NA	NA	PASS	NA	Admixed	0.37	0.63	TRUE
TVu-7155	Tanzania	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-7156	Niger	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7168	United States of America	NA	NA	NA	LR	PASS	NA	Clus. 1	0.78	0.22	TRUE
TVu-7180	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.86	0.14	TRUE

TVu-7185	Tanzania	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-7186	Tanzania	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-7188	Tanzania	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-7190	Niger	13.03	8.37	NA	LR	PASS	NA	Clus. 2	0.12	0.88	TRUE
TVu-7211	Afghanistan	NA	NA	NA	LR	PASS	NA	Clus. 2	0.22	0.78	TRUE
TVu-7229	Afghanistan	NA	NA	NA	LR	PASS	NA	Clus. 2	0.20	0.80	TRUE
TVu-7249	Afghanistan	NA	NA	NA	LR	PASS	NA	Clus. 2	0.20	0.80	TRUE
TVu-7267	Liberia	NA	NA	NA	LR	PASS	NA	Admixed	0.39	0.61	TRUE
TVu-7268	Liberia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.97	0.03	TRUE
TVu-7271	Brazil	NA	NA	NA	NA	PASS	NA	Clus. 1	0.96	0.04	TRUE
TVu-7273	Liberia	NA	NA	NA	LR	PASS	NA	Admixed	0.39	0.61	TRUE
TVu-7274	Nigeria	NA	NA	NA	BRM	PASS	NA	Admixed	0.52	0.48	TRUE
TVu-7275	Sri Lanka	NA	NA	NA	LR	PASS	NA	Admixed	0.55	0.45	TRUE
TVu-7290	Thailand	NA	NA	NA	LR	PASS	NA	Admixed	0.60	0.40	TRUE
TVu-7291	United States of America	NA	NA	NA	BRM	PASS	NA	Admixed	0.50	0.50	TRUE
TVu-7293	Tanzania	NA	NA	NA	Wild	PASS	NA	Admixed	0.47	0.53	TRUE
TVu-7294	Tanzania	NA	NA	NA	Wild	PASS	NA	Admixed	0.47	0.53	TRUE
TVu-7298	Australia	NA	NA	NA	BRM	PASS	NA	Admixed	0.42	0.58	TRUE
TVu-7317	Nigeria	NA	NA	NA	LR	FILTER	TVu-14963, TVu-14978, TVu-15589, TVu-2887, TVu-8123, TVu-8456	NA	NA	NA	FALSE
TVu-7322	Ghana	8.67	-2.25	266	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7325	Ghana	10.08	-0.80	252	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7331	Ghana	7.59	-1.94	398	LR	PASS	NA	Clus. 2	0.01	0.99	TRUE
TVu-7339	Ghana	5.40	-2	86	LR	PASS	NA	Admixed	0.48	0.52	TRUE
TVu-7340	Ghana	5.28	-1.97	86	LR	PASS	NA	Admixed	0.37	0.63	TRUE
TVu-7352	Ghana	6.08	-0.83	123	LR	PASS	NA	Clus. 2	0.27	0.73	TRUE

TVu-7362	Ghana	5.38	-2	86	LR	PASS	NA	Admixed	0.49	0.51	TRUE
TVu-7363	Ghana	6.82	0.43	508	LR	PASS	NA	Admixed	0.52	0.48	TRUE
TVu-7382	Ghana	6.68	0.33	252	LR	PASS	NA	Admixed	0.58	0.42	TRUE
TVu-7383	Ghana	10.57	-0.25	304	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7425	Ghana	7.57	-1.72	302	LR	PASS	NA	Admixed	0.46	0.54	TRUE
TVu-7429	Ghana	11.07	-0.25	252	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7431	Ghana	7.95	-2.05	110	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7434	Ghana	6.97	-1.47	270	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7440	Ghana	5.28	-1.97	263	LR	PASS	NA	Admixed	0.38	0.62	TRUE
TVu-7441	Ghana	7.69	2.11	111	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7443	Ghana	6.75	-0.71	69	LR	PASS	NA	Admixed	0.45	0.55	TRUE
TVu-7456	Nigeria	11.17	4.80	272	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7459	Nigeria	12.47	4.22	272	LR	PASS	NA	Admixed	0.66	0.34	TRUE
TVu-7460	Nigeria	12.47	4.22	272	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7464	Nigeria	12.47	4.22	272	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7509	Nigeria	8.83	9.50	259	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7530	Nigeria	9.02	9.28	259	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7547	Nigeria	8.57	9.67	221	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7559	Nigeria	9.12	9.10	1,276	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7560	Nigeria	9.10	9.10	1,276	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7562	Nigeria	9.10	9.10	1,276	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7566	Nigeria	8.67	9.67	221	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7575	Nigeria	9.15	9.42	1,370	LR	PASS	NA	Clus. 2	0.13	0.87	TRUE
TVu-7585	Nigeria	9.12	9.38	1,370	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7588	Nigeria	9.13	9.10	1,323	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7598	Nigeria	7.58	9.57	198	LR	FILTER	TVu-3710, TVu-4982, TVu-5285, TVu-6236	NA	NA	NA	FALSE
TVu-7605	Mali	14.50	-4.18	272	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7609	Mali	14.40	-3.55	508	LR	FILTER	TVu-10362	NA	NA	NA	FALSE
TVu-7610	Mali	14.40	-3.53	508	LR	PASS	NA	Clus. 2	0.01	0.99	TRUE
TVu-7611	Mali	14.40	-3.53	508	LR	PASS	NA	Clus. 2	0.01	0.99	TRUE
TVu-7612	Mali	14.40	-3.53	508	LR	PASS	NA	Clus. 2	0.01	0.99	TRUE

TVu-7613	Mali	13.80	-4.37	296	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7614	Mali	14.47	-3.30	508	LR	PASS	NA	Clus. 2	0.02	0.98	TRUE
TVu-7625	Mali	14.40	-3.53	508	LR	PASS	NA	Clus. 2	0.01	0.99	TRUE
TVu-7628	Mali	14.47	-3.30	508	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7634	Mali	12.68	-7.90	331	LR	PASS	TVu-7792	Clus. 2	0	1	TRUE
TVu-7638	Mali	13.18	-7.62	331	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7642	Mali	13.95	-8.18	508	LR	PASS	TVu-7654	Clus. 2	0	1	TRUE
TVu-7647	Mali	14.17	-7.60	367	LR	PASS	NA	Clus. 2	0.01	0.99	TRUE
TVu-7654	Mali	13.27	-7.95	508	LR	FILTER	TVu-7642	NA	NA	NA	FALSE
TVu-7664	Mali	11.93	-7.88	331	LR	PASS	NA	Clus. 2	0.15	0.85	TRUE
TVu-7669	Mali	11.42	-7.47	332	LR	PASS	NA	Admixed	0.38	0.62	TRUE
TVu-7670	Mali	11.42	-7.47	332	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7676	Mali	10.77	-7.33	332	LR	PASS	NA	Admixed	0.40	0.60	TRUE
TVu-7677	Mali	10.45	-7.45	332	LR	PASS	NA	Admixed	0.39	0.61	TRUE
TVu-7680	Mali	10.45	-7.45	332	LR	PASS	NA	Clus. 2	0.17	0.83	TRUE
TVu-7684	Mali	11.42	-6.42	332	LR	PASS	NA	Clus. 1	0.80	0.20	TRUE
TVu-7691	Mali	11.32	-5.67	508	LR	PASS	NA	Clus. 2	0.01	0.99	TRUE
TVu-7692	Mali	11.32	-5.67	508	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7696	Mali	11.42	-7.47	332	LR	PASS	NA	Admixed	0.39	0.61	TRUE
TVu-7697	Mali	11.25	-5.82	508	LR	PASS	NA	Admixed	0.38	0.62	TRUE
TVu-7709	Mali	11.38	-7.03	332	LR	PASS	NA	Admixed	0.38	0.62	TRUE
TVu-7713	Mali	10.45	-7.45	332	LR	PASS	NA	Clus. 2	0.03	0.97	TRUE
TVu-7719	Cote d'Ivoire	9.60	-5.20	339	LR	PASS	NA	Admixed	0.39	0.61	TRUE
TVu-7721	Cote d'Ivoire	9.45	-5.62	360	LR	PASS	NA	Admixed	0.40	0.60	TRUE
TVu-7726	Cote d'Ivoire	9.45	-5.62	360	LR	PASS	NA	Admixed	0.39	0.61	TRUE
TVu-7732	Cote d'Ivoire	9.60	-5.20	339	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7733	Cote d'Ivoire	9.60	-5.20	339	LR	PASS	NA	Admixed	0.39	0.61	TRUE
TVu-7739	Cote d'Ivoire	7.70	-5.03	376	LR	PASS	TVu-9357	Admixed	0.40	0.60	TRUE
TVu-7740	Cote d'Ivoire	6.78	-5.27	217	LR	PASS	NA	Clus. 2	0.01	0.99	TRUE
TVu-7741	Cote d'Ivoire	7.70	-5.03	376	LR	PASS	NA	Admixed	0.38	0.62	TRUE
TVu-7742	Cote d'Ivoire	7.70	-5.03	376	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7747	Cote d'Ivoire	6.78	-5.27	339	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7755	Cote d'Ivoire	9.45	-5.62	360	LR	PASS	TVu-9352	Admixed	0.38	0.62	TRUE

TVu-7757	Cote d'Ivoire	9.60	-5.20	339	LR	PASS	NA	Admixed	0.40	0.60	TRUE
TVu-7761	Cote d'Ivoire	5.45	-4.07	73	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7762	Cote d'Ivoire	5.45	-4.07	73	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7764	Cote d'Ivoire	5.93	-4.20	74	LR	FILTER	TVu-13271	NA	NA	NA	FALSE
TVu-7765	Cote d'Ivoire	6.38	-3.87	252	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7768	Cote d'Ivoire	7.70	-5.03	252	LR	PASS	NA	Admixed	0.43	0.57	TRUE
TVu-7775	Cote d'Ivoire	7.70	-5.03	376	LR	PASS	NA	Admixed	0.39	0.61	TRUE
TVu-7788	Cote d'Ivoire	9.27	-2.93	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7792	Cote d'Ivoire	9.22	-3.07	NA	LR	FILTER	TVu-7634	NA	NA	NA	FALSE
TVu-7796	Papua New Guinea	NA	NA	NA	LR	PASS	NA	Admixed	0.49	0.51	TRUE
TVu-7798	Papua New Guinea	NA	NA	NA	LR	PASS	NA	Admixed	0.62	0.38	TRUE
TVu-7827	Nigeria	7.58	5.75	508	LR	PASS	NA	Admixed	0.52	0.48	TRUE
TVu-7829	Nigeria	7.92	5.50	508	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7835	Nigeria	7.17	4.75	252	LR	PASS	NA	Admixed	0.51	0.49	TRUE
TVu-7856	Nigeria	7.83	3.92	292	LR	PASS	NA	Admixed	0.51	0.49	TRUE
TVu-7880	Nigeria	7.83	6.83	NA	LR	PASS	NA	Admixed	0.53	0.47	TRUE
TVu-7881	Nigeria	7.83	6.83	NA	LR	PASS	NA	Admixed	0.52	0.48	TRUE
TVu-7882	Nigeria	7.83	6.83	NA	LR	PASS	NA	Admixed	0.51	0.49	TRUE
TVu-7890	Nigeria	8	6.67	NA	LR	PASS	NA	Admixed	0.52	0.48	TRUE
TVu-7905	Nigeria	8.83	7.83	336	LR	PASS	NA	Admixed	0.52	0.48	TRUE
TVu-7907	Nigeria	8.83	7.83	336	LR	PASS	NA	Admixed	0.53	0.47	TRUE
TVu-7941	Nigeria	9.50	6	281	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7966	Mali	11.42	-7.47	332	LR	PASS	NA	Admixed	0.38	0.62	TRUE
TVu-7967	Mali	11.25	-5.82	375	LR	PASS	NA	Admixed	0.37	0.63	TRUE
TVu-7970	Cote d'Ivoire	9.22	-3.07	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7971	Cote d'Ivoire	7.78	-3.17	NA	LR	PASS	NA	Admixed	0.39	0.61	TRUE
TVu-7987	Cote d'Ivoire	9.60	-5.20	334	LR	PASS	NA	Admixed	0.39	0.61	TRUE
TVu-7991	Nigeria	10.25	4.75	285	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-7999	Ghana	8	-2	NA	LR	PASS	NA	Admixed	0.44	0.56	TRUE
TVu-8010	Nigeria	9.30	6	252	LR	FILTER	TVu-3857	NA	NA	NA	FALSE
TVu-8016	Nigeria	9.28	5.05	127	LR	PASS	NA	Admixed	0.39	0.61	TRUE
TVu-8032	Liberia	6.87	-9.80	312	LR	PASS	NA	Admixed	0.57	0.43	TRUE

TVu-8033	Liberia	6.98	-9.58	286	LR	PASS	NA	Admixed	0.38	0.62	TRUE
TVu-8056	Nigeria	7.48	9.35	252	LR	PASS	NA	Clus. 2	0.15	0.85	TRUE
TVu-8059	Cote d'Ivoire	9.07	-5.17	NA	LR	PASS	NA	Admixed	0.39	0.61	TRUE
TVu-8072	Papua New Guinea	NA	NA	NA	LR	PASS	NA	Admixed	0.58	0.42	TRUE
TVu-8073	Cote d'Ivoire	9.60	-5.20	334	LR	FILTER	TVu-13382	NA	NA	NA	FALSE
TVu-8076	Cote d'Ivoire	6.08	-3.85	252	LR	PASS	NA	Clus. 2	0.02	0.98	TRUE
TVu-8079	Cote d'Ivoire	7.07	-3.97	252	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8082	Cote d'Ivoire	8.03	-2.80	350	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8104	Nigeria	9.12	9.38	1,370	LR	PASS	NA	Clus. 2	0.09	0.91	TRUE
TVu-8108	Nigeria	7.20	9.50	252	NA	PASS	NA	Clus. 2	0.06	0.94	TRUE
TVu-8112	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8121	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8123	Nigeria	10.80	4.77	285	LR	FILTER	TVu-14963, TVu-14978, TVu-15589, TVu-2887, TVu-7317, TVu-8456	NA	NA	NA	FALSE
TVu-8131	Ghana	7.42	-1.42	231	LR	PASS	NA	Admixed	0.47	0.53	TRUE
TVu-8143	Ghana	9.07	-1.83	252	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8157	Ghana	6.57	0.48	252	LR	PASS	NA	Admixed	0.63	0.37	TRUE
TVu-8165	Nigeria	7.20	9.67	144	LR	PASS	NA	Clus. 2	0.05	0.95	TRUE
TVu-8182	Nigeria	7.17	5.33	68	LR	PASS	NA	Admixed	0.53	0.47	TRUE
TVu-8189	Nigeria	8.88	11.33	NA	LR	PASS	NA	Clus. 2	0.04	0.96	TRUE
TVu-8191	Nigeria	8.42	12.13	568	LR	PASS	NA	Clus. 2	0.03	0.97	TRUE
TVu-8215	Nigeria	10.47	13.27	575	LR	PASS	NA	Clus. 2	0.02	0.98	TRUE
TVu-8216	Nigeria	9.83	13.22	575	LR	PASS	NA	Clus. 2	0.06	0.94	TRUE
TVu-8222	Nigeria	10.25	13.03	575	LR	PASS	NA	Clus. 2	0.10	0.90	TRUE
TVu-8228	Nigeria	10.22	12.92	575	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8231	Nigeria	9.03	11.60	350	LR	PASS	NA	Clus. 2	0.11	0.89	TRUE

TVu-8236	Mali	12.67	-8.02	349	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8237	Mali	12.67	-8.02	349	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8244	Mali	13.73	-8.02	508	LR	PASS	NA	Clus. 2	0.05	0.95	TRUE
TVu-8254	Cote d'Ivoire	6.67	-4.22	360	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8259	Burkina Faso	11.08	-2.92	243	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8261	Burkina Faso	11.25	-4.12	302	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8262	Burkina Faso	11.25	-4.12	322	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8274	Burkina Faso	11.72	-4.50	337	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8285	Burkina Faso	11.88	-4.33	317	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8286	Burkina Faso	11.88	-4.33	317	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8291	Burkina Faso	12.08	-4.18	262	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8296	Burkina Faso	11	-5	578	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8306	Burkina Faso	10.57	-5.42	387	LR	PASS	NA	Admixed	0.39	0.61	TRUE
TVu-8308	Burkina Faso	10.63	-5.12	387	LR	PASS	NA	Admixed	0.41	0.59	TRUE
TVu-8309	Burkina Faso	10.63	-5.12	387	LR	PASS	NA	Admixed	0.39	0.61	TRUE
TVu-8310	Burkina Faso	10.63	-5.12	387	LR	PASS	NA	Admixed	0.39	0.61	TRUE
TVu-8313	Burkina Faso	10.83	-4.58	456	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8315	Burkina Faso	11.05	-4.33	299	LR	PASS	NA	Clus. 2	0.02	0.98	TRUE
TVu-8318	Burkina Faso	11.05	-4.33	299	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8330	Tanzania	-6.20	37.17	1,125	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-8331	Tanzania	-6.20	37.17	1,125	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-8332	Tanzania	-5.63	34.80	1,122	LR	PASS	NA	Clus. 1	0.83	0.17	TRUE
TVu-8337	Tanzania	-2.70	33.02	1,193	LR	PASS	NA	Admixed	0.37	0.63	TRUE
TVu-8346	Tanzania	-4.08	37.73	1,020	LR	PASS	NA	Clus. 1	0.98	0.02	TRUE
TVu-8356	Tanzania	-7.68	35.98	1,625	LR	PASS	NA	Clus. 1	0.97	0.03	TRUE
TVu-8357	Tanzania	-8.85	34.83	1,754	LR	PASS	NA	Clus. 1	0.88	0.12	TRUE
TVu-8358	Tanzania	-8.85	34.83	1,754	LR	PASS	NA	Clus. 1	0.91	0.09	TRUE
TVu-8383	United States of America	NA	NA	NA	BRM	FILTER	NA	NA	NA	NA	FALSE
TVu-8389	Papua New Guinea	NA	NA	NA	LR	PASS	NA	Admixed	0.63	0.37	TRUE
TVu-8407	Zambia	NA	NA	NA	LR	PASS	NA	Admixed	0.39	0.61	TRUE
TVu-8408	Niger	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8416	Cameroon	5.97	10.17	1,266	LR	PASS	NA	Clus. 2	0.12	0.88	TRUE

TVu-8422	Mali	14.53	-4.12	272	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8441	Nigeria	11.17	7.63	764	BRM	PASS	NA	Admixed	0.49	0.51	TRUE
TVu-8453	Kenya	NA	NA	NA	LR	FILTER	TVu-1207, TVu-1330, TVu-4642	NA	NA	NA	FALSE
TVu-8454	Kenya	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-8455	Kenya	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-8456	Niger	NA	NA	NA	LR	FILTER	TVu-14963, TVu-14978, TVu-15589, TVu-2887, TVu-7317, TVu-8123	NA	NA	NA	FALSE
TVu-8464	Portugal	NA	NA	NA	LR	PASS	NA	Clus. 1	0.78	0.22	TRUE
TVu-8470	Ghana	10.53	-0.82	252	LR	PASS	NA	Admixed	0.46	0.54	TRUE
TVu-8472	Ghana	6.68	-1.67	579	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8482	Tanzania	-4.58	33.17	372	LR	PASS	NA	Clus. 1	0.89	0.11	TRUE
TVu-8483	Tanzania	-5.18	38.80	NA	LR	PASS	NA	Clus. 1	0.87	0.13	TRUE
TVu-8490	Tanzania	-9.33	34.77	1,625	LR	FILTER	NA	NA	NA	NA	FALSE
TVu-8492	Tanzania	-9.33	34.77	1,625	LR	PASS	NA	Clus. 1	0.88	0.12	TRUE
TVu-8500	Burkina Faso	11.30	-4.37	288	LR	PASS	NA	Admixed	0.39	0.61	TRUE
TVu-8504	Burkina Faso	11.72	-4.50	378	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8512	Burkina Faso	11.42	-4.92	363	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8516	Burkina Faso	10.95	-4.47	508	LR	FILTER	NA	NA	NA	NA	FALSE
TVu-8518	Burkina Faso	10.83	-4.58	299	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8523	Burkina Faso	10.17	-2.95	329	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8574	Nigeria	8.33	4.50	221	LR	PASS	NA	Admixed	0.52	0.48	TRUE
TVu-8579	Nigeria	8.33	4.25	310	LR	PASS	NA	Admixed	0.52	0.48	TRUE
TVu-8600	Togo	6.67	1.27	74	LR	PASS	NA	Admixed	0.54	0.46	TRUE
TVu-8604	Togo	6.92	1.18	102	LR	PASS	NA	Admixed	0.44	0.56	TRUE
TVu-8608	Togo	6.25	NA	70	LR	PASS	NA	Admixed	0.48	0.52	TRUE

TVu-8612	Togo	6.25	1.03	70	LR	PASS	NA	Admixed	0.53	0.47	TRUE
TVu-8619	Togo	6.62	0.88	225	LR	PASS	NA	Admixed	0.55	0.45	TRUE
TVu-8620	Togo	6.62	0.88	225	LR	PASS	NA	Admixed	0.58	0.42	TRUE
TVu-8621	Togo	6.62	0.88	225	LR	PASS	NA	Admixed	0.58	0.42	TRUE
TVu-8622	Togo	6.75	0.87	225	LR	PASS	NA	Admixed	0.51	0.49	TRUE
TVu-8625	Togo	6.47	1.27	74	LR	PASS	NA	Admixed	0.68	0.32	TRUE
TVu-8626	Togo	6.47	1.27	33	LR	PASS	NA	Admixed	0.53	0.47	TRUE
TVu-8628	Togo	6.52	1.32	74	LR	PASS	NA	Admixed	0.42	0.58	TRUE
TVu-8631	Togo	6.58	1.52	33	LR	PASS	NA	Admixed	0.47	0.53	TRUE
TVu-8639	Togo	6.33	1.62	63	LR	FILTER	TVu-10990	NA	NA	NA	FALSE
TVu-8641	Togo	6.33	1.53	65	LR	PASS	NA	Admixed	0.57	0.43	TRUE
TVu-8647	Togo	6.25	1.53	75	LR	PASS	TVu-8683	Admixed	0.45	0.55	TRUE
TVu-8649	Togo	6.17	1.35	6	LR	PASS	NA	Admixed	0.46	0.54	TRUE
TVu-8651	Togo	6.17	1.35	6	LR	PASS	NA	Admixed	0.44	0.56	TRUE
TVu-8656	Benin	6.42	2.37	252	LR	PASS	NA	Admixed	0.57	0.43	TRUE
TVu-8666	Benin	6.70	2.12	87	LR	PASS	NA	Clus. 1	0.78	0.22	TRUE
TVu-8667	Benin	6.70	2.12	87	LR	PASS	NA	Clus. 1	0.95	0.05	TRUE
TVu-8671	Benin	6.70	2.12	87	LR	PASS	NA	Admixed	0.40	0.60	TRUE
TVu-8673	Benin	6.70	2.12	87	LR	PASS	NA	Clus. 1	0.97	0.03	TRUE
TVu-8683	Benin	6.80	2.17	253	LR	FILTER	TVu-8647	NA	NA	NA	FALSE
TVu-8702	Benin	6.47	2.63	39	LR	PASS	NA	Admixed	0.51	0.49	TRUE
TVu-8712	Benin	6.88	2.55	44	LR	PASS	NA	Clus. 2	0.01	0.99	TRUE
TVu-8713	Benin	6.80	2.50	6	LR	PASS	NA	Admixed	0.41	0.59	TRUE
TVu-8719	Benin	6.80	2.50	6	LR	PASS	NA	Admixed	0.43	0.57	TRUE
TVu-8725	Benin	7.17	2	228	LR	PASS	NA	Clus. 2	0.06	0.94	TRUE
TVu-8733	Benin	7.17	2	228	LR	PASS	NA	Admixed	0.49	0.51	TRUE
TVu-8736	Benin	7.27	2.05	NA	LR	PASS	NA	Admixed	0.38	0.62	TRUE
TVu-8742	Benin	6.35	2.43	9	LR	FILTER	TVu-10303, TVu-8783, TVu-8786	NA	NA	NA	FALSE
TVu-8745	Benin	6.35	2.43	9	LR	PASS	NA	Admixed	0.51	0.49	TRUE
TVu-8751	Benin	6.35	2.43	9	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-8758	Benin	6.35	2.43	9	LR	PASS	NA	Admixed	0.52	0.48	TRUE

TVu-8763	Benin	6.35	2.43	9	LR	PASS	NA	Admixed	0.42	0.58	TRUE
TVu-8767	Kenya	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-8769	Tanzania	NA	NA	NA	LR	PASS	NA	Clus. 1	0.97	0.03	TRUE
TVu-8775	NA	NA	NA	NA	LR	PASS	NA	Admixed	0.70	0.30	TRUE
TVu-8777	Tanzania	NA	NA	NA	LR	PASS	NA	Clus. 1	0.94	0.06	TRUE
TVu-8778	Tanzania	NA	NA	NA	LR	PASS	NA	Clus. 1	0.82	0.18	TRUE
TVu-8779	Benin	8	2.37	252	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8781	Benin	8.08	2.55	393	LR	FILTER	TVu-10952	NA	NA	NA	FALSE
TVu-8783	Benin	8.40	2.60	393	LR	PASS	TVu-10303, TVu-8742, TVu-8786	Clus. 1	1	0	TRUE
TVu-8786	Benin	8.75	2.60	393	LR	FILTER	TVu-10303, TVu-8742, TVu-8783	NA	NA	NA	FALSE
TVu-8788	Benin	9.23	2.57	393	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8790	Benin	9.23	2.57	393	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8800	Benin	9.83	2.85	508	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8805	Benin	9.90	2.95	508	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8806	Benin	9.92	3.05	508	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8810	Benin	10.08	2.47	351	LR	PASS	TVu-8817	Clus. 2	0	1	TRUE
TVu-8811	Benin	10.12	2.40	351	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8812	Benin	10.28	2.40	351	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8817	Benin	10.30	2.70	508	LR	FILTER	TVu-8810	NA	NA	NA	FALSE
TVu-8823	Benin	11.13	2.93	292	Wild	PASS	NA	Clus. 2	0.29	0.71	TRUE
TVu-8828	Benin	11.32	3.05	292	LR	FILTER	TVu-3923	NA	NA	NA	FALSE
TVu-8832	Benin	11.30	2.32	508	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8834	Benin	11.20	2.30	508	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8838	Benin	11.17	2.28	302	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8844	Benin	10.38	1.35	461	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8846	Benin	10.27	1.30	461	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8847	Benin	10.27	1.30	461	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8850	Benin	9.83	1.55	508	LR	PASS	NA	Admixed	0.43	0.57	TRUE

TVu-8851	Benin	9.73	1.42	508	LR	PASS	NA	Clus. 2	0.01	0.99	TRUE
TVu-8860	Benin	8.13	1.97	309	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8867	Benin	6.40	1.88	63	LR	PASS	NA	Admixed	0.54	0.46	TRUE
TVu-8877	Benin	6.97	1.83	NA	LR	PASS	NA	Admixed	0.40	0.60	TRUE
TVu-8883	Benin	6.95	1.67	252	LR	PASS	NA	Admixed	0.53	0.47	TRUE
TVu-8888	Benin	7.93	2.07	252	LR	PASS	TVu-8923	Clus. 2	0	1	TRUE
TVu-8889	Benin	7.93	2.07	252	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8892	Benin	7.22	2.33	167	LR	PASS	NA	Admixed	0.50	0.50	TRUE
TVu-8894	Benin	7.22	2.33	167	LR	PASS	NA	Clus. 2	0.11	0.89	TRUE
TVu-8910	Nigeria	8.43	12.07	568	LR	PASS	NA	Clus. 2	0.15	0.85	TRUE
TVu-8916	Nigeria	8.43	12.07	568	LR	PASS	NA	Clus. 2	0.14	0.86	TRUE
TVu-8919	Nigeria	8.43	12.07	568	LR	PASS	NA	Clus. 2	0.14	0.86	TRUE
TVu-8923	Nigeria	8.93	12.10	300	LR	FILTER	TVu-8888	NA	NA	NA	FALSE
TVu-8930	Nigeria	8.85	11.40	350	LR	PASS	NA	Clus. 2	0.11	0.89	TRUE
TVu-8934	Nigeria	8.88	11.33	350	LR	PASS	NA	Clus. 2	0.12	0.88	TRUE
TVu-8945	Nigeria	8.88	11.33	350	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-8973	Nigeria	10.30	13.17	575	LR	PASS	NA	Clus. 2	0.11	0.89	TRUE
TVu-8988	Nigeria	9.93	13.23	575	LR	PASS	NA	Clus. 2	0.28	0.72	TRUE
TVu-8989	Nigeria	9.93	13.23	575	LR	PASS	NA	Clus. 2	0.10	0.90	TRUE
TVu-8990	Nigeria	9.83	13.22	575	LR	PASS	NA	Clus. 2	0.12	0.88	TRUE
TVu-8998	Nigeria	10.37	13.18	565	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-9018	Nigeria	8.42	12.13	568	Wild	PASS	NA	Clus. 2	0.13	0.87	TRUE
TVu-9026	Nigeria	8.88	11.33	350	LR	PASS	NA	Clus. 2	0.17	0.83	TRUE
TVu-9031	Nigeria	8.97	11.90	350	LR	PASS	NA	Clus. 2	0.14	0.86	TRUE
TVu-9049	Cameroon	5.48	10.43	1,438	LR	FILTER	NA	NA	NA	NA	FALSE
TVu-9051	Cameroon	5.48	10.50	1,438	LR	PASS	NA	Admixed	0.50	0.50	TRUE
TVu-9056	Cameroon	5.48	10.43	1,438	LR	PASS	NA	Clus. 1	0.93	0.07	TRUE
TVu-9057	Cameroon	5.48	10.43	1,438	LR	PASS	NA	Admixed	0.66	0.34	TRUE
TVu-9058	Brazil	NA	NA	NA	LR	PASS	NA	Clus. 1	0.95	0.05	TRUE
TVu-9060	Brazil	NA	NA	NA	LR	PASS	NA	Clus. 1	0.89	0.11	TRUE
TVu-9073	India	NA	NA	NA	LR	PASS	NA	Admixed	0.59	0.41	TRUE
TVu-9080	India	NA	NA	NA	LR	PASS	NA	Admixed	0.44	0.56	TRUE
TVu-9095	India	NA	NA	NA	LR	PASS	NA	Admixed	0.46	0.54	TRUE

TVu-9102	Nigeria	6.83	3	68	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-9110	Nigeria	6.92	3.83	64	LR	PASS	NA	Admixed	0.50	0.50	TRUE
TVu-9114	Nigeria	6.83	3	68	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-9131	Nigeria	6.92	2.92	9	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-9135	Nigeria	6.67	3	63	LR	FILTER	NA	NA	NA	NA	FALSE
TVu-9136	Nigeria	7.75	2.75	252	LR	PASS	TVu-10283, TVu-10634	Clus. 2	0	1	TRUE
TVu-9153	Nigeria	8.58	3.42	508	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-9156	Nigeria	7.75	4.42	252	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-9161	Nigeria	7.50	4.58	286	BRM	PASS	NA	Admixed	0.45	0.55	TRUE
TVu-9201	Nigeria	7.67	5.42	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-9226	Tanzania	-5.18	38.80	261	NA	PASS	NA	Clus. 1	1	0	TRUE
TVu-9228	Tanzania	-5.18	38.80	261	LR	PASS	NA	Clus. 1	0.86	0.14	TRUE
TVu-9232	Tanzania	-5.18	38.80	261	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-9233	Tanzania	-7.68	35.98	1,625	LR	PASS	NA	Clus. 1	0.89	0.11	TRUE
TVu-9234	Tanzania	-7.68	35.98	1,625	LR	PASS	NA	Clus. 1	0.88	0.12	TRUE
TVu-9237	Tanzania	-7.68	35.98	1,625	LR	FILTER	TVu-10927	NA	NA	NA	FALSE
TVu-9238	Tanzania	-7.68	35.98	1,625	LR	PASS	NA	Clus. 1	0.87	0.13	TRUE
TVu-9249	Ghana	6.57	0.48	248	LR	PASS	NA	Admixed	0.48	0.52	TRUE
TVu-9252	Burkina Faso	11.17	-4.28	322	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-9256	Burkina Faso	11.53	-4	302	LR	PASS	NA	Admixed	0.39	0.61	TRUE
TVu-9257	Burkina Faso	11.72	-4.50	381	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-9259	Burkina Faso	11.72	-4.50	381	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-9262	Burkina Faso	11.72	-4.50	381	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-9265	Burkina Faso	10.67	-4.80	350	LR	PASS	NA	Admixed	0.38	0.62	TRUE
TVu-9285	Nigeria	6.83	5.83	252	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-9321	Nigeria	5.42	5.83	25	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-9342	Mali	14.47	-3.30	508	LR	PASS	NA	Clus. 2	0.01	0.99	TRUE
TVu-9343	Mali	14.47	-3.30	508	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-9352	Mali	14.17	-7.60	338	LR	FILTER	TVu-7755	NA	NA	NA	FALSE
TVu-9357	Cote d'Ivoire	7.70	-5.03	376	LR	FILTER	TVu-7739	NA	NA	NA	FALSE
TVu-9362	Nigeria	9.08	9.17	259	LR	PASS	NA	Clus. 2	0.28	0.72	TRUE
TVu-9364	Nigeria	7.20	9.50	252	LR	PASS	NA	Clus. 2	0	1	TRUE

TVu-9367	India	12.62	77.93	1,929	LR	PASS	NA	Clus. 2	0.28	0.72	TRUE
TVu-9391	India	23.40	69.07	17	LR	PASS	NA	Clus. 2	0.19	0.81	TRUE
TVu-9393	India	23	72.58	4	LR	PASS	TVu-1744, TVu-3625	Admixed	0.36	0.64	TRUE
TVu-9411	India	20	77	252	LR	PASS	NA	Clus. 2	0.26	0.74	TRUE
TVu-9430	India	16.99	74.13	742	LR	PASS	NA	Admixed	0.33	0.67	TRUE
TVu-9443	Egypt	30.77	31.83	29	LR	PASS	NA	Clus. 2	0.16	0.84	TRUE
TVu-9446	Egypt	30.77	31.83	29	LR	PASS	NA	Clus. 2	0.19	0.81	TRUE
TVu-9457	Egypt	31	31.42	12	LR	PASS	TVu-9463	Clus. 2	0.16	0.84	TRUE
TVu-9461	Egypt	31	31.42	12	LR	PASS	NA	Clus. 2	0.16	0.84	TRUE
TVu-9463	Egypt	31	31.42	12	LR	FILTER	TVu-9457	NA	NA	NA	FALSE
TVu-9468	Egypt	31	31.42	12	LR	PASS	NA	Clus. 2	0.24	0.76	TRUE
TVu-9469	Egypt	31	31.42	12	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-9474	Egypt	31	31.42	12	LR	PASS	NA	Clus. 2	0.23	0.77	TRUE
TVu-9477	Egypt	31	31.42	12	LR	PASS	NA	Clus. 2	0.21	0.79	TRUE
TVu-9480	Egypt	31	31.42	12	LR	PASS	NA	Clus. 2	0.19	0.81	TRUE
TVu-9483	Egypt	31	31.42	12	LR	PASS	NA	Clus. 2	0.19	0.81	TRUE
TVu-9486	Egypt	31	31.42	12	LR	PASS	NA	Clus. 2	0.18	0.82	TRUE
TVu-9487	Egypt	31	31.42	12	LR	PASS	NA	Clus. 2	0.25	0.75	TRUE
TVu-9492	Egypt	31	31.42	12	LR	PASS	NA	Clus. 2	0.19	0.81	TRUE
TVu-9497	Egypt	31.35	31.50	5	LR	PASS	NA	Clus. 2	0.21	0.79	TRUE
TVu-9498	Egypt	31.35	31.50	5	LR	FILTER	TVu-9499, TVu-9506, TVu-9606, TVu-9650, TVu-9676	NA	NA	NA	FALSE
TVu-9499	Egypt	31.35	31.50	5	LR	FILTER	TVu-9498, TVu-9506, TVu-9606, TVu-9650, TVu-9676	NA	NA	NA	FALSE
TVu-9504	Egypt	31.35	31.50	5	LR	PASS	NA	Clus. 2	0.18	0.82	TRUE
TVu-9505	Egypt	31.35	31.50	5	LR	PASS	TVu-9753	Clus. 2	0.23	0.77	TRUE

TVu-9506	Egypt	31.35	31.50	5	LR	PASS	TVu-9498, TVu-9499, TVu-9606, TVu-9650, TVu-9676	Clus. 2	0.16	0.84	TRUE
TVu-9508	Egypt	31.35	31.50	5	LR	PASS	NA	Clus. 2	0.18	0.82	TRUE
TVu-9510	Egypt	31.37	31.97	16	LR	PASS	NA	Clus. 2	0.19	0.81	TRUE
TVu-9514	Egypt	31.37	31.97	16	LR	PASS	TVu-9522	Clus. 2	0.28	0.72	TRUE
TVu-9516	Egypt	31.37	31.97	16	LR	PASS	NA	Admixed	0.43	0.57	TRUE
TVu-9522	Egypt	31.37	31.97	16	LR	FILTER	TVu-9514	NA	NA	NA	FALSE
TVu-9544	Egypt	30.53	31.37	21	LR	PASS	NA	Clus. 2	0.13	0.87	TRUE
TVu-9553	Egypt	30.60	31.52	15	LR	PASS	NA	Clus. 2	0.18	0.82	TRUE
TVu-9554	Egypt	30.60	31.52	15	LR	PASS	NA	Clus. 2	0.18	0.82	TRUE
TVu-9556	Egypt	30.60	31.52	15	LR	PASS	NA	Clus. 2	0.18	0.82	TRUE
TVu-9557	Egypt	30.60	31.52	15	LR	PASS	NA	Clus. 2	0.18	0.82	TRUE
TVu-9576	Egypt	30.78	31	18	LR	PASS	TVu-9579	Clus. 2	0.22	0.78	TRUE
TVu-9579	Egypt	30.78	31	18	LR	FILTER	TVu-9576	NA	NA	NA	FALSE
TVu-9587	Egypt	30.78	31	18	LR	PASS	NA	Clus. 2	0.16	0.84	TRUE
TVu-9596	Egypt	30.78	31	18	LR	PASS	NA	Clus. 2	0.17	0.83	TRUE
TVu-9600	Egypt	30.78	31	18	LR	PASS	NA	Clus. 2	0.15	0.85	TRUE
TVu-9604	Egypt	30.80	30.98	13	LR	PASS	NA	Clus. 2	0.19	0.81	TRUE
TVu-9606	Egypt	30.85	30.87	14	LR	FILTER	TVu-9498, TVu-9499, TVu-9506, TVu-9650, TVu-9676	NA	NA	NA	FALSE
TVu-9609	Egypt	30.85	30.87	14	LR	PASS	NA	Clus. 2	0.17	0.83	TRUE
TVu-9615	Egypt	30.85	30.87	14	LR	PASS	NA	Clus. 2	0.16	0.84	TRUE
TVu-9620	Egypt	30.85	30.87	14	LR	PASS	NA	Clus. 2	0.18	0.82	TRUE
TVu-9621	Egypt	30.85	30.87	14	LR	PASS	NA	Clus. 2	0.17	0.83	TRUE
TVu-9634	Egypt	30.97	30.97	18	LR	PASS	NA	Clus. 2	0.13	0.87	TRUE
TVu-9637	Egypt	30.97	30.97	18	LR	PASS	NA	Clus. 2	0.20	0.80	TRUE
TVu-9640	Egypt	31.01	30.93	15	LR	PASS	NA	Clus. 2	0.18	0.82	TRUE
TVu-9648	Egypt	31.01	30.93	15	LR	PASS	NA	Clus. 2	0.18	0.82	TRUE

TVu-9650	Egypt	31.01	30.93	15	LR	FILTER	TVu-9498, TVu-9499, TVu-9506, TVu-9606, TVu-9676	NA	NA	NA	FALSE
TVu-9651	Egypt	31.01	30.93	15	LR	PASS	NA	Clus. 2	0.18	0.82	TRUE
TVu-9663	Egypt	31.01	30.93	15	LR	PASS	NA	Clus. 2	0.16	0.84	TRUE
TVu-9666	Egypt	31.01	30.93	15	LR	PASS	NA	Clus. 2	0.15	0.85	TRUE
TVu-9671	Egypt	31.01	30.93	15	LR	PASS	NA	Clus. 2	0.15	0.85	TRUE
TVu-9672	Egypt	31.01	30.93	15	LR	PASS	NA	Clus. 2	0.19	0.81	TRUE
TVu-9676	Egypt	31.20	31.01	15	LR	FILTER	TVu-9498, TVu-9499, TVu-9506, TVu-9606, TVu-9650	NA	NA	NA	FALSE
TVu-9684	Egypt	31.20	31.01	15	LR	PASS	NA	Clus. 2	0.17	0.83	TRUE
TVu-9701	Egypt	31.20	30.40	21	LR	PASS	NA	Clus. 2	0.16	0.84	TRUE
TVu-9716	Egypt	31	30.47	18	LR	PASS	NA	Clus. 2	0.18	0.82	TRUE
TVu-9724	Egypt	31.01	30.32	15	LR	PASS	NA	Clus. 2	0.21	0.79	TRUE
TVu-9725	Egypt	31.01	30.32	15	LR	PASS	NA	Clus. 2	0.17	0.83	TRUE
TVu-9732	Egypt	31.01	30.32	15	LR	PASS	NA	Admixed	0.57	0.43	TRUE
TVu-9739	Egypt	31.01	30.32	15	LR	PASS	NA	Clus. 2	0.16	0.84	TRUE
TVu-9749	Egypt	29.30	30.98	29	LR	PASS	NA	Clus. 2	0.16	0.84	TRUE
TVu-9751	Egypt	29.30	30.98	29	LR	PASS	NA	Clus. 2	0.20	0.80	TRUE
TVu-9753	Egypt	29.30	30.98	29	LR	FILTER	TVu-9505	NA	NA	NA	FALSE
TVu-9755	Egypt	29.30	30.98	29	LR	PASS	NA	Clus. 2	0.21	0.79	TRUE
TVu-9756	Egypt	29.30	30.98	29	LR	PASS	NA	Clus. 2	0.18	0.82	TRUE
TVu-9761	Egypt	30	31.20	21	LR	PASS	NA	Clus. 2	0.16	0.84	TRUE
TVu-9765	Egypt	30	31.20	21	LR	PASS	NA	Clus. 2	0.17	0.83	TRUE
TVu-9775	Nigeria	NA	NA	NA	BRM	PASS	NA	Admixed	0.67	0.33	TRUE
TVu-9782	Nigeria	NA	NA	NA	BRM	PASS	NA	Admixed	0.45	0.55	TRUE
TVu-9789	Nigeria	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.92	0.08	TRUE
TVu-9792	Malawi	-16.54	35.01	78	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-9801	Malawi	-16.58	35.12	100	LR	PASS	TVu-9811	Clus. 1	1	0	TRUE

TVu-9811	Malawi	-16.50	35.21	58	LR	FILTER	TVu-9801	NA	NA	NA	FALSE
TVu-9814	Malawi	-16.50	35.21	58	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-9817	Malawi	-12.08	34.06	508	LR	PASS	TVu-9848	Clus. 1	1	0	TRUE
TVu-9820	Malawi	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-9835	Malawi	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-9836	Malawi	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-9842	Malawi	-15.81	35.65	781	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-9843	Malawi	-15.81	35.65	781	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-9848	Malawi	-13.50	34	1,276	LR	FILTER	TVu-9817	NA	NA	NA	FALSE
TVu-9851	Malawi	-13.50	34	1,276	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-9862	Malawi	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-9865	Malawi	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-9866	Malawi	-15.65	35.02	734	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-9868	Malawi	-15.65	35.02	734	LR	FILTER	TVu-15118, TVu-15433, TVu-15571, TVu-9869	NA	NA	NA	FALSE
TVu-9869	Malawi	-15.65	35.02	734	LR	FILTER	TVu-15118, TVu-15433, TVu-15571, TVu-9868	NA	NA	NA	FALSE
TVu-9901	Malawi	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-9909	Malawi	13.58	33.17	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-9913	Malawi	13.58	33.17	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-9914	Malawi	13.58	33.17	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-9917	Malawi	-15.81	35.65	781	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-9929	Malawi	-15.92	35.05	1,109	LR	PASS	NA	Clus. 1	1	0	TRUE

TVu-9930	Malawi	-15.92	35.05	1,109	LR	FILTER	TVu-13468, TVu-15107, TVu-15117, TVu-15131, TVu-15360, TVu-15445, TVu-15490	NA	NA	NA	FALSE
TVu-9934	Malawi	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-9944	Malawi	-13.28	33.53	1,049	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-9952	Cote d'Ivoire	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-9956	Burkina Faso	NA	NA	NA	BRM	PASS	TVu-11610, TVu-14845	Clus. 2	0	1	TRUE
TVu-9976	Burkina Faso	NA	NA	NA	BRM	FILTER	TVu-15323	NA	NA	NA	FALSE
TVu-9977	Burkina Faso	NA	NA	NA	BRM	PASS	NA	Clus. 2	0	1	TRUE
TVu-10004	Nigeria	9.12	6.28	252	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-10005	Nigeria	9.12	6.28	252	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-10030	Nigeria	9.08	5.78	111	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-10032	Nigeria	8.85	6.52	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-10033	Nigeria	9.17	6.52	272	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-10037	Nigeria	9.17	6.52	272	LR	PASS	NA	Admixed	0.52	0.48	TRUE
TVu-10056	Nigeria	8.92	5.83	111	LR	PASS	TVu-6775	Clus. 2	0	1	TRUE
TVu-10065	Nigeria	9.05	5.85	111	LR	FILTER	TVu-4924, TVu-4946, TVu-4976, TVu-4984, TVu-5020, TVu-5029, TVu-5031,	NA	NA	NA	FALSE

							TVu-5035, TVu-5040, TVu-5052, TVu-5055, TVu-5057, TVu-5247, TVu-5314				
TVu-10068	Nigeria	9.05	5.85	111	LR	PASS	NA	Admixed	0.45	0.55	TRUE
TVu-10073	Nigeria	9.58	6.07	111	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-10086	Nigeria	9.35	5.82	111	LR	FILTER	NA	NA	NA	NA	FALSE
TVu-10100	Colombia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.90	0.10	TRUE
TVu-10107	Turkey	NA	NA	NA	LR	PASS	NA	Clus. 1	0.84	0.16	TRUE
TVu-10110	Paraguay	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-10111	Nigeria	NA	NA	NA	LR	FILTER	TVu-1412, TVu-1536, TVu-1549, TVu-1707, TVu-2300	NA	NA	NA	FALSE
TVu-10132	United States of America	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-10153	India	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-10173	India	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-10178	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.80	0.20	TRUE
TVu-10179	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.87	0.13	TRUE
TVu-10199	Australia	NA	NA	NA	LR	FILTER	TVu-14524, TVu-14525, TVu-14568	NA	NA	NA	FALSE
TVu-10201	Australia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.99	0.01	TRUE
TVu-10204	Brazil	NA	NA	NA	LR	PASS	TVu-14117	Clus. 1	0.99	0.01	TRUE
TVu-10205	Nepal	NA	NA	NA	LR	PASS	NA	Clus. 1	0.71	0.29	TRUE
TVu-10206	Nepal	NA	NA	NA	LR	FILTER	TVu-109, TVu-	NA	NA	NA	FALSE

							14891, TVu-16343, TVu-16408, TVu-18, TVu-1975, TVu-1996, TVu-1999, TVu-36, TVu-374, TVu-745				
TVu-10255	India	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-10281	Benin	10.38	1.35	450	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-10283	Nigeria	NA	NA	NA	LR	FILTER	TVu-10634, TVu-9136	NA	NA	NA	FALSE
TVu-10284	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 1	0.78	0.22	TRUE
TVu-10288	Nigeria	10.43	13.22	575	NA	PASS	NA	Clus. 2	0	1	TRUE
TVu-10300	Togo	6.47	1.27	NA	LR	PASS	NA	Admixed	0.55	0.45	TRUE
TVu-10303	Benin	6.42	2.37	228	LR	FILTER	TVu-8742, TVu-8783, TVu-8786	NA	NA	NA	FALSE
TVu-10305	Benin	6.42	2.37	228	LR	PASS	NA	Admixed	0.67	0.33	TRUE
TVu-10310	Nigeria	9.30	12.23	252	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-10311	Somalia	NA	NA	NA	LR	PASS	NA	Admixed	0.58	0.42	TRUE
TVu-10313	Somalia	NA	NA	NA	LR	PASS	NA	Admixed	0.60	0.40	TRUE
TVu-10322	India	NA	NA	NA	LR	PASS	NA	Admixed	0.44	0.56	TRUE
TVu-10343	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.90	0.10	TRUE
TVu-10351	Mali	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-10360	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 2	0.03	0.97	TRUE
TVu-10361	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 2	0.05	0.95	TRUE
TVu-10362	Mali	NA	NA	NA	LR	PASS	TVu-7609	Clus. 2	0	1	TRUE

TVu-10363	Papua New Guinea	NA	NA	NA	LR	PASS	NA	Admixed	0.53	0.47	TRUE
TVu-10365	Cote d'Ivoire	NA	NA	NA	LR	PASS	NA	Admixed	0.38	0.62	TRUE
TVu-10366	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.86	0.14	TRUE
TVu-10373	Niger	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-10383	Tanzania	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-10394	Portugal	NA	NA	NA	LR	PASS	NA	Clus. 1	0.84	0.16	TRUE
TVu-10396	Portugal	NA	NA	NA	LR	PASS	NA	Clus. 1	0.82	0.18	TRUE
TVu-10400	United States of America	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.82	0.18	TRUE
TVu-10404	Mali	12.67	-8.02	338	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-10407	Bangladesh	NA	NA	NA	LR	PASS	NA	Admixed	0.58	0.42	TRUE
TVu-10408	Nigeria	12.55	8.45	476	LR	PASS	NA	Admixed	0.40	0.60	TRUE
TVu-10409	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.75	0.25	TRUE
TVu-10435	Jamaica	NA	NA	NA	LR	FILTER	NA	NA	NA	NA	FALSE
TVu-10438	Nigeria	12.55	8.45	476	Weedy	PASS	NA	Clus. 2	0.29	0.71	TRUE
TVu-10440	Tanzania	-6.83	38.92	252	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-10442	Tanzania	-6.77	37.08	572	LR	PASS	TVu-1280	Clus. 1	1	0	TRUE
TVu-10454	Tanzania	-7.67	35.70	1,625	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-10456	Gambia	13.70	-15.17	20	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-10460	Sierra Leone	7.85	-11.97	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-10465	Burkina Faso	NA	NA	NA	LR	PASS	NA	Admixed	0.37	0.63	TRUE
TVu-10466	Burkina Faso	NA	NA	NA	LR	PASS	NA	Admixed	0.36	0.64	TRUE
TVu-10471	India	28.58	70.30	NA	LR	PASS	NA	Admixed	0.34	0.66	TRUE
TVu-10479	Niger	NA	NA	NA	BRM	PASS	NA	Admixed	0.46	0.54	TRUE
TVu-10513	Nigeria	7.48	3.75	252	BRM	PASS	NA	Clus. 1	0.70	0.30	TRUE
TVu-10545	Nigeria	13.29	5.42	280	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-10559	Nigeria	13.22	5.50	317	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-10634	Nigeria	7.53	10.57	NA	LR	FILTER	TVu-10283, TVu-9136	NA	NA	NA	FALSE
TVu-10687	Nigeria	11.07	7.70	671	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-10745	Sierra Leone	8.98	-13.15	13	LR	PASS	NA	Clus. 2	0.10	0.90	TRUE
TVu-10751	Sierra Leone	8.55	-13.17	NA	LR	PASS	NA	Admixed	0.40	0.60	TRUE

TVu-10754	Benin	6.37	2.48	7	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-10806	Tanzania	-3.65	33.40	1,276	LR	PASS	NA	Clus. 1	0.86	0.14	TRUE
TVu-10825	Cameroon	10.63	13.60	1,020	LR	PASS	NA	Clus. 2	0.08	0.92	TRUE
TVu-10829	Cameroon	10.52	13.58	1,085	LR	PASS	NA	Clus. 2	0.02	0.98	TRUE
TVu-10835	Cameroon	9.58	13.78	291	LR	PASS	NA	Clus. 2	0.13	0.87	TRUE
TVu-10875	Burkina Faso	10.63	-5.12	350	LR	PASS	NA	Clus. 2	0.29	0.71	TRUE
TVu-10892	India	15	75	698	LR	PASS	NA	Admixed	0.41	0.59	TRUE
TVu-10910	Malawi	-13.35	33.92	NA	LR	PASS	NA	Clus. 1	0.85	0.15	TRUE
TVu-10915	Burkina Faso	NA	NA	NA	LR	PASS	NA	Clus. 2	0.19	0.81	TRUE
TVu-10918	Burkina Faso	NA	NA	NA	LR	PASS	NA	Clus. 2	0.01	0.99	TRUE
TVu-10919	Burkina Faso	NA	NA	NA	LR	PASS	NA	Clus. 2	0.01	0.99	TRUE
TVu-10922	Tanzania	-2.67	32.67	1,276	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-10927	Tanzania	-7.68	35.98	1,625	LR	PASS	TVu-9237	Admixed	0.54	0.46	TRUE
TVu-10935	Benin	10.30	2.38	351	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-10942	Benin	9.82	1.73	508	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-10952	Nigeria	8.88	11.33	NA	LR	PASS	TVu-8781	Clus. 2	0	1	TRUE
TVu-10972	Nigeria	8.85	5.77	NA	LR	PASS	NA	Admixed	0.52	0.48	TRUE
TVu-10973	Nigeria	8.85	5.77	252	LR	PASS	NA	Clus. 2	0.03	0.97	TRUE
TVu-10990	Benin	6.88	2.55	44	LR	PASS	TVu-8639	Admixed	0.55	0.45	TRUE
TVu-10992	Benin	7.17	2	252	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-10993	Benin	7.17	2	252	LR	PASS	NA	Clus. 2	0.06	0.94	TRUE
TVu-11008	Cameroon	10.60	14.32	422	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-11009	Cameroon	11.03	14.15	358	LR	PASS	NA	Clus. 2	0.04	0.96	TRUE
TVu-11011	Cameroon	11.03	14.15	358	LR	PASS	NA	Clus. 2	0.02	0.98	TRUE
TVu-11013	Cameroon	11.03	14.15	358	LR	PASS	TVu-11014	Clus. 2	0.04	0.96	TRUE
TVu-11014	Cameroon	11.03	14.15	358	LR	FILTER	TVu-11013	NA	NA	NA	FALSE
TVu-11015	Cameroon	11.03	14.15	358	LR	PASS	NA	Clus. 2	0.04	0.96	TRUE
TVu-11017	Cameroon	10.95	14.15	422	LR	PASS	NA	Clus. 2	0.03	0.97	TRUE
TVu-11030	Cameroon	10.18	14.83	319	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-11040	Cameroon	10.10	14.45	377	LR	PASS	NA	Clus. 2	0.13	0.87	TRUE
TVu-11041	Cameroon	10.10	14.45	377	LR	PASS	NA	Clus. 2	0.08	0.92	TRUE
TVu-11045	Cameroon	10.60	14.33	422	LR	PASS	NA	Clus. 2	0.18	0.82	TRUE
TVu-11048	Cameroon	10.60	14.33	422	LR	PASS	NA	Clus. 2	0.05	0.95	TRUE

TVu-11061	Cameroon	10.73	14.22	422	LR	PASS	NA	Clus. 2	0.08	0.92	TRUE
TVu-11078	Cameroon	10.75	13.82	833	LR	PASS	NA	Clus. 2	0.13	0.87	TRUE
TVu-11082	Cameroon	10.75	13.82	833	LR	PASS	NA	Clus. 2	0.01	0.99	TRUE
TVu-11105	Cameroon	10.80	13.85	764	LR	PASS	NA	Clus. 2	0.15	0.85	TRUE
TVu-11123	Cameroon	10.87	13.88	508	LR	PASS	NA	Clus. 2	0.05	0.95	TRUE
TVu-11187	Cameroon	9.43	13.37	237	LR	PASS	NA	Clus. 2	0.10	0.90	TRUE
TVu-11188	Cameroon	9.43	13.37	237	LR	PASS	NA	Clus. 2	0.14	0.86	TRUE
TVu-11197	Cameroon	9.72	13.55	237	LR	PASS	NA	Clus. 2	0.15	0.85	TRUE
TVu-11213	Cameroon	9.43	13.37	237	LR	PASS	NA	Clus. 2	0.16	0.84	TRUE
TVu-11215	Cameroon	9.30	13.40	244	LR	PASS	NA	Clus. 2	0.13	0.87	TRUE
TVu-11294	Cameroon	9.72	13.55	1,085	LR	PASS	NA	Clus. 2	0.12	0.88	TRUE
TVu-11330	Cameroon	5.87	11.10	1,059	LR	PASS	NA	Admixed	0.57	0.43	TRUE
TVu-11382	Cameroon	4.85	9.78	1,195	LR	PASS	NA	Admixed	0.64	0.36	TRUE
TVu-11410	Gambia	13.43	-15.82	43	LR	PASS	NA	Clus. 2	0.02	0.98	TRUE
TVu-11411	Gambia	13.67	15.03	11	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-11460	Philippines	NA	NA	NA	LR	PASS	NA	Admixed	0.69	0.31	TRUE
TVu-11462	Philippines	NA	NA	NA	LR	PASS	NA	Admixed	0.62	0.38	TRUE
TVu-11480	Philippines	NA	NA	NA	LR	PASS	NA	Admixed	0.64	0.36	TRUE
TVu-11485	Philippines	NA	NA	NA	LR	FILTER	TVu-1	NA	NA	NA	FALSE
TVu-11488	Philippines	NA	NA	NA	LR	PASS	NA	Admixed	0.64	0.36	TRUE
TVu-11500	Philippines	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-11503	Philippines	NA	NA	NA	LR	PASS	NA	Admixed	0.69	0.31	TRUE
TVu-11610	Cote d'Ivoire	6.78	-5.27	NA	LR	FILTER	TVu-14845, TVu-9956	NA	NA	NA	FALSE
TVu-11788	Malawi	-9.83	33.88	508	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-11952	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-11953	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-11954	Sudan	15.83	32.83	NA	LR	PASS	NA	Clus. 2	0.28	0.72	TRUE
TVu-11955	Sudan	15.67	32.50	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-11959	Sudan	12.73	34.13	433	LR	FILTER	TVu-11963, TVu-11971	NA	NA	NA	FALSE
TVu-11960	Sudan	14.08	32.45	412	LR	PASS	NA	Admixed	0.51	0.49	TRUE

TVu-11963	Sudan	12.73	34.13	433	LR	FILTER	TVu-11959, TVu-11971	NA	NA	NA	FALSE
TVu-11971	Sudan	12.73	34.13	433	LR	PASS	TVu-11959, TVu-11963	Clus. 2	0.26	0.74	TRUE
TVu-11977	Sudan	12.73	34.13	433	LR	FILTER	TVu-1000, TVu-1452, TVu-14602	NA	NA	NA	FALSE
TVu-11990	Sudan	NA	NA	NA	LR	PASS	NA	Clus. 2	0.28	0.72	TRUE
TVu-12139	India	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-12340	Mozambique	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-12351	Mozambique	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-12354	Mozambique	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-12357	Mozambique	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-12415	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.96	0.04	TRUE
TVu-12430	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-12431	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-12432	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-12449	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-12470	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.89	0.11	TRUE
TVu-12526	Yemen	15.70	43.60	1,791	LR	PASS	NA	Admixed	0.31	0.69	TRUE
TVu-12546	India	NA	NA	NA	LR	PASS	NA	Admixed	0.48	0.52	TRUE
TVu-12556	India	NA	NA	NA	LR	PASS	NA	Admixed	0.60	0.40	TRUE
TVu-12560	India	NA	NA	NA	LR	PASS	NA	Admixed	0.69	0.31	TRUE
TVu-12565	India	NA	NA	NA	LR	PASS	NA	Admixed	0.46	0.54	TRUE
TVu-12597	India	NA	NA	NA	LR	FILTER	TVu-274, TVu-6365	NA	NA	NA	FALSE
TVu-12608	India	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-12626	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.99	0.01	TRUE
TVu-12637	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.85	0.15	TRUE
TVu-12646	India	NA	NA	NA	LR	FILTER	TVu-12937, TVu-1973	NA	NA	NA	FALSE

TVu-12705	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.99	0.01	TRUE
TVu-12710	India	NA	NA	NA	LR	PASS	NA	Clus. 2	0.20	0.80	TRUE
TVu-12746	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.80	0.20	TRUE
TVu-12780	India	NA	NA	NA	LR	FILTER	NA	NA	NA	NA	FALSE
TVu-12786	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.75	0.25	TRUE
TVu-12792	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.79	0.21	TRUE
TVu-12802	India	NA	NA	NA	LR	PASS	NA	Admixed	0.44	0.56	TRUE
TVu-12804	India	NA	NA	NA	LR	PASS	NA	Admixed	0.50	0.50	TRUE
TVu-12848	India	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-12863	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.85	0.15	TRUE
TVu-12873	India	NA	NA	NA	LR	PASS	NA	Admixed	0.40	0.60	TRUE
TVu-12897	India	NA	NA	NA	LR	PASS	NA	Admixed	0.43	0.57	TRUE
TVu-12914	India	NA	NA	NA	LR	PASS	NA	Admixed	0.53	0.47	TRUE
TVu-12923	India	NA	NA	NA	LR	PASS	NA	Admixed	0.54	0.46	TRUE
TVu-12929	India	NA	NA	NA	LR	PASS	TVu-15686	Clus. 1	1	0	TRUE
TVu-12937	India	NA	NA	NA	LR	FILTER	TVu-12646, TVu-1973	NA	NA	NA	FALSE
TVu-12961	India	NA	NA	NA	LR	PASS	NA	Admixed	0.41	0.59	TRUE
TVu-12963	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.76	0.24	TRUE
TVu-12968	India	NA	NA	NA	LR	FILTER	TVu-2891, TVu-3107	NA	NA	NA	FALSE
TVu-12990	India	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-12996	Madagascar	-18.97	48.58	514	LR	PASS	NA	Clus. 1	0.95	0.05	TRUE
TVu-12997	Madagascar	-18.97	48.58	514	LR	PASS	NA	Clus. 1	0.84	0.16	TRUE
TVu-13001	Madagascar	-18.93	48.23	1,020	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-13004	Madagascar	-20.33	44.50	35	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-13015	Madagascar	-23.13	44.15	558	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-13017	Madagascar	-18.92	47.53	1,288	LR	PASS	NA	Admixed	0.52	0.48	TRUE
TVu-13019	Madagascar	-18.92	47.53	1,288	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-13035	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.96	0.04	TRUE
TVu-13088	Benin	11.13	2.93	292	Wild	PASS	NA	Clus. 2	0.29	0.71	TRUE
TVu-13090	Cameroon	9.22	13.48	1,276	Wild	PASS	TVu-13094	Clus. 2	0.26	0.74	TRUE
TVu-13091	Cameroon	6.75	11.82	1,077	Wild	PASS	NA	Admixed	0.35	0.65	TRUE

TVu-13093	Nigeria	NA	NA	NA	Wild	PASS	NA	Clus. 2	0.29	0.71	TRUE
TVu-13094	Nigeria	9.28	6.28	117	Wild	FILTER	TVu-13090	NA	NA	NA	FALSE
TVu-13095	Nigeria	9.52	6.10	252	Wild	PASS	NA	Clus. 2	0.27	0.73	TRUE
TVu-13096	Niger	NA	NA	NA	Wild	PASS	NA	Clus. 2	0.28	0.72	TRUE
TVu-13097	Niger	NA	NA	NA	Wild	PASS	NA	Clus. 2	0.28	0.72	TRUE
TVu-13118	India	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-13124	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.82	0.18	TRUE
TVu-13147	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.87	0.13	TRUE
TVu-13176	India	NA	NA	NA	LR	PASS	NA	Clus. 1	0.92	0.08	TRUE
TVu-13232	Zambia	-14.08	31.17	1,021	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-13234	Zambia	-13.58	32.58	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-13235	Zambia	-9.42	31.33	1,566	LR	PASS	NA	Clus. 1	0.80	0.20	TRUE
TVu-13241	Benin	11.03	2.88	292	LR	PASS	NA	Admixed	0.59	0.41	TRUE
TVu-13249	United States of America	NA	NA	NA	BRM	PASS	NA	Admixed	0.31	0.69	TRUE
TVu-13271	Burkina Faso	12.46	-1.56	303	LR	PASS	TVu-7764	Clus. 2	0.01	0.99	TRUE
TVu-13283	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.92	0.08	TRUE
TVu-13295	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.83	0.17	TRUE
TVu-13297	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.91	0.09	TRUE
TVu-13299	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.99	0.01	TRUE
TVu-13305	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-13310	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.95	0.05	TRUE
TVu-13316	Zambia	NA	NA	NA	LR	PASS	TVu-13334	Clus. 1	0.97	0.03	TRUE
TVu-13334	Zambia	NA	NA	NA	LR	FILTER	TVu-13316	NA	NA	NA	FALSE
TVu-13344	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.96	0.04	TRUE
TVu-13358	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.96	0.04	TRUE
TVu-13361	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.93	0.07	TRUE
TVu-13367	Zambia	NA	NA	NA	LR	FILTER	NA	NA	NA	NA	FALSE
TVu-13368	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.95	0.05	TRUE
TVu-13373	Burkina Faso	NA	NA	NA	LR	PASS	NA	Admixed	0.38	0.62	TRUE
TVu-13382	Burkina Faso	NA	NA	NA	LR	PASS	TVu-8073	Admixed	0.39	0.61	TRUE
TVu-13388	Burkina Faso	NA	NA	NA	LR	PASS	TVu-13390	Admixed	0.37	0.63	TRUE
TVu-13390	Burkina Faso	NA	NA	NA	LR	FILTER	TVu-13388	NA	NA	NA	FALSE
TVu-13395	Burkina Faso	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE

TVu-13398	Malawi	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-13403	Nigeria	6.20	6.80	57	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-13410	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.94	0.06	TRUE
TVu-13411	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.99	0.01	TRUE
TVu-13417	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.96	0.04	TRUE
TVu-13420	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.98	0.02	TRUE
TVu-13421	Zambia	NA	NA	NA	LR	FILTER	TVu-14255, TVu-15388, TVu-15487, TVu-15601	NA	NA	NA	FALSE
TVu-13424	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.97	0.03	TRUE
TVu-13436	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.99	0.01	TRUE
TVu-13437	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.98	0.02	TRUE
TVu-13440	Kenya	-0.75	34.60	NA	LR	PASS	NA	Clus. 1	0.96	0.04	TRUE
TVu-13445	Kenya	-1.05	34.45	1,322	LR	FILTER	NA	NA	NA	NA	FALSE
TVu-13448	Kenya	-0.75	34.60	NA	LR	PASS	TVu-15055	Clus. 2	0.02	0.98	TRUE
TVu-13457	Kenya	-0.42	34.20	1,125	LR	PASS	NA	Clus. 1	0.96	0.04	TRUE
TVu-13463	Kenya	-0.42	34.20	1,125	LR	PASS	NA	Clus. 1	0.97	0.03	TRUE
TVu-13468	Kenya	-0.42	34.20	1,125	LR	FILTER	TVu-15107, TVu-15117, TVu-15131, TVu-15360, TVu-15445, TVu-15490, TVu-9930	NA	NA	NA	FALSE

TVu-13470	Kenya	-0.45	34.25	1,125	LR	PASS	NA	Clus. 1	0.99	0.01	TRUE
TVu-13474	Kenya	-0.35	34.80	1,493	LR	PASS	NA	Clus. 1	0.95	0.05	TRUE
TVu-13480	Kenya	-0.17	34.93	1,154	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-13485	Kenya	0.07	34.27	1,224	LR	PASS	NA	Clus. 1	0.99	0.01	TRUE
TVu-13491	Kenya	0.20	34.20	1,207	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-13492	Kenya	0.20	34.23	1,207	LR	PASS	NA	Clus. 1	0.96	0.04	TRUE
TVu-13495	Kenya	0.12	34.18	1,185	LR	PASS	NA	Clus. 1	0.99	0.01	TRUE
TVu-13496	Kenya	0.12	34.18	1,185	LR	PASS	NA	Clus. 1	0.97	0.03	TRUE
TVu-13500	Kenya	0.12	34.10	1,185	Wild	PASS	NA	Admixed	0.67	0.33	TRUE
TVu-13506	Kenya	0.17	34.93	1,154	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-13508	Kenya	0.17	34.93	1,154	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-13521	Guinea	NA	NA	NA	LR	PASS	NA	Clus. 2	0.24	0.76	TRUE
TVu-13533	Guinea	NA	NA	NA	LR	PASS	NA	Clus. 2	0.17	0.83	TRUE
TVu-13674	Nigeria	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.94	0.06	TRUE
TVu-13677	Nigeria	NA	NA	NA	BRM	PASS	NA	Admixed	0.42	0.58	TRUE
TVu-13683	Nigeria	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.77	0.23	TRUE
TVu-13685	Kenya	-0.32	34.93	1,493	LR	PASS	NA	Admixed	0.68	0.32	TRUE
TVu-13746	Brazil	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.99	0.01	TRUE
TVu-13778	Brazil	NA	NA	NA	BRM	PASS	TVu-13779	Clus. 1	0.94	0.06	TRUE
TVu-13779	Brazil	NA	NA	NA	BRM	FILTER	TVu-13778	NA	NA	NA	FALSE
TVu-13790	Brazil	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.98	0.02	TRUE
TVu-13797	Brazil	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.88	0.12	TRUE
TVu-13804	Brazil	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.98	0.02	TRUE
TVu-13814	Brazil	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.96	0.04	TRUE
TVu-13821	Sri Lanka	NA	NA	NA	LR	PASS	NA	Clus. 1	0.98	0.02	TRUE
TVu-13830	Central African Republic	NA	NA	NA	LR	PASS	NA	Admixed	0.48	0.52	TRUE
TVu-13831	Central African Republic	NA	NA	NA	LR	PASS	NA	Clus. 2	0.12	0.88	TRUE
TVu-13832	Central African Republic	NA	NA	NA	LR	FILTER	TVu-13846, TVu-14042	NA	NA	NA	FALSE

TVu-13834	Central African Republic	NA	NA	NA	LR	PASS	NA	Clus. 1	0.93	0.07	TRUE
TVu-13838	Central African Republic	NA	NA	NA	LR	PASS	NA	Clus. 2	0.15	0.85	TRUE
TVu-13839	Central African Republic	NA	NA	NA	LR	PASS	NA	Admixed	0.44	0.56	TRUE
TVu-13845	Central African Republic	NA	NA	NA	LR	PASS	NA	Admixed	0.44	0.56	TRUE
TVu-13846	Central African Republic	NA	NA	NA	LR	FILTER	TVu-13832, TVu-14042	NA	NA	NA	FALSE
TVu-13847	Central African Republic	NA	NA	NA	LR	PASS	NA	Clus. 2	0.15	0.85	TRUE
TVu-13850	Central African Republic	NA	NA	NA	LR	PASS	NA	Admixed	0.46	0.54	TRUE
TVu-13857	Central African Republic	NA	NA	NA	LR	PASS	NA	Admixed	0.43	0.57	TRUE
TVu-13859	Central African Republic	NA	NA	NA	LR	PASS	NA	Clus. 2	0.08	0.92	TRUE
TVu-13863	Central African Republic	NA	NA	NA	LR	PASS	NA	Clus. 2	0.16	0.84	TRUE
TVu-13866	Central African Republic	NA	NA	NA	LR	PASS	NA	Clus. 2	0.15	0.85	TRUE

TVu-13867	Central African Republic	NA	NA	NA	LR	PASS	NA	Clus. 2	0.12	0.88	TRUE
TVu-13871	Central African Republic	NA	NA	NA	LR	PASS	NA	Clus. 1	0.72	0.28	TRUE
TVu-13872	Central African Republic	NA	NA	NA	LR	PASS	NA	Clus. 1	0.72	0.28	TRUE
TVu-13873	Central African Republic	NA	NA	NA	LR	PASS	NA	Clus. 2	0.15	0.85	TRUE
TVu-13874	Central African Republic	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-13880	Central African Republic	NA	NA	NA	LR	PASS	TVu-14856	Admixed	0.49	0.51	TRUE
TVu-13882	Central African Republic	NA	NA	NA	LR	FILTER	TVu-3791, TVu-3853	NA	NA	NA	FALSE
TVu-13887	Central African Republic	NA	NA	NA	LR	PASS	NA	Clus. 1	0.96	0.04	TRUE
TVu-13891	Central African Republic	NA	NA	NA	LR	PASS	NA	Clus. 2	0.08	0.92	TRUE
TVu-13892	Central African Republic	NA	NA	NA	LR	PASS	NA	Admixed	0.48	0.52	TRUE
TVu-13908	Botswana	NA	NA	NA	LR	PASS	NA	Admixed	0.42	0.58	TRUE
TVu-13919	Botswana	NA	NA	NA	LR	PASS	NA	Clus. 1	0.73	0.27	TRUE
TVu-13932	Botswana	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-13933	Botswana	NA	NA	NA	LR	PASS	TVu-14533	Clus. 1	1	0	TRUE
TVu-13939	Botswana	NA	NA	NA	LR	PASS	NA	Admixed	0.49	0.51	TRUE

TVu-13947	Botswana	NA	NA	NA	LR	PASS	TVu-14229	Clus. 1	0.73	0.27	TRUE
TVu-13950	Botswana	NA	NA	NA	LR	PASS	TVu-15805	Admixed	0.59	0.41	TRUE
TVu-13953	Botswana	NA	NA	NA	LR	PASS	NA	Clus. 1	0.97	0.03	TRUE
TVu-13956	Union of Soviet Socialist Republics	NA	NA	NA	LR	PASS	NA	Clus. 2	0.13	0.87	TRUE
TVu-13958	Union of Soviet Socialist Republics	NA	NA	NA	LR	PASS	NA	Admixed	0.57	0.43	TRUE
TVu-13965	Union of Soviet Socialist Republics	NA	NA	NA	LR	PASS	TVu-14558	Admixed	0.61	0.39	TRUE
TVu-13966	Union of Soviet Socialist Republics	NA	NA	NA	LR	PASS	NA	Clus. 2	0.20	0.80	TRUE
TVu-13968	Union of Soviet Socialist Republics	NA	NA	NA	LR	PASS	NA	Admixed	0.41	0.59	TRUE
TVu-13973	Union of Soviet Socialist Republics	NA	NA	NA	LR	PASS	NA	Clus. 2	0.14	0.86	TRUE
TVu-13979	Union of Soviet Socialist Republics	NA	NA	NA	LR	PASS	NA	Admixed	0.38	0.62	TRUE
TVu-13982	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.95	0.05	TRUE
TVu-13983	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.89	0.11	TRUE
TVu-13986	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.89	0.11	TRUE
TVu-13990	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.97	0.03	TRUE

TVu-13994	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.79	0.21	TRUE
TVu-13997	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.82	0.18	TRUE
TVu-13998	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.96	0.04	TRUE
TVu-14002	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.98	0.02	TRUE
TVu-14003	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-14012	Nigeria	NA	NA	NA	BRM	PASS	NA	Admixed	0.62	0.38	TRUE
TVu-14025	Brazil	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.95	0.05	TRUE
TVu-14032	Brazil	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.97	0.03	TRUE
TVu-14042	Central African Republic	NA	NA	NA	LR	PASS	TVu-13832, TVu-13846	Clus. 2	0.01	0.99	TRUE
TVu-14049	Central African Republic	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-14054	Central African Republic	NA	NA	NA	LR	PASS	NA	Clus. 2	0.08	0.92	TRUE
TVu-14056	Central African Republic	NA	NA	NA	LR	PASS	NA	Clus. 2	0.16	0.84	TRUE
TVu-14061	Central African Republic	NA	NA	NA	LR	PASS	NA	Clus. 2	0.14	0.86	TRUE
TVu-14067	Central African Republic	NA	NA	NA	LR	PASS	NA	Clus. 2	0.14	0.86	TRUE
TVu-14069	Central African Republic	NA	NA	NA	LR	PASS	NA	Clus. 2	0.14	0.86	TRUE
TVu-14080	Central African Republic	NA	NA	NA	LR	PASS	NA	Clus. 2	0.16	0.84	TRUE

TVu-14082	Central African Republic	NA	NA	NA	LR	PASS	NA	Clus. 2	0.11	0.89	TRUE
TVu-14084	Central African Republic	NA	NA	NA	LR	PASS	NA	Clus. 2	0.15	0.85	TRUE
TVu-14090	Central African Republic	NA	NA	NA	LR	PASS	NA	Clus. 2	0.12	0.88	TRUE
TVu-14109	Central African Republic	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-14117	Central African Republic	NA	NA	NA	LR	FILTER	TVu-10204	NA	NA	NA	FALSE
TVu-14134	Botswana	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-14136	Botswana	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-14137	Union of Soviet Socialist Republics	NA	NA	NA	LR	PASS	NA	Clus. 1	0.95	0.05	TRUE
TVu-14143	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.93	0.07	TRUE
TVu-14144	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.89	0.11	TRUE
TVu-14146	Kenya	NA	NA	NA	LR	PASS	NA	Clus. 1	0.97	0.03	TRUE
TVu-14171	Nigeria	NA	NA	NA	BRM	PASS	NA	Admixed	0.56	0.44	TRUE
TVu-14172	Nigeria	NA	NA	NA	BRM	PASS	NA	Admixed	0.62	0.38	TRUE
TVu-14175	Nigeria	NA	NA	NA	BRM	PASS	NA	Admixed	0.37	0.63	TRUE
TVu-14184	Nigeria	NA	NA	NA	BRM	PASS	NA	Clus. 2	0.14	0.86	TRUE
TVu-14185	Nigeria	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.72	0.28	TRUE
TVu-14190	Nigeria	NA	NA	NA	BRM	PASS	NA	Admixed	0.48	0.52	TRUE
TVu-14191	Nigeria	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.73	0.27	TRUE
TVu-14195	Nigeria	NA	NA	NA	BRM	PASS	NA	Admixed	0.51	0.49	TRUE
TVu-14196	Nigeria	NA	NA	NA	BRM	PASS	NA	Admixed	0.56	0.44	TRUE
TVu-14197	Nigeria	NA	NA	NA	BRM	FILTER	NA	NA	NA	NA	FALSE

TVu-14198	Nigeria	NA	NA	NA	BRM	PASS	NA	Clus. 1	0.81	0.19	TRUE
TVu-14207	Botswana	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-14224	Botswana	NA	NA	NA	LR	PASS	NA	Admixed	0.53	0.47	TRUE
TVu-14225	Botswana	NA	NA	NA	LR	PASS	NA	Admixed	0.64	0.36	TRUE
TVu-14229	Botswana	NA	NA	NA	LR	FILTER	TVu-13947	NA	NA	NA	FALSE
TVu-14234	Botswana	NA	NA	NA	LR	FILTER	NA	NA	NA	NA	FALSE
TVu-14240	Botswana	NA	NA	NA	LR	PASS	NA	Admixed	0.57	0.43	TRUE
TVu-14242	Botswana	NA	NA	NA	LR	PASS	TVu-14317	Clus. 1	1	0	TRUE
TVu-14246	Botswana	NA	NA	NA	LR	PASS	NA	Admixed	0.38	0.62	TRUE
TVu-14248	Botswana	NA	NA	NA	LR	PASS	NA	Admixed	0.47	0.53	TRUE
TVu-14253	Botswana	NA	NA	NA	LR	PASS	NA	Admixed	0.38	0.62	TRUE
TVu-14255	Botswana	NA	NA	NA	LR	FILTER	TVu-13421, TVu-15388, TVu-15487, TVu-15601	NA	NA	NA	FALSE
TVu-14260	Botswana	NA	NA	NA	LR	FILTER	TVu-15979, TVu-1832	NA	NA	NA	FALSE
TVu-14272	Botswana	NA	NA	NA	LR	PASS	NA	Admixed	0.48	0.52	TRUE
TVu-14273	Botswana	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-14290	Botswana	NA	NA	NA	LR	FILTER	TVu-14325, TVu-14700, TVu-14721, TVu-14886, TVu-14890, TVu-14914,	NA	NA	NA	FALSE

							TVu-15424, TVu-15968, TVu-16422, TVu-6838, TVu-7149				
TVu-14291	Botswana	NA	NA	NA	LR	PASS	NA	Clus. 1	0.99	0.01	TRUE
TVu-14299	Botswana	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-14308	Botswana	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-14313	Botswana	NA	NA	NA	LR	PASS	NA	Admixed	0.53	0.47	TRUE
TVu-14314	Botswana	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-14317	Botswana	NA	NA	NA	LR	FILTER	TVu-14242	NA	NA	NA	FALSE
TVu-14318	Botswana	NA	NA	NA	LR	PASS	NA	Clus. 1	0.98	0.02	TRUE
TVu-14321	Botswana	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-14325	Botswana	NA	NA	NA	LR	FILTER	TVu-14290, TVu-14700, TVu-14721, TVu-14886, TVu-14890, TVu-14914, TVu-15424, TVu-15968, TVu-16422,	NA	NA	NA	FALSE

							TVu-6838, TVu-7149				
TVu-14327	Botswana	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-14336	Senegal	14.75	-16.77	22	LR	FILTER	TVu-14807, TVu-14827	NA	NA	NA	FALSE
TVu-14337	Senegal	14.75	-16.77	22	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-14341	Senegal	14.62	-16.25	7	LR	PASS	NA	Clus. 2	0.08	0.92	TRUE
TVu-14344	Senegal	14.62	-16.25	7	LR	PASS	NA	Clus. 2	0.05	0.95	TRUE
TVu-14345	Senegal	14.62	-16.25	7	LR	PASS	NA	Clus. 2	0.07	0.93	TRUE
TVu-14346	Senegal	15.03	-15.77	25	LR	PASS	NA	Clus. 2	0.07	0.93	TRUE
TVu-14348	Senegal	15.12	-15.73	25	LR	PASS	NA	Clus. 2	0.05	0.95	TRUE
TVu-14356	Senegal	15.62	-16.25	45	LR	PASS	NA	Clus. 2	0.07	0.93	TRUE
TVu-14357	Senegal	15.62	-16.25	45	LR	PASS	NA	Clus. 2	0.07	0.93	TRUE
TVu-14358	Senegal	15.48	-16.35	45	LR	FILTER	TVu-5168, TVu-7144	NA	NA	NA	FALSE
TVu-14361	Senegal	15.48	-16.35	45	LR	PASS	NA	Admixed	0.31	0.69	TRUE
TVu-14380	Senegal	15.13	-16.12	43	LR	PASS	NA	Clus. 2	0.09	0.91	TRUE
TVu-14387	Senegal	15.93	-16.25	45	LR	PASS	NA	Clus. 2	0.07	0.93	TRUE
TVu-14393	Senegal	16.43	-15.72	NA	LR	PASS	TVu-14396	Clus. 2	0.06	0.94	TRUE
TVu-14395	Senegal	15.32	-16.13	40	LR	PASS	NA	Clus. 2	0.07	0.93	TRUE
TVu-14396	Senegal	16.47	-15.20	11	LR	FILTER	TVu-14393	NA	NA	NA	FALSE
TVu-14401	Senegal	15.50	-13.27	15	LR	PASS	NA	Clus. 2	0.09	0.91	TRUE
TVu-14402	Senegal	15.48	-15.25	15	LR	PASS	NA	Clus. 2	0.07	0.93	TRUE
TVu-14405	Senegal	15.38	-15.23	29	LR	PASS	NA	Clus. 2	0.08	0.92	TRUE
TVu-14406	Senegal	15.38	-15.23	29	LR	PASS	NA	Clus. 2	0.07	0.93	TRUE
TVu-14410	Senegal	15.32	-15.45	29	LR	PASS	NA	Clus. 2	0.07	0.93	TRUE
TVu-14417	Senegal	15.50	-16	29	LR	PASS	NA	Clus. 2	0.08	0.92	TRUE
TVu-14429	Senegal	14.12	-15.77	8	LR	PASS	NA	Clus. 2	0.26	0.74	TRUE
TVu-14432	Senegal	14	-14.23	21	LR	PASS	NA	Clus. 2	0.05	0.95	TRUE
TVu-14434	Senegal	13.97	-14.52	21	LR	FILTER	TVu-1985, TVu-1986, TVu-332, TVu-470,	NA	NA	NA	FALSE

							TVu-492, TVu-493				
TVu-14446	Senegal	13.27	-13.90	21	LR	FILTER	NA	NA	NA	NA	FALSE
TVu-14473	Senegal	NA	NA	NA	LR	PASS	NA	Clus. 1	0.97	0.03	TRUE
TVu-14484	Senegal	NA	NA	NA	LR	FILTER	TVu-123	NA	NA	NA	FALSE
TVu-14487	Senegal	NA	NA	NA	LR	PASS	NA	Clus. 1	0.95	0.05	TRUE
TVu-14500	Senegal	NA	NA	NA	LR	FILTER	NA	NA	NA	NA	FALSE
TVu-14502	Senegal	NA	NA	NA	LR	PASS	NA	Clus. 1	0.95	0.05	TRUE
TVu-14505	Senegal	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-14512	Senegal	NA	NA	NA	LR	FILTER	TVu-1836, TVu-2274	NA	NA	NA	FALSE
TVu-14522	Senegal	NA	NA	NA	LR	PASS	NA	Clus. 1	0.98	0.02	TRUE
TVu-14523	Senegal	NA	NA	NA	LR	PASS	NA	Admixed	0.47	0.53	TRUE
TVu-14524	Senegal	NA	NA	NA	LR	FILTER	TVu-10199, TVu-14525, TVu-14568	NA	NA	NA	FALSE
TVu-14525	Senegal	NA	NA	NA	LR	PASS	TVu-10199, TVu-14524, TVu-14568	Clus. 1	1	0	TRUE
TVu-14528	Senegal	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-14530	Senegal	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-14531	Senegal	NA	NA	NA	LR	PASS	NA	Clus. 1	0.76	0.24	TRUE
TVu-14533	Mali	14.50	-9	252	LR	FILTER	TVu-13933	NA	NA	NA	FALSE
TVu-14539	Mali	15.08	-7.83	301	LR	PASS	NA	Clus. 2	0.07	0.93	TRUE
TVu-14541	Mali	15	-7.50	259	LR	PASS	NA	Clus. 2	0.07	0.93	TRUE
TVu-14543	Mali	13.25	-6	274	LR	PASS	NA	Clus. 2	0.07	0.93	TRUE
TVu-14550	Mali	14.50	-3.17	326	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-14558	Mali	14.50	-4.18	272	LR	FILTER	TVu-13965	NA	NA	NA	FALSE
TVu-14564	Mali	12.83	-7.83	330	LR	PASS	NA	Clus. 1	1	0	TRUE

TVu-14568	Ethiopia	NA	NA	NA	LR	FILTER	TVu-10199, TVu-14524, TVu-14525	NA	NA	NA	FALSE
TVu-14580	Mali	NA	NA	NA	LR	PASS	NA	Clus. 1	0.96	0.04	TRUE
TVu-14593	Mali	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-14598	Mali	NA	NA	NA	LR	PASS	TVu-7070	Admixed	0.53	0.47	TRUE
TVu-14602	Mali	NA	NA	NA	LR	FILTER	TVu-1000, TVu-11977, TVu-1452	NA	NA	NA	FALSE
TVu-14604	Mali	NA	NA	NA	LR	PASS	NA	Clus. 1	0.96	0.04	TRUE
TVu-14621	Mali	NA	NA	NA	LR	PASS	NA	Clus. 1	0.82	0.18	TRUE
TVu-14623	Mali	NA	NA	NA	LR	PASS	NA	Clus. 1	0.87	0.13	TRUE
TVu-14626	Mali	NA	NA	NA	LR	PASS	TVu-15884	Admixed	0.46	0.54	TRUE
TVu-14632	Central African Republic	NA	NA	NA	LR	PASS	NA	Admixed	0.69	0.31	TRUE
TVu-14633	Central African Republic	NA	NA	NA	LR	PASS	NA	Admixed	0.58	0.42	TRUE
TVu-14634	Central African Republic	NA	NA	NA	LR	PASS	NA	Clus. 1	0.74	0.26	TRUE
TVu-14635	Central African Republic	4.80	16.05	558	LR	FILTER	NA	NA	NA	NA	FALSE
TVu-14642	Botswana	NA	NA	NA	LR	PASS	NA	Clus. 1	0.99	0.01	TRUE
TVu-14652	Botswana	NA	NA	NA	LR	PASS	NA	Clus. 1	0.97	0.03	TRUE
TVu-14656	Botswana	NA	NA	NA	LR	PASS	NA	Admixed	0.52	0.48	TRUE
TVu-14667	Botswana	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-14669	Botswana	NA	NA	NA	LR	PASS	NA	Clus. 1	0.89	0.11	TRUE
TVu-14682	Botswana	NA	NA	NA	LR	PASS	NA	Clus. 1	0.96	0.04	TRUE

TVu-14683	Botswana	NA	NA	NA	LR	PASS	NA	Clus. 1	0.97	0.03	TRUE
TVu-14686	Botswana	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-14691	Botswana	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-14693	Botswana	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-14700	Botswana	NA	NA	NA	LR	FILTER	TVu-14290, TVu-14325, TVu-14721, TVu-14886, TVu-14890, TVu-14914, TVu-15424, TVu-15968, TVu-16422, TVu-6838, TVu-7149	NA	NA	NA	FALSE
TVu-14701	Botswana	NA	NA	NA	LR	PASS	TVu-14702	Clus. 1	1	0	TRUE
TVu-14702	Botswana	NA	NA	NA	LR	FILTER	TVu-14701	NA	NA	NA	FALSE
TVu-14705	Botswana	NA	NA	NA	LR	PASS	NA	Clus. 1	0.95	0.05	TRUE
TVu-14711	Botswana	NA	NA	NA	LR	PASS	NA	Clus. 1	0.99	0.01	TRUE
TVu-14719	Botswana	NA	NA	NA	LR	PASS	NA	Clus. 1	0.92	0.08	TRUE
TVu-14721	Botswana	NA	NA	NA	LR	FILTER	TVu-14290, TVu-14325, TVu-14700,	NA	NA	NA	FALSE

							TVu-14886, TVu-14890, TVu-14914, TVu-15424, TVu-15968, TVu-16422, TVu-6838, TVu-7149				
TVu-14726	Botswana	NA	NA	NA	LR	FILTER	NA	NA	NA	NA	FALSE
TVu-14745	Botswana	NA	NA	NA	LR	PASS	NA	Clus. 1	0.99	0.01	TRUE
TVu-14746	Botswana	NA	NA	NA	LR	PASS	NA	Clus. 1	0.99	0.01	TRUE
TVu-14759	Botswana	NA	NA	NA	LR	FILTER	TVu-45, TVu-7069	NA	NA	NA	FALSE
TVu-14761	Botswana	NA	NA	NA	LR	PASS	NA	Admixed	0.49	0.51	TRUE
TVu-14788	Senegal	14.63	-16.13	23	LR	PASS	NA	Clus. 2	0.07	0.93	TRUE
TVu-14795	Senegal	15.38	-15.87	29	LR	FILTER	TVu-14939, TVu-161	NA	NA	NA	FALSE
TVu-14807	Senegal	15.05	-16.60	40	LR	FILTER	TVu-14336, TVu-14827	NA	NA	NA	FALSE
TVu-14813	Senegal	15.02	-16.27	40	LR	PASS	NA	Clus. 2	0.06	0.94	TRUE
TVu-14827	Senegal	15.32	-15.45	20	LR	PASS	TVu-14336, TVu-14807	Clus. 2	0	1	TRUE
TVu-14830	Senegal	14.27	-16.38	6	LR	PASS	NA	Clus. 2	0.07	0.93	TRUE
TVu-14834	Senegal	14.07	-15.62	6	LR	PASS	NA	Clus. 2	0.06	0.94	TRUE
TVu-14839	Senegal	13.10	-12.60	116	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-14841	Senegal	13.27	-13.90	21	LR	PASS	NA	Clus. 1	0.88	0.12	TRUE

TVu-14843	Senegal	13.77	-16.33	49	LR	PASS	NA	Clus. 2	0.07	0.93	TRUE
TVu-14845	Mali	14.08	-8.33	44	LR	FILTER	TVu-11610, TVu-9956	NA	NA	NA	FALSE
TVu-14850	Mali	15.08	-9.83	22	LR	PASS	NA	Clus. 2	0.08	0.92	TRUE
TVu-14856	Central African Republic	7	19.17	508	LR	FILTER	TVu-13880	NA	NA	NA	FALSE
TVu-14861	China	NA	NA	NA	LR	PASS	TVu-14868	Admixed	0.55	0.45	TRUE
TVu-14862	China	NA	NA	NA	LR	PASS	NA	Admixed	0.49	0.51	TRUE
TVu-14868	China	NA	NA	NA	LR	FILTER	TVu-14861	NA	NA	NA	FALSE
TVu-14875	China	NA	NA	NA	LR	PASS	NA	Admixed	0.52	0.48	TRUE
TVu-14876	China	NA	NA	NA	LR	PASS	NA	Admixed	0.57	0.43	TRUE
TVu-14886	Botswana	-25.78	24.60	1,281	LR	FILTER	TVu-14290, TVu-14325, TVu-14700, TVu-14721, TVu-14890, TVu-14914, TVu-15424, TVu-15968, TVu-16422, TVu-6838, TVu-7149	NA	NA	NA	FALSE
TVu-14890	Botswana	-23.08	27.75	837	LR	FILTER	TVu-14290,	NA	NA	NA	FALSE

							TVu-14325, TVu-14700, TVu-14721, TVu-14886, TVu-14914, TVu-15424, TVu-15968, TVu-16422, TVu-6838, TVu-7149				
TVu-14891	Botswana	-22.33	28.67	772	LR	FILTER	TVu-10206, TVu-109, TVu-16343, TVu-16408, TVu-18, TVu-1975, TVu-1996, TVu-1999, TVu-36, TVu-374, TVu-745	NA	NA	NA	FALSE
TVu-14892	Botswana	-21	27.25	989	LR	PASS	NA	Clus. 1	0.98	0.02	TRUE
TVu-14904	Botswana	-23.08	26.75	1,009	LR	PASS	TVu-15840	Clus. 1	0.97	0.03	TRUE

TVu-14905	Botswana	-23.08	26.75	1,009	LR	FILTER	TVu-347, TVu-565	NA	NA	NA	FALSE
TVu-14906	Niger	13.68	1.79	206	LR	FILTER	TVu-14919, TVu-4733	NA	NA	NA	FALSE
TVu-14914	Niger	14.45	0.77	222	LR	FILTER	TVu-14290, TVu-14325, TVu-14700, TVu-14721, TVu-14886, TVu-14890, TVu-15424, TVu-15968, TVu-16422, TVu-6838, TVu-7149	NA	NA	NA	FALSE
TVu-14915	Niger	14.45	0.77	222	LR	PASS	NA	Admixed	0.59	0.41	TRUE
TVu-14919	Niger	14.47	1.45	252	LR	FILTER	TVu-14906, TVu-4733	NA	NA	NA	FALSE
TVu-14921	Niger	14.53	1.27	460	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-14923	Niger	13.42	1.42	252	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-14924	Niger	12.83	1.42	252	Wild	PASS	NA	Clus. 1	0.97	0.03	TRUE
TVu-14931	Niger	3.25	3.25	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-14932	Niger	3.25	3.25	252	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-14935	Niger	14	5.68	262	Wild	FILTER	NA	NA	NA	NA	FALSE

TVu-14939	Niger	13.70	6.85	262	LR	FILTER	TVu-14795, TVu-161	NA	NA	NA	FALSE
TVu-14949	Niger	13.70	7.88	373	Weedy	PASS	NA	Clus. 2	0	1	TRUE
TVu-14962	Niger	13.77	7.92	373	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-14963	Niger	13.77	7.92	373	LR	FILTER	TVu-14978, TVu-15589, TVu-2887, TVu-7317, TVu-8123, TVu-8456	NA	NA	NA	FALSE
TVu-14967	Niger	13.07	8.25	446	LR	FILTER	TVu-15866, TVu-315, TVu-387, TVu-763	NA	NA	NA	FALSE
TVu-14968	Niger	13.20	8.43	453	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-14970	Niger	13.83	8.50	446	LR	PASS	NA	Clus. 2	0.02	0.98	TRUE
TVu-14971	Niger	13.83	8.50	446	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-14978	Niger	13.07	8.83	446	LR	FILTER	TVu-14963, TVu-15589, TVu-2887, TVu-7317, TVu-8123, TVu-8456	NA	NA	NA	FALSE
TVu-14980	Niger	13.10	8.95	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-14992	Niger	13.50	9.50	453	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-14996	Niger	13.37	12.47	285	LR	PASS	NA	Admixed	0.54	0.46	TRUE
TVu-15008	Niger	14.03	5.98	NA	LR	PASS	NA	Admixed	0.40	0.60	TRUE
TVu-15011	Niger	13.93	6.25	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-15016	Niger	14.02	6.03	NA	LR	PASS	NA	Clus. 2	0	1	TRUE

TVu-15017	Niger	14.02	6.03	NA	LR	FILTER	NA	NA	NA	NA	FALSE
TVu-15019	Niger	14.02	6.03	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-15029	Niger	14.76	5.77	395	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-15035	Niger	14.76	5.77	395	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-15037	Niger	14.95	5.32	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-15053	Zambia	-16.50	27.53	895	LR	PASS	NA	Clus. 1	0.97	0.03	TRUE
TVu-15055	Botswana	-19.08	22.58	986	Wild	FILTER	TVu-13448	NA	NA	NA	FALSE
TVu-15056	Zambia	-15.52	23.25	1,053	LR	PASS	NA	Clus. 1	0.95	0.05	TRUE
TVu-15058	Zambia	-17.75	25.87	764	LR	PASS	NA	Clus. 1	0.99	0.01	TRUE
TVu-15076	Zambia	-14.52	28.05	1,280	LR	PASS	TVu-15077	Clus. 1	1	0	TRUE
TVu-15077	Zambia	-10.50	33.25	NA	LR	FILTER	TVu-15076	NA	NA	NA	FALSE
TVu-15086	Malawi	-14.97	34.93	608	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-15088	Malawi	-15.02	35.12	608	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-15089	Malawi	-15.13	35.25	608	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-15107	Malawi	-15.98	35.40	820	LR	FILTER	TVu-13468, TVu-15117, TVu-15131, TVu-15360, TVu-15445, TVu-15490, TVu-9930	NA	NA	NA	FALSE
TVu-15112	Malawi	-15.40	35.43	781	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-15113	Malawi	-15.40	35.43	781	LR	FILTER	NA	NA	NA	NA	FALSE
TVu-15114	Malawi	-15.05	35.37	508	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-15116	Malawi	-15.05	35.40	508	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-15117	Malawi	-15.05	35.40	508	LR	PASS	TVu-13468, TVu-	Clus. 1	1	0	TRUE

							15107, TVu-15131, TVu-15360, TVu-15445, TVu-15490, TVu-9930				
TVu-15118	Malawi	-15.05	35.40	508	LR	FILTER	TVu-15433, TVu-15571, TVu-9868, TVu-9869	NA	NA	NA	FALSE
TVu-15120	Malawi	-14.43	35.62	712	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-15121	Malawi	-14.55	35.22	508	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-15131	Malawi	-13.75	34.40	536	LR	FILTER	TVu-13468, TVu-15107, TVu-15117, TVu-15360, TVu-15445, TVu-15490, TVu-9930	NA	NA	NA	FALSE
TVu-15140	Malawi	-11.17	34.38	1,253	LR	PASS	NA	Clus. 1	0.99	0.01	TRUE
TVu-15141	Malawi	-11.38	33.98	1,253	LR	PASS	TVu-15146	Clus. 1	0.99	0.01	TRUE
TVu-15142	Malawi	-11.22	33.85	1,253	LR	PASS	TVu-15143	Clus. 1	1	0	TRUE
TVu-15143	Malawi	-11.22	33.85	1,253	LR	FILTER	TVu-15142	NA	NA	NA	FALSE

TVu-15146	Malawi	-10.20	34.03	508	LR	FILTER	TVu-15141	NA	NA	NA	FALSE
TVu-15147	Malawi	-10.20	34.03	508	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-15149	Malawi	-11.40	33.83	1,276	LR	PASS	NA	Clus. 1	0.93	0.07	TRUE
TVu-15151	Malawi	-11.05	33.63	1,276	LR	PASS	TVu-15913	Clus. 1	0.75	0.25	TRUE
TVu-15158	Cameroon	4.90	10.87	575	LR	PASS	NA	Clus. 1	0.70	0.30	TRUE
TVu-15161	Cameroon	5.43	10.23	1,438	LR	FILTER	NA	NA	NA	NA	FALSE
TVu-15164	Cameroon	6.38	10.18	1,109	LR	PASS	NA	Clus. 2	0.13	0.87	TRUE
TVu-15166	Cameroon	5.98	10.73	NA	LR	PASS	NA	Admixed	0.59	0.41	TRUE
TVu-15170	Cameroon	5.80	11.43	1,150	LR	PASS	NA	Admixed	0.57	0.43	TRUE
TVu-15171	Cameroon	6.03	11.53	1,150	LR	PASS	NA	Admixed	0.60	0.40	TRUE
TVu-15184	Cameroon	5.77	9.73	1,266	LR	PASS	NA	Admixed	0.62	0.38	TRUE
TVu-15186	Cameroon	5.73	9.27	1,266	LR	PASS	NA	Admixed	0.62	0.38	TRUE
TVu-15187	Cameroon	5.72	9.30	126	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-15190	Cameroon	5.38	9.40	126	LR	PASS	NA	Admixed	0.60	0.40	TRUE
TVu-15191	Cameroon	5.10	9.35	126	LR	PASS	NA	Clus. 1	0.77	0.23	TRUE
TVu-15197	Cameroon	4.68	9.45	126	LR	PASS	NA	Clus. 1	0.75	0.25	TRUE
TVu-15198	Cameroon	4.73	9.52	244	LR	PASS	NA	Clus. 1	0.74	0.26	TRUE
TVu-15200	Cameroon	5	10	638	LR	PASS	NA	Admixed	0.59	0.41	TRUE
TVu-15201	Cameroon	3.75	10.18	25	LR	PASS	NA	Clus. 2	0.11	0.89	TRUE
TVu-15202	Republic of the Congo	-4.12	13.03	508	LR	PASS	NA	Clus. 1	0.74	0.26	TRUE
TVu-15204	Republic of the Congo	-4.05	13.12	508	LR	PASS	NA	Clus. 1	0.73	0.27	TRUE
TVu-15208	Congo	-3.52	13.45	508	LR	PASS	NA	Clus. 1	0.83	0.17	TRUE
TVu-15223	Republic of the Congo	-4.85	12.05	NA	LR	PASS	NA	Clus. 1	0.75	0.25	TRUE
TVu-15224	Republic of the Congo	-4.85	12.05	NA	LR	PASS	NA	Clus. 1	0.74	0.26	TRUE
TVu-15225	Congo	-4.78	11.86	17	LR	PASS	NA	Clus. 1	0.96	0.04	TRUE
TVu-15229	Republic of the Congo	-3.43	12.23	330	LR	PASS	NA	Clus. 1	0.73	0.27	TRUE
TVu-15230	Congo	-3.57	12.33	330	LR	FILTER	NA	NA	NA	NA	FALSE
TVu-15238	Republic of the Congo	-3.55	13.42	508	LR	PASS	NA	Admixed	0.67	0.33	TRUE

TVu-15239	Republic of the Congo	-4.38	14.92	317	LR	PASS	NA	Admixed	0.70	0.30	TRUE
TVu-15240	Republic of the Congo	-3.48	15.43	610	LR	PASS	NA	Clus. 1	0.73	0.27	TRUE
TVu-15242	Republic of the Congo	-2.65	15.63	610	LR	PASS	TVu-15243	Clus. 1	0.72	0.28	TRUE
TVu-15243	Republic of the Congo	-2.48	15.60	611	LR	FILTER	TVu-15242	NA	NA	NA	FALSE
TVu-15251	Chad	12.92	14.80	286	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-15256	Chad	12.35	15.10	299	LR	PASS	NA	Clus. 2	0.08	0.92	TRUE
TVu-15258	Chad	11.57	15.42	299	LR	PASS	NA	Clus. 2	0.22	0.78	TRUE
TVu-15259	Chad	11.57	15.42	299	LR	PASS	TVu-16461	Clus. 2	0	1	TRUE
TVu-15262	Chad	10.80	15.58	294	LR	PASS	NA	Clus. 2	0.04	0.96	TRUE
TVu-15279	Chad	8.30	18.52	365	LR	PASS	NA	Admixed	0.47	0.53	TRUE
TVu-15285	Chad	9.27	18.07	365	LR	PASS	NA	Admixed	0.50	0.50	TRUE
TVu-15295	Chad	12.97	16.53	303	LR	PASS	NA	Clus. 2	0.06	0.94	TRUE
TVu-15299	Chad	12.88	16.77	303	LR	PASS	NA	Clus. 2	0.08	0.92	TRUE
TVu-15301	Chad	13.08	17.23	303	LR	PASS	NA	Admixed	0.41	0.59	TRUE
TVu-15307	Chad	13.30	19.35	336	LR	PASS	NA	Clus. 2	0.07	0.93	TRUE
TVu-15308	Chad	13.33	19.55	360	LR	FILTER	NA	NA	NA	NA	FALSE
TVu-15309	Chad	13.33	19.55	360	LR	PASS	NA	Clus. 2	0.14	0.86	TRUE
TVu-15312	Chad	12.37	19.48	508	LR	PASS	NA	Clus. 2	0.02	0.98	TRUE
TVu-15313	Chad	12.18	18.63	508	LR	PASS	NA	Clus. 2	0.01	0.99	TRUE
TVu-15315	Chad	12.03	18.20	508	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-15323	Chad	9.38	15.07	508	LR	PASS	TVu-9976	Clus. 2	0	1	TRUE
TVu-15332	Chad	8.45	16.35	508	LR	PASS	NA	Clus. 2	0.06	0.94	TRUE
TVu-15340	Chad	7.90	16.03	508	LR	PASS	NA	Admixed	0.54	0.46	TRUE
TVu-15341	Chad	7.83	15.80	508	LR	PASS	NA	Clus. 2	0.11	0.89	TRUE
TVu-15350	Tanzania	-5.02	38.30	301	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-15352	Tanzania	-4.68	38.30	513	LR	PASS	NA	Clus. 1	0.86	0.14	TRUE
TVu-15353	Tanzania	-4.68	38.12	513	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-15354	Tanzania	-3.33	37.55	854	LR	PASS	NA	Clus. 1	0.93	0.07	TRUE
TVu-15355	Tanzania	-3.33	37.55	854	LR	PASS	NA	Clus. 1	1	0	TRUE

TVu-15360	Tanzania	-4.90	29.67	NA	LR	FILTER	TVu-13468, TVu-15107, TVu-15117, TVu-15131, TVu-15445, TVu-15490, TVu-9930	NA	NA	NA	FALSE
TVu-15362	Tanzania	-8.85	34.05	1,697	LR	PASS	NA	Clus. 1	0.99	0.01	TRUE
TVu-15365	Tanzania	-8.85	34.87	1,754	LR	PASS	NA	Clus. 1	0.83	0.17	TRUE
TVu-15368	Tanzania	-7.78	35.68	1,625	LR	PASS	NA	Clus. 1	0.89	0.11	TRUE
TVu-15371	Tanzania	-7.78	35.68	1,625	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-15375	Tanzania	-7.73	35.92	1,625	LR	PASS	NA	Clus. 1	0.84	0.16	TRUE
TVu-15378	Tanzania	-7.45	36.57	1,625	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-15379	Tanzania	-7.33	37.12	517	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-15381	Tanzania	-6.62	38.35	508	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-15388	Zimbabwe	-17.63	29.02	1,227	LR	PASS	TVu-13421, TVu-14255, TVu-15487, TVu-15601	Clus. 1	0.97	0.03	TRUE
TVu-15391	Lesotho	-29.30	27.58	1,600	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-15395	Lesotho	-28.83	28.21	1,850	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-15399	Lesotho	-29.70	27.52	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-15400	Lesotho	-29.70	27.52	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-15407	Lesotho	-30.47	27.75	1,532	LR	PASS	NA	Clus. 1	0.99	0.01	TRUE
TVu-15411	Lesotho	-30.20	27.95	NA	LR	PASS	NA	Clus. 1	0.97	0.03	TRUE

TVu-15413	Lesotho	-30	28.50	NA	LR	PASS	NA	Clus. 1	0.98	0.02	TRUE
TVu-15420	Lesotho	-29.13	27.63	1,551	LR	PASS	NA	Clus. 1	0.97	0.03	TRUE
TVu-15424	Lesotho	-28.58	28.25	1,655	LR	FILTER	TVu-14290, TVu-14325, TVu-14700, TVu-14721, TVu-14886, TVu-14890, TVu-14914, TVu-15968, TVu-16422, TVu-6838, TVu-7149	NA	NA	NA	FALSE
TVu-15426	Lesotho	-28.57	28.42	1,549	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-15431	Swaziland	-27.03	31.40	NA	LR	PASS	TVu-15442	Clus. 1	1	0	TRUE
TVu-15433	Swaziland	-26.12	31.15	1,276	LR	FILTER	TVu-15118, TVu-15571, TVu-9868, TVu-9869	NA	NA	NA	FALSE
TVu-15440	Swaziland	-27.10	31.22	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-15441	Swaziland	-26.48	31.40	764	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-15442	Swaziland	-26.48	31.40	764	LR	FILTER	TVu-15431	NA	NA	NA	FALSE
TVu-15444	Swaziland	-26.88	30.93	1,358	LR	PASS	NA	Clus. 1	0.98	0.02	TRUE

TVu-15445	Swaziland	-26.88	30.93	1,358	LR	FILTER	TVu-13468, TVu-15107, TVu-15117, TVu-15131, TVu-15360, TVu-15490, TVu-9930	NA	NA	NA	FALSE
TVu-15446	Swaziland	-26.37	31.43	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-15448	Swaziland	-26.37	31.43	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-15450	Zimbabwe	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-15452	Zimbabwe	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-15453	Zimbabwe	NA	NA	NA	LR	PASS	NA	Clus. 1	0.97	0.03	TRUE
TVu-15454	Zimbabwe	NA	NA	NA	LR	PASS	NA	Clus. 1	0.98	0.02	TRUE
TVu-15459	Zimbabwe	NA	NA	NA	LR	PASS	NA	Clus. 1	0.98	0.02	TRUE
TVu-15460	Zimbabwe	NA	NA	NA	LR	PASS	TVu-15486	Clus. 1	0.95	0.05	TRUE
TVu-15461	Zimbabwe	NA	NA	NA	LR	PASS	NA	Clus. 1	0.99	0.01	TRUE
TVu-15462	Zimbabwe	NA	NA	NA	LR	PASS	NA	Clus. 1	0.96	0.04	TRUE
TVu-15467	Zimbabwe	NA	NA	NA	LR	PASS	NA	Clus. 2	0.22	0.78	TRUE
TVu-15468	Zimbabwe	NA	NA	NA	LR	PASS	NA	Clus. 1	0.96	0.04	TRUE
TVu-15470	Zimbabwe	NA	NA	NA	LR	PASS	NA	Clus. 1	0.96	0.04	TRUE
TVu-15471	Zimbabwe	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-15472	Zimbabwe	NA	NA	NA	LR	PASS	NA	Clus. 1	0.97	0.03	TRUE
TVu-15474	Zimbabwe	NA	NA	NA	LR	PASS	NA	Clus. 1	0.97	0.03	TRUE
TVu-15477	Zimbabwe	NA	NA	NA	LR	PASS	NA	Clus. 1	0.97	0.03	TRUE
TVu-15482	Zimbabwe	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-15485	Zimbabwe	NA	NA	NA	LR	PASS	NA	Clus. 1	0.98	0.02	TRUE
TVu-15486	Zimbabwe	NA	NA	NA	LR	FILTER	TVu-15460	NA	NA	NA	FALSE

TVu-15487	Zimbabwe	NA	NA	NA	LR	FILTER	TVu-13421, TVu-14255, TVu-15388, TVu-15601	NA	NA	NA	FALSE
TVu-15488	Zimbabwe	NA	NA	NA	LR	PASS	NA	Clus. 1	0.98	0.02	TRUE
TVu-15490	Zimbabwe	NA	NA	NA	LR	FILTER	TVu-13468, TVu-15107, TVu-15117, TVu-15131, TVu-15360, TVu-15445, TVu-9930	NA	NA	NA	FALSE
TVu-15500	Burkina Faso	NA	NA	NA	BRM	PASS	NA	Admixed	0.37	0.63	TRUE
TVu-15503	Burkina Faso	NA	NA	NA	BRM	PASS	NA	Clus. 2	0	1	TRUE
TVu-15520	Burkina Faso	NA	NA	NA	BRM	PASS	NA	Clus. 2	0.13	0.87	TRUE
TVu-15523	Burkina Faso	NA	NA	NA	BRM	PASS	NA	Clus. 2	0.26	0.74	TRUE
TVu-15531	Burkina Faso	NA	NA	NA	BRM	PASS	NA	Clus. 2	0	1	TRUE
TVu-15533	Burkina Faso	NA	NA	NA	BRM	PASS	NA	Admixed	0.46	0.54	TRUE
TVu-15546	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 2	0.28	0.72	TRUE
TVu-15548	Ethiopia	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-15551	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.90	0.10	TRUE
TVu-15553	Burkina Faso	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-15554	Burkina Faso	NA	NA	NA	LR	PASS	NA	Clus. 1	0.93	0.07	TRUE
TVu-15555	Burkina Faso	NA	NA	NA	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-15560	Nigeria	NA	NA	NA	LR	PASS	NA	Clus. 1	0.92	0.08	TRUE

TVu-15563	Syrian Arab Republic	NA	NA	NA	LR	PASS	NA	Admixed	0.41	0.59	TRUE
TVu-15564	Syrian Arab Republic	NA	NA	NA	LR	PASS	NA	Clus. 2	0.13	0.87	TRUE
TVu-15565	Syrian Arab Republic	NA	NA	NA	LR	PASS	NA	Clus. 2	0.15	0.85	TRUE
TVu-15569	Botswana	NA	NA	NA	LR	FILTER	TVu-16440, TVu-6994	NA	NA	NA	FALSE
TVu-15570	Tanzania	-3.48	35.85	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-15571	Tanzania	NA	NA	NA	LR	PASS	TVu-15118, TVu-15433, TVu-9868, TVu-9869	Clus. 1	1	0	TRUE
TVu-15576	Chad	9.35	15.50	508	LR	PASS	NA	Clus. 2	0.15	0.85	TRUE
TVu-15578	Chad	8.58	16.43	401	LR	PASS	NA	Clus. 2	0.09	0.91	TRUE
TVu-15585	Malawi	NA	NA	NA	LR	PASS	NA	Admixed	0.64	0.36	TRUE
TVu-15589	Niger	13.70	6.85	373	LR	PASS	TVu-14963, TVu-14978, TVu-2887, TVu-7317, TVu-8123, TVu-8456	Clus. 2	0.07	0.93	TRUE
TVu-15591	Niger	13.92	5.95	252	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-15601	Zimbabwe	NA	NA	NA	LR	FILTER	TVu-13421, TVu-14255, TVu-15388, TVu-15487	NA	NA	NA	FALSE

TVu-15610	Nigeria	7.48	3.75	252	BRM	PASS	NA	Admixed	0.35	0.65	TRUE
TVu-15617	Nigeria	7.48	3.75	252	BRM	PASS	NA	Clus. 1	0.75	0.25	TRUE
TVu-15636	Nigeria	7.48	3.75	252	BRM	PASS	NA	Admixed	0.48	0.52	TRUE
TVu-15639	Nigeria	7.48	3.75	252	BRM	PASS	NA	Admixed	0.39	0.61	TRUE
TVu-15651	Nigeria	7.48	3.75	252	BRM	PASS	NA	Admixed	0.66	0.34	TRUE
TVu-15653	Nigeria	7.48	3.75	252	BRM	PASS	NA	Admixed	0.48	0.52	TRUE
TVu-15654	Nigeria	7.48	3.75	252	BRM	PASS	NA	Admixed	0.63	0.37	TRUE
TVu-15656	Nigeria	7.48	3.75	252	BRM	PASS	TVu-15777	Clus. 1	0.82	0.18	TRUE
TVu-15657	Nigeria	7.48	3.75	252	BRM	PASS	NA	Admixed	0.51	0.49	TRUE
TVu-15660	Nigeria	7.48	3.75	252	BRM	PASS	NA	Clus. 2	0.16	0.84	TRUE
TVu-15661	Nigeria	7.48	3.75	252	BRM	PASS	NA	Clus. 1	0.83	0.17	TRUE
TVu-15662	Nigeria	7.48	3.75	252	BRM	PASS	NA	Clus. 1	0.92	0.08	TRUE
TVu-15676	Nigeria	7.48	3.75	252	BRM	PASS	NA	Clus. 1	0.82	0.18	TRUE
TVu-15685	Nigeria	7.48	3.75	252	BRM	FILTER	TVu-202, TVu-238, TVu-243, TVu-697, TVu-990	NA	NA	NA	FALSE
TVu-15686	Nigeria	7.48	3.75	252	BRM	FILTER	TVu-12929	NA	NA	NA	FALSE
TVu-15687	Nigeria	7.48	3.75	252	BRM	PASS	NA	Admixed	0.34	0.66	TRUE
TVu-15688	Nigeria	7.48	3.75	252	BRM	PASS	NA	Clus. 2	0.29	0.71	TRUE
TVu-15694	Nigeria	7.48	3.75	252	BRM	PASS	NA	Admixed	0.44	0.56	TRUE
TVu-15695	Nigeria	7.48	3.75	252	BRM	PASS	NA	Admixed	0.43	0.57	TRUE
TVu-15710	Nigeria	7.48	3.75	252	BRM	PASS	NA	Admixed	0.51	0.49	TRUE
TVu-15719	Nigeria	7.48	3.75	252	BRM	PASS	NA	Admixed	0.45	0.55	TRUE
TVu-15721	Nigeria	7.48	3.75	252	BRM	PASS	NA	Admixed	0.59	0.41	TRUE
TVu-15725	Nigeria	7.48	3.75	252	BRM	PASS	NA	Clus. 1	0.78	0.22	TRUE
TVu-15742	Nigeria	7.48	3.75	252	BRM	PASS	NA	Clus. 1	0.72	0.28	TRUE
TVu-15751	Nigeria	7.48	3.75	252	BRM	PASS	NA	Clus. 2	0.25	0.75	TRUE
TVu-15762	Nigeria	7.48	3.75	252	BRM	PASS	NA	Admixed	0.42	0.58	TRUE
TVu-15775	Nigeria	7.48	3.75	252	BRM	PASS	NA	Admixed	0.62	0.38	TRUE
TVu-15777	Nigeria	7.48	3.75	252	BRM	FILTER	TVu-15656	NA	NA	NA	FALSE
TVu-15805	Nigeria	7.48	3.75	252	BRM	FILTER	TVu-13950	NA	NA	NA	FALSE
TVu-15810	Nigeria	7.48	3.75	252	BRM	PASS	NA	Admixed	0.67	0.33	TRUE

TVu-15811	Nigeria	7.48	3.75	252	BRM	PASS	NA	Admixed	0.57	0.43	TRUE
TVu-15834	Nigeria	7.48	3.75	252	BRM	PASS	NA	Clus. 2	0.20	0.80	TRUE
TVu-15840	Nigeria	7.48	3.75	252	BRM	FILTER	TVu-14904	NA	NA	NA	FALSE
TVu-15852	Chad	9.35	15.50	508	LR	PASS	NA	Clus. 2	0.06	0.94	TRUE
TVu-15853	Chad	10.85	16.12	324	LR	PASS	NA	Clus. 2	0	1	TRUE
TVu-15854	Niger	NA	NA	NA	LR	PASS	NA	Clus. 2	0.22	0.78	TRUE
TVu-15860	Yemen	NA	NA	NA	LR	PASS	NA	Admixed	0.32	0.68	TRUE
TVu-15861	Yemen	NA	NA	NA	LR	PASS	NA	Clus. 2	0.27	0.73	TRUE
TVu-15866	Nigeria	NA	NA	NA	LR	FILTER	TVu-14967, TVu-315, TVu-387, TVu-763	NA	NA	NA	FALSE
TVu-15873	Ghana	NA	NA	NA	LR	PASS	NA	Admixed	0.46	0.54	TRUE
TVu-15877	Ghana	NA	NA	NA	LR	PASS	NA	Admixed	0.46	0.54	TRUE
TVu-15878	Ghana	NA	NA	NA	LR	PASS	NA	Admixed	0.45	0.55	TRUE
TVu-15884	Ghana	NA	NA	NA	LR	FILTER	TVu-14626	NA	NA	NA	FALSE
TVu-15887	Ghana	NA	NA	NA	LR	PASS	NA	Clus. 2	0.15	0.85	TRUE
TVu-15890	Ghana	NA	NA	NA	LR	PASS	NA	Clus. 2	0.03	0.97	TRUE
TVu-15892	Ghana	NA	NA	NA	LR	PASS	NA	Admixed	0.37	0.63	TRUE
TVu-15895	Ghana	NA	NA	NA	LR	PASS	NA	Admixed	0.38	0.62	TRUE
TVu-15898	Ghana	NA	NA	NA	LR	PASS	NA	Clus. 1	0.76	0.24	TRUE
TVu-15900	Ghana	NA	NA	NA	LR	PASS	NA	Admixed	0.67	0.33	TRUE
TVu-15904	Ghana	NA	NA	NA	LR	PASS	NA	Admixed	0.45	0.55	TRUE
TVu-15910	Oman	NA	NA	NA	LR	PASS	NA	Clus. 1	0.73	0.27	TRUE
TVu-15913	Oman	NA	NA	NA	LR	FILTER	TVu-15151	NA	NA	NA	FALSE
TVu-15917	Oman	NA	NA	NA	LR	PASS	NA	Clus. 1	0.73	0.27	TRUE
TVu-15926	Oman	NA	NA	NA	LR	PASS	NA	Admixed	0.45	0.55	TRUE
TVu-15940	Oman	NA	NA	NA	LR	PASS	NA	Admixed	0.55	0.45	TRUE
TVu-15945	Oman	NA	NA	NA	LR	PASS	NA	Admixed	0.44	0.56	TRUE
TVu-15968	Botswana	NA	NA	NA	LR	FILTER	TVu-14290, TVu-14325,	NA	NA	NA	FALSE

							TVu-14700, TVu-14721, TVu-14886, TVu-14890, TVu-14914, TVu-15424, TVu-16422, TVu-6838, TVu-7149				
TVu-15973	Botswana	NA	NA	NA	LR	PASS	NA	Admixed	0.63	0.37	TRUE
TVu-15976	Botswana	NA	NA	NA	LR	PASS	NA	Admixed	0.46	0.54	TRUE
TVu-15979	Botswana	NA	NA	NA	LR	FILTER	TVu-14260, TVu-1832	NA	NA	NA	FALSE
TVu-15982	Botswana	NA	NA	NA	LR	PASS	NA	Clus. 1	0.82	0.18	TRUE
TVu-15985	Botswana	NA	NA	NA	LR	PASS	NA	Admixed	0.66	0.34	TRUE
TVu-15986	Botswana	NA	NA	NA	LR	PASS	TVu-4557	Admixed	0.49	0.51	TRUE
TVu-15988	Botswana	NA	NA	NA	LR	PASS	NA	Clus. 1	0.90	0.10	TRUE
TVu-15993	Botswana	NA	NA	NA	LR	PASS	NA	Admixed	0.65	0.35	TRUE
TVu-15995	Botswana	NA	NA	NA	LR	PASS	NA	Clus. 1	0.71	0.29	TRUE
TVu-16029	Somalia	2.25	45.42	9	LR	PASS	NA	Admixed	0.68	0.32	TRUE
TVu-16188	Gabon	0.15	10.78	NA	LR	PASS	NA	Clus. 2	0.12	0.88	TRUE
TVu-16191	Gabon	0.65	9.76	8	LR	PASS	NA	Clus. 2	0.11	0.89	TRUE
TVu-16200	Italy	NA	NA	NA	LR	PASS	NA	Clus. 2	0.15	0.85	TRUE
TVu-16220	Italy	NA	NA	NA	LR	PASS	NA	Clus. 2	0.28	0.72	TRUE
TVu-16222	Italy	NA	NA	NA	LR	PASS	NA	Clus. 2	0.13	0.87	TRUE
TVu-16225	Italy	NA	NA	NA	LR	PASS	NA	Clus. 2	0.14	0.86	TRUE

TVu-16229	Italy	NA	NA	NA	LR	PASS	NA	Clus. 2	0.14	0.86	TRUE
TVu-16237	Italy	NA	NA	NA	LR	PASS	NA	Admixed	0.41	0.59	TRUE
TVu-16239	Italy	NA	NA	NA	LR	PASS	NA	Admixed	0.52	0.48	TRUE
TVu-16253	Italy	NA	NA	NA	LR	PASS	NA	Admixed	0.54	0.46	TRUE
TVu-16268	Italy	NA	NA	NA	LR	PASS	NA	Clus. 2	0.14	0.86	TRUE
TVu-16269	Italy	NA	NA	NA	LR	PASS	NA	Admixed	0.59	0.41	TRUE
TVu-16278	Italy	NA	NA	NA	LR	PASS	NA	Clus. 2	0.13	0.87	TRUE
TVu-16280	Italy	NA	NA	NA	LR	PASS	NA	Clus. 2	0.15	0.85	TRUE
TVu-16298	Italy	NA	NA	NA	LR	PASS	NA	Admixed	0.37	0.63	TRUE
TVu-16300	Italy	NA	NA	NA	LR	PASS	NA	Admixed	0.42	0.58	TRUE
TVu-16304	Italy	NA	NA	NA	LR	PASS	NA	Admixed	0.58	0.42	TRUE
TVu-16320	Italy	NA	NA	NA	LR	PASS	TVu-16321	Admixed	0.33	0.67	TRUE
TVu-16334	Italy	NA	NA	NA	LR	PASS	NA	Admixed	0.39	0.61	TRUE
TVu-16336	Italy	NA	NA	NA	LR	PASS	NA	Admixed	0.31	0.69	TRUE
TVu-16343	Benin	7.18	2.01	252	LR	FILTER	TVu-10206, TVu-109, TVu-14891, TVu-16408, TVu-18, TVu-1975, TVu-1996, TVu-1999, TVu-36, TVu-374, TVu-745	NA	NA	NA	FALSE
TVu-16368	Benin	NA	NA	NA	LR	PASS	NA	Admixed	0.47	0.53	TRUE
TVu-16372	Benin	6.80	1.78	72	LR	PASS	NA	Admixed	0.47	0.53	TRUE
TVu-16390	Benin	6.68	2.68	NA	LR	PASS	NA	Admixed	0.48	0.52	TRUE
TVu-16393	Benin	6.65	2.01	78	LR	PASS	NA	Admixed	0.63	0.37	TRUE
TVu-16399	Benin	6.58	2.01	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-16400	Benin	6.58	2.01	NA	LR	PASS	NA	Admixed	0.63	0.37	TRUE

TVu-16403	Benin	9.50	2.25	75	LR	PASS	NA	Admixed	0.44	0.56	TRUE
TVu-16408	Benin	7.01	1.95	200	LR	FILTER	TVu-10206, TVu-109, TVu-14891, TVu-16343, TVu-18, TVu-1975, TVu-1996, TVu-1999, TVu-36, TVu-374, TVu-745	NA	NA	NA	FALSE
TVu-16414	Nigeria	NA	NA	NA	LR	FILTER	NA	NA	NA	NA	FALSE
TVu-16422	Chad	NA	NA	NA	LR	FILTER	TVu-14290, TVu-14325, TVu-14700, TVu-14721, TVu-14886, TVu-14890, TVu-14914, TVu-15424, TVu-15968,	NA	NA	NA	FALSE

							TVu-6838, TVu-7149				
TVu-16424	Chad	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-16429	Chad	NA	NA	NA	LR	PASS	NA	Clus. 1	0.90	0.10	TRUE
TVu-16430	Chad	NA	NA	NA	LR	PASS	NA	Clus. 1	0.87	0.13	TRUE
TVu-16431	Chad	9.25	18.65	365	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-16433	Chad	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-16438	Chad	8.20	16.18	508	LR	PASS	NA	Admixed	0.54	0.46	TRUE
TVu-16440	Botswana	NA	NA	NA	LR	FILTER	TVu-15569, TVu-6994	NA	NA	NA	FALSE
TVu-16449	Australia	NA	NA	NA	NA	PASS	TVu-3641	Admixed	0.33	0.67	TRUE
TVu-16459	Italy	NA	NA	NA	LR	PASS	NA	Clus. 1	1	0	TRUE
TVu-16461	Chad	12.17	16.06	NA	LR	FILTER	TVu-15259	NA	NA	NA	FALSE
TVu-16465	Nigeria	NA	NA	NA	BRM	PASS	NA	Admixed	0.46	0.54	TRUE
TVu-16467	Nigeria	NA	NA	NA	BRM	PASS	NA	Admixed	0.34	0.66	TRUE
TVu-16475	Nigeria	NA	NA	NA	BRM	PASS	NA	Admixed	0.51	0.49	TRUE
TVu-16483	Nigeria	NA	NA	NA	BRM	PASS	NA	Admixed	0.54	0.46	TRUE
TVu-16486	Nigeria	NA	NA	NA	BRM	PASS	NA	Clus. 2	0.25	0.75	TRUE
TVu-16487	Nigeria	NA	NA	NA	BRM	PASS	NA	Clus. 2	0.09	0.91	TRUE
TVu-16503	Nigeria	NA	NA	NA	BRM	PASS	NA	Clus. 2	0	1	TRUE
TVu-16504	Nigeria	NA	NA	NA	BRM	PASS	NA	Admixed	0.49	0.51	TRUE
TVu-16505	Nigeria	NA	NA	NA	BRM	PASS	NA	Admixed	0.49	0.51	TRUE
TVu-16510	Nigeria	NA	NA	NA	BRM	PASS	NA	Admixed	0.45	0.55	TRUE
TVu-16513	Nigeria	NA	NA	NA	BRM	PASS	NA	Clus. 2	0.15	0.85	TRUE
TVu-16516	Nigeria	NA	NA	NA	NA	PASS	NA	Clus. 2	0	1	TRUE
TVu-16521	Guinea	NA	NA	NA	LR	PASS	NA	Admixed	0.40	0.60	TRUE
TVu-16528	Guinea	NA	NA	NA	LR	PASS	NA	Admixed	0.31	0.69	TRUE
TVu-16531	Guinea	NA	NA	NA	LR	PASS	NA	Clus. 2	0.04	0.96	TRUE
TVu-16534	Guinea	NA	NA	NA	LR	PASS	NA	Admixed	0.43	0.57	TRUE
TVu-16536	Guinea	NA	NA	NA	LR	PASS	NA	Clus. 2	0.02	0.98	TRUE
TVu-16544	Guinea	NA	NA	NA	LR	PASS	NA	Clus. 2	0.01	0.99	TRUE
TVu-16545	Guinea	NA	NA	NA	LR	PASS	TVu-16573	Admixed	0.59	0.41	TRUE
TVu-16550	Guinea	NA	NA	NA	LR	PASS	NA	Admixed	0.42	0.58	TRUE

TVu-16554	Guinea	NA	NA	NA	LR	PASS	NA	Clus. 2	0.23	0.77	TRUE
TVu-16555	Guinea	NA	NA	NA	LR	PASS	NA	Clus. 2	0.25	0.75	TRUE
TVu-16566	Guinea	NA	NA	NA	LR	PASS	NA	Clus. 2	0.27	0.73	TRUE
TVu-16573	Guinea	NA	NA	NA	LR	FILTER	TVu-16545	NA	NA	NA	FALSE
TVu-16574	Guinea	NA	NA	NA	LR	PASS	NA	Admixed	0.39	0.61	TRUE
TVu-16575	Guinea	NA	NA	NA	LR	PASS	NA	Clus. 2	0.28	0.72	TRUE
TVu-16594	Mali	NA	NA	NA	NA	PASS	NA	Clus. 1	1	0	TRUE
TVu-16602	Mali	NA	NA	NA	NA	PASS	NA	Clus. 2	0.02	0.98	TRUE
TVu-16607	Mali	NA	NA	NA	NA	PASS	NA	Clus. 2	0.20	0.80	TRUE
TVu-16610	Mali	NA	NA	NA	NA	PASS	NA	Clus. 2	0.16	0.84	TRUE
TVu-16616	Mali	NA	NA	NA	NA	PASS	NA	Clus. 1	0.95	0.05	TRUE
TVu-16624	Mali	NA	NA	NA	NA	PASS	NA	Clus. 2	0.30	0.70	TRUE
TVu-16628	Mali	NA	NA	NA	NA	PASS	NA	Clus. 1	1	0	TRUE
TVu-16637	Zambia	NA	NA	NA	LR	PASS	NA	Clus. 1	0.93	0.07	TRUE
TVu-16646	Nigeria	NA	NA	NA	BRM	PASS	NA	Admixed	0.37	0.63	TRUE
TVu-16722	Nigeria	7.48	3.75	252	BRM	PASS	NA	Clus. 2	0.23	0.77	TRUE
TVu-16158	Algeria	36.71	3.16	NA	NA	FILTER	NA	NA	NA	NA	FALSE
TVu-1975	NA	NA	NA	NA	NA	FILTER	TVu-10206, TVu-109, TVu-14891, TVu-16343, TVu-16408, TVu-18, TVu-1996, TVu-1999, TVu-36, TVu-374, TVu-745	NA	NA	NA	FALSE
TVu-16402	Benin	NA	NA	NA	NA	PASS	NA	Admixed	0.43	0.57	TRUE
TVu-16358	Benin	NA	NA	NA	NA	PASS	NA	Clus. 2	0	1	TRUE

TVu-14256	Botswana	NA	NA	NA	NA	PASS	NA	Clus. 2	0	1	TRUE
TVu-14266	Botswana	NA	NA	NA	NA	PASS	NA	Admixed	0.54	0.46	TRUE
TVu-16317	Italy	NA	NA	NA	NA	PASS	NA	Clus. 2	0.15	0.85	TRUE
TVu-16321	Italy	NA	NA	NA	NA	FILTER	TVu-16320	NA	NA	NA	FALSE
TVu-16409	Kenya	NA	NA	NA	NA	FILTER	NA	NA	NA	NA	FALSE
TVu-15609	Nigeria	NA	NA	NA	NA	PASS	NA	Clus. 1	0.97	0.03	TRUE
TVu-14504	Senegal	NA	NA	NA	NA	PASS	NA	Clus. 1	0.83	0.17	TRUE
TVu-14463	Senegal	NA	NA	NA	NA	PASS	NA	Clus. 2	0.16	0.84	TRUE
TVu-14485	Senegal	NA	NA	NA	NA	PASS	NA	Clus. 1	1	0	TRUE
TVu-14630	Zambia	NA	NA	NA	NA	PASS	NA	Clus. 1	0.90	0.10	TRUE
TVu-16454	China	NA	NA	NA	NA	PASS	NA	Admixed	0.56	0.44	TRUE

Columns: Lat. = Latitude, Long. = Longitude, Elev. = Elevation, Bio. Status = Biological Status, Geno. filter = Genotype filter, K2 assign. = K2 assignment, Clus1 anc. = Cluster 1 ancestry, Clus2 anc. = Cluster 2 ancestry. Values for Bio. Status: LR = Traditional cultivar/ Landrace, BRM = Breeding/ Research Material.

Table 3.S2 List of phenotypes used in GWAS

ID	Phenotype	Category 1	Category 2	Type	Recoded	Combined IITA traits	Used breeding
1	Days to first flowering	Days to first flowering	Maturity	CONTINUOUS	FALSE	NA	Y
2	Days to first ripe pod	Days to first ripe pod	Maturity	CONTINUOUS	FALSE	NA	Y
3	No of main branches	No of main branches	Plant_Architecture	CONTINUOUS	FALSE	NA	N
4	No of main stem nodes	No of main stem nodes	Plant_Architecture	CONTINUOUS	FALSE	NA	N
5	Terminal leaflet length	Terminal leaflet length	Leaf_Morphology	CONTINUOUS	FALSE	NA	N
6	Terminal leaflet width	Terminal leaflet width	Leaf_Morphology	CONTINUOUS	FALSE	NA	N
7	Pod length	Pod length	Pod_Morphology	CONTINUOUS	FALSE	NA	N
8	Pod width	Pod width	Pod_Morphology	CONTINUOUS	FALSE	NA	N
9	No of locules/pod	No of locules/pod	Pod_Morphology	CONTINUOUS	FALSE	NA	N
10	Number of pods affected by Maruca	Number of pods affected by Maruca	Disease_Suceptibility	CONTINUOUS	FALSE	NA	N
11	Number of pods unaffected by Maruca	Number of pods unaffected by Maruca	Disease_Suceptibility	CONTINUOUS	FALSE	NA	N
12	Number of pods affected by Laspeyresia	Number of pods affected by Laspeyresia	Disease_Suceptibility	CONTINUOUS	FALSE	NA	N
13	Number of pods unaffected by Laspeyresia	Number of pods unaffected by Laspeyresia	Disease_Suceptibility	CONTINUOUS	FALSE	NA	N

14	Percentage of Sulphur (combustion & titration)	Percentage of Sulphur (combustion & titration)	Disease_Suceptibility	CONTINUOUS	FALSE	NA	N
15	Percentage of Nitrogen (colorimetric analysis)	Percentage of Nitrogen (colorimetric analysis)	Disease_Suceptibility	CONTINUOUS	FALSE	NA	N
53	Terminal leaflet shape_Globose	Terminal leaflet shape	Leaf_Morphology	BINARY	TRUE	NA	N
54	Terminal leaflet shape_Hastate (Lanceolate)	Terminal leaflet shape	Leaf_Morphology	BINARY	TRUE	NA	N
55	Terminal leaflet shape_Sub-Globose	Terminal leaflet shape	Leaf_Morphology	BINARY	TRUE	NA	N
56	Terminal leaflet shape_Sub-hastate	Terminal leaflet shape	Leaf_Morphology	BINARY	TRUE	NA	N
66	Eye pattern_A10:Eye absent	Eye pattern	Seed_Pigmentation	BINARY	TRUE	NA	N
71	Eye pattern_A60:the eye fills the narrow groove all around the hilum. similar to Kabba (K) group but no specks on body. flower pigment pattern is 1.	Eye pattern	Seed_Pigmentation	BINARY	TRUE	NA	N
72	Eye pattern_A61:Similar to A60 but	Eye pattern	Seed_Pigmentation	BINARY	TRUE	NA	N

	flower pigment pattern is 5.						
73	Eye pattern_A70:eye starts in a groove at either side of the hilum and spills out slightly in front of it. flower pigment pattern is 1.	Eye pattern	Seed_Pigmentation	BINARY	TRUE	NA	N
74	Eye pattern_A81:A thin line of pigment starts at back of the hilum (h) and moves along each side of it. A narrow clear space found b/w eye & H. Flower pigment pattern is 6.	Eye pattern	Seed_Pigmentation	BINARY	TRUE	NA	N
97	Eye pattern_S00:Self Colored	Eye pattern	Seed_Pigmentation	BINARY	TRUE	NA	N
1C	Pattern of pigmentation on plant	Pattern of pigmentation on plant	Plant_Pigmentation	BINARY	TRUE	NA	N
2C	Pattern of pigmentation on flower	Pattern of pigmentation on flower	Flower_Pigmentation	BINARY	TRUE	NA	N
226	Incidence of Other Diseases_Nothing	Incidence of Other Diseases	Disease_Suceptibility	BINARY	TRUE	NA	N

227	Incidence of Other Diseases_Red freckle - Septoria	Incidence of Other Diseases	Disease_Suceptibility	BINARY	TRUE	NA	N
228	Incidence of Other Diseases_Sclerotium rot	Incidence of Other Diseases	Disease_Suceptibility	BINARY	TRUE	NA	N
229	Incidence of Other Diseases_Undefined code	Incidence of Other Diseases	Disease_Suceptibility	BINARY	TRUE	NA	N
233	Incidence of Other Diseases_Wet stem rot	Incidence of Other Diseases	Disease_Suceptibility	BINARY	TRUE	NA	N
3C	Pattern of pigmentation on green pod	Pattern of pigmentation on green pod	Pod_Pigmentation	BINARY	TRUE	NA	N
4C	Plant growth habit	Plant growth habit	Plant_Architecture	DISCRETE	TRUE	NA	Y
5C	Twining tendency	Twining tendency	Plant_Architecture	DISCRETE	TRUE	NA	N
6C	Growth vigor	Growth vigor	Plant_Architecture	DISCRETE	TRUE	NA	N
7C	Determinacy	Determinacy	Plant_Architecture	DISCRETE	TRUE	NA	N
8C	Peduncle length	Peduncle length	Inflorescence_Morphology	DISCRETE	TRUE	NA	N
9C	Raceme position	Raceme position	Inflorescence_Morphology	DISCRETE	TRUE	NA	N
10C	No of pods/peduncle	No of pods/peduncle	Inflorescence_Morphology	DISCRETE	TRUE	NA	Y
11C	Pod attachment to peduncle	Pod attachment to peduncle	Inflorescence_Morphology	DISCRETE	TRUE	NA	N
12C	Pod shape	Pod shape	Pod_Morphology	DISCRETE	TRUE	NA	N
13C	Hilum ring	Eye pattern	Seed_Pigmentation	BINARY	TRUE	Eye pattern_A20:line by hilum	N

						(H).straight:narrow band of pigment on each side of H: similar to E10 but pigment does not extend completely behind H.; Eye pattern_A40:small hilum ring. similar to N40 but eye more restricted in front of hilum.flower pigment pattern is 1.; Eye pattern_A41:restricted hilum ring. similar to A40 but flower pigment pattern is 3.; Eye pattern_A42:limited hilum ring. similar to A40. differentiated definitely by crossing.; Eye pattern_N40:Narrow Eye(Hilum ring).Eye fills the narrow groove(G.) around hilum(H.) & spills out of this G in front of the H for a short distance & presents an indistinct margin in front; Eye pattern_N41:Hilum ring:specks similar	

						to N40 but with specks distributed uniformly over body.; Eye pattern_N80:Hilum ring:speckled keel. similar to N40 but with specks predominantly on keel.; Eye pattern_N84:Hilum ring:lightly speckled keel. similar to N80 but with specks less dense.	
14C	Small eye	Eye pattern	Seed_Pigmentation	BINARY	TRUE	Eye pattern_E10:Small eye.Eye encircles the back of hilum(H.) in a narrow ring:widens slightly at the sides of H. & extends in a straight band at either sides of H.; Eye pattern_E30:Small eye-large. similar to E10: but eye at sides of the hilum is wider than that of E10.; Eye pattern_E50:Broad eye. eye is triangle:with the hilum inside: the	N

						front of the hilum resting on the base of the triangle.; Eye pattern_E58:Broad eye:spotted keel.similar to E40 but with spotted keel.	
15C	Large eye	Eye pattern	Seed_Pigmentation	BINARY	TRUE	Eye pattern_H11:Large eye. Heart shaped eye: with indentation at front of hilum; Eye pattern_H18:Large eye: spotted keel. Similar to H11 but with spotted keel; Eye pattern_H28:Large eye: spoted keel: dilute. Similar to H18 but with flower pigment pattern 1; Eye pattern_H29:Very Large eye. a large semi-circle of pigment almost covering each half of the seed: with the center of the beans of each semi-circle at the hilum; Eye pattern_H30:Large eye to	N

						holstein.similar to H11 but splashes of pigment spilling over in front of hilum: the splashes having a distinct margin; Eye pattern_H38:Large eye to holstein.spotted keel. similar to H30 but with splashes of pigment on keel.	
16C	Holstein	Eye pattern	Seed_Pigmentation	BINARY	TRUE	Eye pattern_H40:holstein 40 to 60.pigment extends out in front of hilum from the large eye and covers 40-60% of seed; Eye pattern_H48:holstein 40 to 60:spotted keel. Similar to H40 with splashes of pigment on keel joining with the pigment of the eye; Eye pattern_H60:holstein 60 to 80l. Pigment extends out in front of hilum from the large eye and covers 60-80% of the seed.; Eye	N

						pattern_H80:holstein 80 to 95. Pigment extends out in front of hilum from the large eye and covers 60-80% of the seed.	
17C	Speckled	Eye pattern	Seed_Pigmentation	BINARY	TRUE	Eye pattern_K10:Densely speckled. speckles uniform over body; Eye pattern_K20:Lightly speckled. speckles uniform over body; Eye pattern_K30:Very Lightly speckled. speckles uniform over body; Eye pattern_K38:speckled keel.	N
18C	Watson	Eye pattern	Seed_Pigmentation	BINARY	TRUE	Eye pattern_W11:Normal Watson; Eye pattern_W15:Watson with dark or speckled body; Eye pattern_W20:Watson dilute.The margin in front of the hilum becomes more restricted; Eye pattern_W30:Watson blotched.Large	N

						blotches of pigment from eye move onto body; Eye pattern_W31:Watson blotched:dilute.blotches are much less pronounced. Flowering pigment pattern is 4; Eye pattern_W35:Watson speckled. Speckling tends to occur in blotches; Eye pattern_W55:Watson: nearly self colored. Eye covers almost entire seed except for small portion of micropylar end.	
19C	Black	Eye color	Seed_Pigmentation	BINARY	TRUE	Eye color_B10:Purple; Eye color_B20:Solid black: gray body; Eye color_B30:Solid black; Eye color_B41:black with light spots of tan; Eye color_B45:black with light spots of red; Eye color_B51:black	Y

						spots with speckling on tan	
20C	Blue	Eye color	Seed_Pigmentation	BINARY	TRUE	Eye color_B71:blue covering tan; Eye color_B75:blue covering red; Eye color_T16:buff with blue tinge; Eye color_X71:blue covering mottled on tan; Eye color_X81:blue covering solid brown	N
21C	Tan	Eye color	Seed_Pigmentation	BINARY	TRUE	Eye color_M11:brown mottling on tan; Eye color_M60:solid brown over tan; Eye color_S11:Speckling on tan; Eye color_S61:Speckling on tan with clear areas:as though speckles had erased with random strokes; Eye color_T10:Tan or buff; Eye color_T20:dark tan; Eye color_T41:light orange tan; Eye color_T44:medium orange tan; Eye color_V11:Speckled with mottling on tan; Eye	N

						color_V61:Speckled with clear areas and mottling on buff; Eye color_V71:solid brown with speckling on tan; Eye color_X51:black spots with mottling on tan	
22C	Red	Eye color	Seed_Pigmentation	BINARY	TRUE	Eye color_M12:brown mottling on orange; Eye color_M15:brown mottling on red; Eye color_M65:solid brown over red; Eye color_R10:maroon; Eye color_R40:red; Eye color_R70:pink; Eye color_S15:Speckling on red; Eye color_S62:Speckling on orange with clear areas; Eye color_X55:black spots with mottling on red	N
23C	Brown	Eye color	Seed_Pigmentation	BINARY	TRUE	Eye color_S63:Speckling on brown with clear areas; Eye color_T57:reddish brown; Eye	N

						color_T60:brown; Eye color_X61:black spots on solid brown	
24C	White	Eye color	Seed_Pigmentation	BINARY	TRUE	Eye color_W20:white body: used only with A10 eye; Eye color_W21:white body: black eye; Eye color_W22:white body: red eye; Eye color_W23:white body: mottled eye; Eye color_W25:white body: tan eye	N
25C	Cream	Eye color	Seed_Pigmentation	BINARY	TRUE	Eye color_W40:cream body: used only with A10 eye; Eye color_W41:cream body: black eye; Eye color_W42:cream body: red eye; Eye color_W43:cream body: mottled eye; Eye color_W45:cream body: tan eye	N
26C	Brown splash	Eye color	Seed_Pigmentation	BINARY	TRUE	Eye color_W60:brown splash on body:used only with A10 eye; Eye color_W61:brown	N

						splash on body: black eye; Eye color_W62:brown splash on body: red eye; Eye color_W65:brown splash on body: tan eye	
27C	Gray	Eye color	Seed_Pigmentation	BINARY	TRUE	Eye color_W70:gray body:used only with A10 eye; Eye color_W71:gray body: black eye; Eye color_W80:gray body with brown splash: used only with A10 eye; Eye color_W81:gray body with brown splash: black eye	N
28C	Testa texture	Testa texture	Seed_Morphology	DISCRETE	TRUE	NA	Y
29C	Seed size	Seed size	Seed_Morphology	DISCRETE	TRUE	NA	Y
30C	Seed length	Seed length	Seed_Morphology	DISCRETE	TRUE	NA	N
31C	Seed thickness	Seed thickness	Seed_Morphology	DISCRETE	TRUE	NA	N
32C	Seed Crowding in pod	Seed Crowding in pod	Seed_Morphology	DISCRETE	TRUE	NA	N
33C	Incidence of Leaf Spot (C. Canescens)	Incidence of Leaf Spot (C. Canescens)	Disease_Suceptibility	BINARY	TRUE	NA	N
34C	Incidence of Leaf Spot (C. Cruenta)	Incidence of Leaf Spot (C. Cruenta)	Disease_Suceptibility	DISCRETE	TRUE	NA	N

35C	Incidence of Bacterial Pustule	Incidence of Bacterial Pustule	Disease_Suceptibility	DISCRETE	TRUE	NA	N
36C	Incidence of Bacterial Blight	Incidence of Bacterial Blight	Disease_Suceptibility	BINARY	TRUE	NA	N
37C	Incidence of Target Spot	Incidence of Target Spot	Disease_Suceptibility	BINARY	TRUE	NA	N
38C	Incidence of Rust	Incidence of Rust	Disease_Suceptibility	BINARY	TRUE	NA	N
39C	Incidence of Cowpea Mosaic Virus	Incidence of Cowpea Mosaic Virus	Disease_Suceptibility	DISCRETE	TRUE	NA	N
40C	Incidence of Anthracnose	Incidence of Anthracnose	Disease_Suceptibility	DISCRETE	TRUE	NA	N
41C	Web blight	Incidence of Other Diseases	Disease_Suceptibility	DISCRETE	TRUE	Incidence of Other Diseases_Web blight - moderate; Incidence of Other Diseases_Web blight - severe; Incidence of Other Diseases_Web blight - unspecified	N

Table 3.S3 Phenotype codes by state for GWAS

Phenotype	**IITA phenotype**	**State**	**Value**
Black	Eye color_B10:Purple	control	0
Black	Eye color_B10:Purple	case	1
Black	Eye color_B20:Solid black: gray body	control	0
Black	Eye color_B20:Solid black: gray body	case	1
Black	Eye color_B30:Solid black	control	0
Black	Eye color_B30:Solid black	case	1
Black	Eye color_B41:black with light spots of tan	control	0
Black	Eye color_B41:black with light spots of tan	case	1
Black	Eye color_B45:black with light spots of red	control	0
Black	Eye color_B45:black with light spots of red	case	1
Black	Eye color_B51:black spots with speckling on tan	control	0
Black	Eye color_B51:black spots with speckling on tan	case	1
Blue	Eye color_B71:blue covering tan	control	0
Blue	Eye color_B71:blue covering tan	case	1
Blue	Eye color_B75:blue covering red	control	0
Blue	Eye color_B75:blue covering red	case	1
Blue	Eye color_T16:buff with blue tinge	control	0
Blue	Eye color_T16:buff with blue tinge	case	1
Blue	Eye color_X71:blue covering mottled on tan	control	0
Blue	Eye color_X71:blue covering mottled on tan	case	1
Blue	Eye color_X81:blue covering solid brown	control	0
Blue	Eye color_X81:blue covering solid brown	case	1
Brown	Eye color_S63:Speckling on brown with clear areas	control	0
Brown	Eye color_S63:Speckling on brown with clear areas	case	1
Brown	Eye color_T57:reddish brown	control	0
Brown	Eye color_T57:reddish brown	case	1
Brown	Eye color_T60:brown	control	0
Brown	Eye color_T60:brown	case	1
Brown	Eye color_X61:black spots on solid brown	control	0
Brown	Eye color_X61:black spots on solid brown	case	NA
Brown splash	Eye color_W60:brown splash on body:used only with A10 eye	control	0
Brown splash	Eye color_W60:brown splash on body:used only with A10 eye	case	1
Brown splash	Eye color_W61:brown splash on body: black eye	control	0
Brown splash	Eye color_W61:brown splash on body: black eye	case	1
Brown splash	Eye color_W62:brown splash on body: red eye	control	0

Brown splash	Eye color_W62:brown splash on body: red eye	case	1
Brown splash	Eye color_W65:brown splash on body: tan eye	control	0
Brown splash	Eye color_W65:brown splash on body: tan eye	case	1
Cream	Eye color_W40:cream body: used only with A10 eye	control	0
Cream	Eye color_W40:cream body: used only with A10 eye	case	1
Cream	Eye color_W41:cream body: black eye	control	0
Cream	Eye color_W41:cream body: black eye	case	1
Cream	Eye color_W42:cream body: red eye	control	0
Cream	Eye color_W42:cream body: red eye	case	1
Cream	Eye color_W43:cream body: mottled eye	control	0
Cream	Eye color_W43:cream body: mottled eye	case	1
Cream	Eye color_W45:cream body: tan eye	control	0
Cream	Eye color_W45:cream body: tan eye	case	1
Determinacy	Determinacy	Indeterminate main stem	1
Determinacy	Determinacy	Determinate main stem	2
Gray	Eye color_W70:gray body:used only with A10 eye	control	0
Gray	Eye color_W70:gray body:used only with A10 eye	case	1
Gray	Eye color_W71:gray body: black eye	control	0
Gray	Eye color_W71:gray body: black eye	case	1
Gray	Eye color_W80:gray body with brown splash: used only with A10 eye	control	0
Gray	Eye color_W80:gray body with brown splash: used only with A10 eye	case	1
Gray	Eye color_W81:gray body with brown splash: black eye	control	0
Gray	Eye color_W81:gray body with brown splash: black eye	case	NA
Growth vigor	Growth vigor	Vigorous - Height < 37.5cm and Width < 75cm	1
Growth vigor	Growth vigor	Intermediate - Height > 37.5cm or Width > 75cm	2
Growth vigor	Growth vigor	Vigorous - Height > 37.5cm and Width > 75cm	3
Growth vigor	Growth vigor	Very Vigorous - Height > 50cm and Width > 1m	4

Hilum ring	Eye pattern_A20:line by hilum (H).straight:narrow band of pigment on each side of H: similar to E10 but pigment does not extend completely behind H.	control	0
Hilum ring	Eye pattern_A20:line by hilum (H).straight:narrow band of pigment on each side of H: similar to E10 but pigment does not extend completely behind H.	case	1
Hilum ring	Eye pattern_A40:small hilum ring. similar to N40 but eye more restricted in front of hilum.flower pigment pattern is 1.	control	0
Hilum ring	Eye pattern_A40:small hilum ring. similar to N40 but eye more restricted in front of hilum.flower pigment pattern is 1.	case	1
Hilum ring	Eye pattern_A41:restricted hilum ring. similar to A40 but flower pigment pattern is 3.	control	0
Hilum ring	Eye pattern_A41:restricted hilum ring. similar to A40 but flower pigment pattern is 3.	case	1
Hilum ring	Eye pattern_A42:limited hilum ring. similar to A40. differentiated definitely by crossing.	control	0
Hilum ring	Eye pattern_A42:limited hilum ring. similar to A40. differentiated definitely by crossing.	case	1
Hilum ring	Eye pattern_N40:Narrow Eye(Hilum ring).Eye fills the narrow groove(G.) around hilum(H.) & spills out of this G in front of the H for a short distance & presents an indistinct margin in front	control	0
Hilum ring	Eye pattern_N40:Narrow Eye(Hilum ring).Eye fills the narrow groove(G.) around hilum(H.) & spills out of this G in front of the H for a short distance & presents an indistinct margin in front	case	1
Hilum ring	Eye pattern_N41:Hilum ring:specks similar to N40 but with specks distributed uniformly over body.	control	0
Hilum ring	Eye pattern_N41:Hilum ring:specks similar to N40 but with specks distributed uniformly over body.	case	1
Hilum ring	Eye pattern_N80:Hilum ring:speckled keel. similar to N40 but with specks predominantly on keel.	control	0
Hilum ring	Eye pattern_N80:Hilum ring:speckled keel. similar to N40 but with specks predominantly on keel.	case	1
Hilum ring	Eye pattern_N84:Hilum ring:lightly speckled keel. similar to N80 but with specks less dense.	control	0

Hilum ring	Eye pattern_N84:Hilum ring:lightly speckled keel. similar to N80 but with specks less dense.	case	1
Holstein	Eye pattern_H40:holstein 40 to 60.pigment extends out in front of hilum from the large eye and covers 40-60% of seed	control	0
Holstein	Eye pattern_H40:holstein 40 to 60.pigment extends out in front of hilum from the large eye and covers 40-60% of seed	case	1
Holstein	Eye pattern_H48:holstein 40 to 60:spotted keel. Similar to H40 with splashes of pigment on keel joining with the pigment of the eye	control	0
Holstein	Eye pattern_H48:holstein 40 to 60:spotted keel. Similar to H40 with splashes of pigment on keel joining with the pigment of the eye	case	1
Holstein	Eye pattern_H60:holstein 60 to 80l. Pigment extends out in front of hilum from the large eye and covers 60-80% of the seed.	control	0
Holstein	Eye pattern_H60:holstein 60 to 80l. Pigment extends out in front of hilum from the large eye and covers 60-80% of the seed.	case	1
Holstein	Eye pattern_H80:holstein 80 to 95. Pigment extends out in front of hilum from the large eye and covers 60-80% of the seed.	control	0
Holstein	Eye pattern_H80:holstein 80 to 95. Pigment extends out in front of hilum from the large eye and covers 60-80% of the seed.	case	1
Incidence of Anthracnose	Incidence of Anthracnose	None or hypersensitive	0
Incidence of Anthracnose	Incidence of Anthracnose	Few small lesions	1
Incidence of Anthracnose	Incidence of Anthracnose	Many small lesions	2
Incidence of Anthracnose	Incidence of Anthracnose	Many large lesions	3
Incidence of Anthracnose	Incidence of Anthracnose	Few large lesions	4
Incidence of Anthracnose	Incidence of Anthracnose	Coalesced lesions	5
Incidence of Anthracnose	Incidence of Anthracnose	Segregating	6
Incidence of Bacterial Blight	Incidence of Bacterial Blight	None	0

Incidence of Bacterial Blight	Incidence of Bacterial Blight	Some	1
Incidence of Bacterial Pustule	Incidence of Bacterial Pustule	None	0
Incidence of Bacterial Pustule	Incidence of Bacterial Pustule	Very light:occasional scattered leaf spots	1
Incidence of Bacterial Pustule	Incidence of Bacterial Pustule	Light:scattered spots, no more than 1 per leaf, on more than half the leaves	2
Incidence of Bacterial Pustule	Incidence of Bacterial Pustule	Light/Moderate:2 or 3 spots/leaf, on few leaves	3
Incidence of Bacterial Pustule	Incidence of Bacterial Pustule	Moderate:2 or 3 spots/leaf, on most of the leaves	4
Incidence of Bacterial Pustule	Incidence of Bacterial Pustule	Moderate/Severe: heavy spotting on a few leaves	5
Incidence of Bacterial Pustule	Incidence of Bacterial Pustule	Segregating	6
Incidence of Bacterial Pustule	Incidence of Bacterial Pustule	Severe:Heavy spotting on most leaves with yellowing	7
Incidence of Cowpea Mosaic Virus	Incidence of Cowpea Mosaic Virus	None	0
Incidence of Cowpea Mosaic Virus	Incidence of Cowpea Mosaic Virus	Yellow mosaic	1
Incidence of Cowpea Mosaic Virus	Incidence of Cowpea Mosaic Virus	Green mottle	2
Incidence of Cowpea Mosaic Virus	Incidence of Cowpea Mosaic Virus	Bright yellow fleck	3
Incidence of Leaf Spot (C. Canescens)	Incidence of Leaf Spot (C. Canescens)	None	0
Incidence of Leaf Spot (C. Canescens)	Incidence of Leaf Spot (C. Canescens)	Very light:occasional scattered leaf spots	1
Incidence of Leaf Spot (C. Cruenta)	Incidence of Leaf Spot (C. Cruenta)	None	0

Incidence of Leaf Spot (C. Cruenta)	Incidence of Leaf Spot (C. Cruenta)	Very light:occasional scattered leaf spots	1
Incidence of Leaf Spot (C. Cruenta)	Incidence of Leaf Spot (C. Cruenta)	Light:scattered spots, no more than 1 per leaf, on more than half the leaves	2
Incidence of Leaf Spot (C. Cruenta)	Incidence of Leaf Spot (C. Cruenta)	Light/Moderate:2 or 3 spots/leaf, on few leaves	3
Incidence of Leaf Spot (C. Cruenta)	Incidence of Leaf Spot (C. Cruenta)	Moderate:2 or 3 spots/leaf, on most of the leaves	4
Incidence of Leaf Spot (C. Cruenta)	Incidence of Leaf Spot (C. Cruenta)	Moderate/Severe: heavy spotting on a few leaves	5
Incidence of Leaf Spot (C. Cruenta)	Incidence of Leaf Spot (C. Cruenta)	Segregating	6
Incidence of Leaf Spot (C. Cruenta)	Incidence of Leaf Spot (C. Cruenta)	Severe:Heavy spotting on most leaves with yellowing	7
Incidence of Rust	Incidence of Rust	None	0
Incidence of Rust	Incidence of Rust	Some	1
Incidence of Target Spot	Incidence of Target Spot	None	0
Incidence of Target Spot	Incidence of Target Spot	Some	1
Large eye	Eye pattern_H11:Large eye. Heart shaped eye: with indentation at front of hilum	control	0
Large eye	Eye pattern_H11:Large eye. Heart shaped eye: with indentation at front of hilum	case	1
Large eye	Eye pattern_H18:Large eye: spotted keel. Similar to H11 but with spotted keel	control	0
Large eye	Eye pattern_H18:Large eye: spotted keel. Similar to H11 but with spotted keel	case	1
Large eye	Eye pattern_H28:Large eye: spoted keel: dilute. Similar to H18 but with flower pigment pattern 1	control	0
Large eye	Eye pattern_H28:Large eye: spoted keel: dilute. Similar to H18 but with flower pigment pattern 1	case	1
Large eye	Eye pattern_H29:Very Large eye. a large semi-circle of pigment almost covering each half of the seed: with the center of the beans of each semi-circle at the hilum	control	0

Large eye	Eye pattern_H29:Very Large eye. a large semi-circle of pigment almost covering each half of the seed: with the center of the beans of each semi-circle at the hilum	case	1
Large eye	Eye pattern_H30:Large eye to holstein.similar to H11 but splashes of pigment spilling over in front of hilum: the splashes having a distinct margin	control	0
Large eye	Eye pattern_H30:Large eye to holstein.similar to H11 but splashes of pigment spilling over in front of hilum: the splashes having a distinct margin	case	1
Large eye	Eye pattern_H38:Large eye to holstein.spotted keel. similar to H30 but with splashes of pigment on keel.	control	0
Large eye	Eye pattern_H38:Large eye to holstein.spotted keel. similar to H30 but with splashes of pigment on keel.	case	1
No of pods/peduncle	No of pods/peduncle	Less than 2	1
No of pods/peduncle	No of pods/peduncle	2 to 3	2
No of pods/peduncle	No of pods/peduncle	4 or more	3
Pattern of pigmentation on flower	Pattern of pigmentation on flower	None	0
Pattern of pigmentation on flower	Pattern of pigmentation on flower	Completely Pigmented	1
Pattern of pigmentation on flower	Pattern of pigmentation on flower	Wing & Standard petal has pigmented margin	1
Pattern of pigmentation on flower	Pattern of pigmentation on flower	Wing has pigmented upper margin; standard petal pigmented	1
Pattern of pigmentation on flower	Pattern of pigmentation on flower	Wing is pigmented ; Petal is lightly pigmented	1
Pattern of pigmentation on flower	Pattern of pigmentation on flower	Wing pigmented petal has light V-shape pattern	1
Pattern of pigmentation on green pod	Pattern of pigmentation on green pod	None	0
Pattern of pigmentation on green pod	Pattern of pigmentation on green pod	Pigmented Sutures	1

Pattern of pigmentation on green pod	Pattern of pigmentation on green pod	Pigmented tip	1
Pattern of pigmentation on green pod	Pattern of pigmentation on green pod	Pigmented valves,green sutures	1
Pattern of pigmentation on green pod	Pattern of pigmentation on green pod	Splashes of Pigment	1
Pattern of pigmentation on green pod	Pattern of pigmentation on green pod	Uniform pigment	1
Pattern of pigmentation on plant	Pattern of pigmentation on plant	None or Very pale	0
Pattern of pigmentation on plant	Pattern of pigmentation on plant	Almost Solid	1
Pattern of pigmentation on plant	Pattern of pigmentation on plant	Extensive	1
Pattern of pigmentation on plant	Pattern of pigmentation on plant	Moderate on base and tip of petioles	1
Peduncle length	Peduncle length	Short - average length < 5cm	1
Peduncle length	Peduncle length	Long - Average length > 5cm	2
Plant growth habit	Plant growth habit	Prostrate: plant completely flat on ground: branches spread for several meters	1
Plant growth habit	Plant growth habit	SemiProstrate: Main stem upto 20cm or more above ground; branches spread 1-4m	2
Plant growth habit	Plant growth habit	Intermediate:most lower branches touch the ground	3
Plant growth habit	Plant growth habit	Semi-Erect: branches tend to be perpendicular to main stem but do not touch ground	4

Plant growth habit	Plant growth habit	Erect : branches less acute than above	5
Plant growth habit	Plant growth habit	Acute erect: branches form acute angle with main stem	6
Plant growth habit	Plant growth habit	Climbing	7
Pod attachment to peduncle	Pod attachment to peduncle	Angle of 30° to 90°	1
Pod attachment to peduncle	Pod attachment to peduncle	Erect	2
Pod attachment to peduncle	Pod attachment to peduncle	Pendant	3
Pod shape	Pod shape	Straight	1
Pod shape	Pod shape	Curved	2
Pod shape	Pod shape	Coiled	3
Raceme position	Raceme position	In all layers of canopy	1
Raceme position	Raceme position	In upper leaf layers	2
Raceme position	Raceme position	Above Foliage	3
Red	Eye color_M12:brown mottling on orange	control	0
Red	Eye color_M12:brown mottling on orange	case	1
Red	Eye color_M15:brown mottling on red	control	0
Red	Eye color_M15:brown mottling on red	case	1
Red	Eye color_M65:solid brown over red	control	0
Red	Eye color_M65:solid brown over red	case	1
Red	Eye color_R10:maroon	control	0
Red	Eye color_R10:maroon	case	1
Red	Eye color_R40:red	control	0
Red	Eye color_R40:red	case	1
Red	Eye color_R70:pink	control	0
Red	Eye color_R70:pink	case	1
Red	Eye color_S15:Speckling on red	control	0
Red	Eye color_S15:Speckling on red	case	1
Red	Eye color_S62:Speckling on orange with clear areas	control	0
Red	Eye color_S62:Speckling on orange with clear areas	case	1
Red	Eye color_X55:black spots with mottling on red	control	0
Red	Eye color_X55:black spots with mottling on red	case	NA
Seed Crowding in pod	Seed Crowding in pod	Non-crowder:no compression at all in pod	0
Seed Crowding in pod	Seed Crowding in pod	Semi-Crowder:slight	1

		indentation of seed ends	
Seed Crowding in pod	Seed Crowding in pod	Crowder:marked compression of seeds	2
Seed Crowding in pod	Seed Crowding in pod	Extreme crowder:seed so compressd that width is greater than length	3
Seed length	Seed length	Very Short - Length equal to Width	0
Seed length	Seed length	Short - slightly longer than it is wide	1
Seed length	Seed length	Intermediate - twice as long as wide	2
Seed length	Seed length	Long - thrice as long as wide	3
Seed length	Seed length	Very Long - at least four times as long as wide	4
Seed size	Seed size	48mg/10 seeds	48
Seed size	Seed size	117mg/10 seeds	117
Seed size	Seed size	189mg/10 seeds	189
Seed size	Seed size	472mg/10 seeds	472
Seed size	Seed size	810mg/10 seeds	810
Seed size	Seed size	1400mg/10 seeds	1400
Seed size	Seed size	2150mg/10 seeds	2150
Seed size	Seed size	2880mg/10 seeds	2880
Seed size	Seed size	3370mg/10 seeds	3370
Seed thickness	Seed thickness	Very Flat - thickness half the width	1
Seed thickness	Seed thickness	Flat - thickness two-thirds the width	2
Seed thickness	Seed thickness	Intermediate - thickness slightly less than the width	3
Seed thickness	Seed thickness	Thick - thickness equal to width	4
Small eye	Eye pattern_E10:Small eye.Eye encircles the back of hilum(H.) in a narrow ring:widens slightly at the sides of H. & extends in a straight band at either sides of H.	control	0

Small eye	Eye pattern_E10:Small eye.Eye encircles the back of hilum(H.) in a narrow ring:widens slightly at the sides of H. & extends in a straight band at either sides of H.	case	1
Small eye	Eye pattern_E30:Small eye-large. similar to E10: but eye at sides of the hilum is wider than that of E10.	control	0
Small eye	Eye pattern_E30:Small eye-large. similar to E10: but eye at sides of the hilum is wider than that of E10.	case	1
Small eye	Eye pattern_E50:Broad eye. eye is triangle:with the hilum inside: the front of the hilum resting on the base of the triangle.	control	0
Small eye	Eye pattern_E50:Broad eye. eye is triangle:with the hilum inside: the front of the hilum resting on the base of the triangle.	case	1
Small eye	Eye pattern_E58:Broad eye:spotted keel.similar to E40 but with spotted keel.	control	0
Small eye	Eye pattern_E58:Broad eye:spotted keel.similar to E40 but with spotted keel.	case	1
Speckled	Eye pattern_K10:Densely speckled. speckles uniform over body	control	0
Speckled	Eye pattern_K10:Densely speckled. speckles uniform over body	case	1
Speckled	Eye pattern_K20:Lightly speckled. speckles uniform over body	control	0
Speckled	Eye pattern_K20:Lightly speckled. speckles uniform over body	case	1
Speckled	Eye pattern_K30:Very Lightly speckled. speckles uniform over body	control	0
Speckled	Eye pattern_K30:Very Lightly speckled. speckles uniform over body	case	1
Speckled	Eye pattern_K38:speckled keel.	control	0
Speckled	Eye pattern_K38:speckled keel.	case	1
Tan	Eye color_M11:brown mottling on tan	control	0
Tan	Eye color_M11:brown mottling on tan	case	1
Tan	Eye color_M60:solid brown over tan	control	0
Tan	Eye color_M60:solid brown over tan	case	1
Tan	Eye color_S11:Speckling on tan	control	0
Tan	Eye color_S11:Speckling on tan	case	1
Tan	Eye color_S61:Speckling on tan with clear areas:as though speckles had erased with random strokes	control	0
Tan	Eye color_S61:Speckling on tan with clear areas:as though speckles had erased with random strokes	case	1

Tan	Eye color_T10:Tan or buff	control	0
Tan	Eye color_T10:Tan or buff	case	1
Tan	Eye color_T20:dark tan	control	0
Tan	Eye color_T20:dark tan	case	1
Tan	Eye color_T41:light orange tan	control	0
Tan	Eye color_T41:light orange tan	case	1
Tan	Eye color_T44:medium orange tan	control	0
Tan	Eye color_T44:medium orange tan	case	1
Tan	Eye color_V11:Speckled with mottling on tan	control	0
Tan	Eye color_V11:Speckled with mottling on tan	case	1
Tan	Eye color_V61:Speckled with clear areas and mottling on buff	control	0
Tan	Eye color_V61:Speckled with clear areas and mottling on buff	case	1
Tan	Eye color_V71:solid brown with speckling on tan	control	0
Tan	Eye color_V71:solid brown with speckling on tan	case	1
Tan	Eye color_X51:black spots with mottling on tan	control	0
Tan	Eye color_X51:black spots with mottling on tan	case	NA
Testa texture	Testa texture	S:Smooth	1
Testa texture	Testa texture	R:Rough	2
Testa texture	Testa texture	I:Intermediate	3
Testa texture	Testa texture	W:Wrinkled	4
Testa texture	Testa texture	P:Split	5
Testa texture	Testa texture	S-W:Smooth & Wrinkled	6
Testa texture	Testa texture	L:Loose	7
Testa texture	Testa texture	S/W:Smooth Eye;Wrinkled Body	8
Testa texture	Testa texture	I-W:Intermediate & Wrinkled	9
Testa texture	Testa texture	R-W:Rough & Wrinkled	10
Twining tendency	Twining tendency	None	1
Twining tendency	Twining tendency	Moderate	2
Twining tendency	Twining tendency	Pronounced	3
Watson	Eye pattern_W11:Normal Watson	control	0
Watson	Eye pattern_W11:Normal Watson	case	1
Watson	Eye pattern_W15:Watson with dark or speckled body	control	0
Watson	Eye pattern_W15:Watson with dark or speckled body	case	1

Watson	Eye pattern_W20:Watson dilute.The margin in front of the hilum becomes more restricted	control	0
Watson	Eye pattern_W20:Watson dilute.The margin in front of the hilum becomes more restricted	case	1
Watson	Eye pattern_W30:Watson blotched.Large blotches of pigment from eye move onto body	control	0
Watson	Eye pattern_W30:Watson blotched.Large blotches of pigment from eye move onto body	case	1
Watson	Eye pattern_W31:Watson blotched:dilute.blotches are much less pronounced. Flowering pigment pattern is 4	control	0
Watson	Eye pattern_W31:Watson blotched:dilute.blotches are much less pronounced. Flowering pigment pattern is 4	case	1
Watson	Eye pattern_W35:Watson speckled. Speckling tends to occur in blotches	control	0
Watson	Eye pattern_W35:Watson speckled. Speckling tends to occur in blotches	case	1
Watson	Eye pattern_W55:Watson: nearly self colored. Eye covers almost entire seed except for small portion of micropylar end.	control	0
Watson	Eye pattern_W55:Watson: nearly self colored. Eye covers almost entire seed except for small portion of micropylar end.	case	1
Web blight	Incidence of Other Diseases - Web blight	unspecified	0
Web blight	Incidence of Other Diseases - Web blight	moderate	1
Web blight	Incidence of Other Diseases - Web blight	severe	2
White	Eye color_W20:white body: used only with A10 eye	control	0
White	Eye color_W20:white body: used only with A10 eye	case	1
White	Eye color_W21:white body: black eye	control	0
White	Eye color_W21:white body: black eye	case	1
White	Eye color_W22:white body: red eye	control	0
White	Eye color_W22:white body: red eye	case	1
White	Eye color_W23:white body: mottled eye	control	0
White	Eye color_W23:white body: mottled eye	case	1
White	Eye color_W25:white body: tan eye	control	0
White	Eye color_W25:white body: tan eye	case	1

Table 3.S4 Wilcoxon tests for differences in quantitative phenotypes

ID	Phenotype	Median Admixed	Median Cluster 1	Median Cluster 2	Wilcoxon P value
1	Days to first flowering	45	48	53	1.76E-15
2	Days to first ripe pod	67	70	78	1.93E-25
3	No of main branches	5	5	5	4.82E-01
4	No of main stem nodes	10	11	11	2.71E-04
5	Terminal leaflet length	116	123	111	7.53E-27
6	Terminal leaflet width	72	81	70	1.65E-33
7	Pod length	158.50	166	134	6.93E-72
8	Pod width	7	7	6	2.29E-12
9	No of locules/pod	15	17	12	8.48E-110
10	Number of pods affected by Maruca	75	45.50	70	1.20E-01
11	Number of pods unaffected by Maruca	53	34.50	48.50	1.68E-01
12	Number of pods affected by Laspeyresia	70	38	56	9.14E-02
13	Number of pods unaffected by Laspeyresia	62	32.50	45.50	7.49E-02
14	Percentage of Sulphur (combustion & titration)	0.15	0.16	0.16	4.27E-01
15	Percentage of Nitrogen (colorimetric analysis)	4.13	4.19	4.01	8.66E-03
4C	Plant growth habit	3	3	2	4.25E-26
5C	Twining tendency	1	1	1	3.09E-05
6C	Growth vigor	2	2	2	1.72E-03
7C	Determinacy	1	1	1	6.41E-01
8C	Peduncle length	2	2	2	1.96E-01
9C	Raceme position	2	1	2	3.97E-20
10C	No of pods/peduncle	2	2	2	5.90E-02
11C	Pod attachment to peduncle	1	1	1	2.65E-01
12C	Pod shape	2	2	2	7.23E-01
28C	Testa texture	1	1	2	1.66E-130
29C	Seed size	810	810	1,400	1.47E-20
30C	Seed length	1	1	1	3.07E-17
31C	Seed thickness	3	3	3	1.04E-13
32C	Seed Crowding in pod	0	1	1	4.17E-05
34C	Incidence of Leaf Spot (C. Cruenta)	0	0	0	7.25E-01
35C	Incidence of Bacterial Pustule	0	0	0	9.92E-03

39C	Incidence of Cowpea Mosaic Virus	1	1	1	5.70E-01
40C	Incidence of Anthracnose	4.50	5	2	1.08E-06
41C	Web blight	0	0	0	2.28E-01

Table 3.S5 Fisher's exact test statistics for qualitative phenotypes

ID	Phenotype	Freq Admixed	Freq Cluster 1	Freq Cluster 2	Fisher P value
53	Terminal leaflet shape_Globose	0.02	0.05	0.02	1.33E-03
54	Terminal leaflet shape_Hastate (Lanceolate)	0.03	0.01	0.02	8.02E-02
55	Terminal leaflet shape_Sub-Globose	0.60	0.75	0.63	1.26E-05
56	Terminal leaflet shape_Sub-hastate	0.35	0.19	0.33	3.44E-08
66	Eye pattern_A10:Eye absent	0.02	0.02	0.03	2.19E-01
71	Eye pattern_A60:the eye fills the narrow groove all around the hilum. similar to Kabba (K) group but no specks on body. flower pigment pattern is 1.	0.01	0	0.07	8.42E-12
72	Eye pattern_A61:Similar to A60 but flower pigment pattern is 5.	0.01	0	0.04	4.80E-07
73	Eye pattern_A70:eye starts in a groove at either side of the hilum and spills out slightly in front of it. flower pigment pattern is 1.	0.04	0.01	0.01	1E+00
74	Eye pattern_A81:A thin line of pigment starts at back of the hilum (h) and moves along each side of it. A narrow clear space found b/w eye & H. Flower pigment pattern is 6.	0	0	0	4.65E-01
97	Eye pattern_S00:Self Colored	0.55	0.84	0.18	4.20E-116
1C	Pattern of pigmentation on plant	0.77	0.79	0.82	3.10E-01
2C	Pattern of pigmentation on flower	0.86	0.95	0.82	6.76E-13
226	Incidence of Other Diseases_Nothing	0.38	0.42	0.40	6.35E-01
227	Incidence of Other Diseases_Red freckle - Septoria	0	0	0	4.79E-01
228	Incidence of Other Diseases_Sclerotium rot	0.01	0	0.03	5.53E-03
229	Incidence of Other Diseases_Undefined code	0.01	0.02	0.01	4.52E-01
233	Incidence of Other Diseases_Wet stem rot	0.02	0.03	0	3.10E-02
3C	Pattern of pigmentation on green pod	0.37	0.35	0.35	9E-01
13C	Hilum ring	0.12	0.05	0.37	6.16E-43
14C	Small eye	0.15	0.04	0.14	5.72E-08
15C	Large eye	0.03	0.01	0.01	3.64E-01
16C	Holstein	0.05	0.02	0.01	1.26E-01
17C	Speckled	0	0	0.08	7.62E-14

18C	Watson	0.03	0.01	0.08	3.66E-09
19C	Black	0.10	0.07	0.19	3.01E-09
20C	Blue	0.02	0.05	0.05	5.87E-01
21C	Tan	0.39	0.57	0.31	2.62E-18
22C	Red	0.17	0.15	0.02	6.19E-17
23C	Brown	0.16	0.11	0.05	9.33E-05
24C	White	0.08	0.02	0.29	3.81E-37
25C	Cream	0.05	0.02	0.06	1.73E-03
26C	Brown splash	0.01	0	0.01	1.29E-01
27C	Gray	0	0	0	1E+00
33C	Incidence of Leaf Spot (C. Canescens)	0.01	0.02	0.03	5.31E-01
36C	Incidence of Bacterial Blight	0.04	0.06	0.05	1E+00
37C	Incidence of Target Spot	0.05	0.02	0.11	2.32E-05
38C	Incidence of Rust	0.03	0.01	0.04	6.87E-02

Table 3.S6 Significantly associated regions in GWAS

ID	Chr	Start	End	Tag SNP	BP	Linked SNPs
17C	Vu01	1208460	1549752	2_37214	1549752	2_42551
72	Vu01	1208460	1549752	2_42551	1208460	NA
7	Vu01	1330630	1330630	2_00801	1330630	NA
4	Vu01	2454065	2454065	2_32083	2454065	NA
72	Vu01	5280109	6663744	2_15976	5681560	2_44199,2_25970
72	Vu01	5280109	5681560	2_30548	5280109	2_44199,2_25970,2_15976
17C	Vu01	5681560	7534125	2_25970	6640374	2_44199
72	Vu01	5681560	7650234	2_44199	6663744	2_25970,2_28600
17C	Vu01	6640374	7650234	2_03341	6761905	2_43100,2_44199,2_50508,2_54974,2_45818,2_25970
17C	Vu01	6663744	8246046	2_54974	7650234	2_45818,2_50508
66	Vu01	7140117	7140117	2_51198	7140117	NA
72	Vu01	7534125	9164694	2_53723	8246046	2_24407,2_02365,2_54738,2_47433,2_31765,2_31764,2_25970,2_54879,2_55184,2_51536,2_49221,2_28600,2_42696,2_44199,2_47460,2_38415,2_48815,2_43826
72	Vu01	9152465	10172727	2_49221	9287997	2_38415,2_54879,2_31765,2_55184,2_24407,2_31764,2_02365,2_54738,2_00841,2_39768,2_42696,2_51536,2_43826,2_48815,2_47433,2_47460,2_37939
66	Vu01	9813768	10635534	2_41391	9813768	2_38814
72	Vu01	10172727	11706102	2_52840	11167321	2_03438,2_51536,2_39768,2_00841,2_55184,2_38415,2_52698,2_54879,2_47433,2_02365,2_54738,2_37939,2_28339,2_31764,2_40552,2_32823,2_43826,2_48815,2_49221,2_10013,2_24407,2_37777,2_38797,2_53043,2_31765
72	Vu01	10406957	12228956	2_37777	11343102	2_03438,2_53043,2_40552,2_38797
66	Vu01	10635534	12302016	2_31470	11532475	2_38814,2_41391
72	Vu01	10795047	12627974	2_38797	11706102	2_53043
72	Vu01	11229705	13144449	2_53043	12228956	NA
66	Vu01	11532475	12302016	2_26641	11984584	2_39172,2_31470,2_38814

71	Vu01	11706102	13516834	2_09597	12627974	2_25266,2_31787,2_33737,2_29819,2_51300,2_02759,2_32932,2_00170,2_00830,2_24511,2_55287,2_38769,2_40108,2_45708,2_46699,2_41679
71	Vu01	12857259	14619649	2_55287	13775666	2_25266,2_29819,2_31787,2_24511,2_51300,2_32932,2_33737,2_38769,2_02759,2_40108,2_00170,2_00830,2_46699,2_41679,2_41729,2_45708
71	Vu01	16613696	17068485	2_52112	16865137	2_28050,2_00597,2_38560,2_49092,2_38384
66	Vu01	17423601	18954157	2_38041	18076564	2_10693,2_39036,2_05668,2_38340,2_28909,2_43193,2_55397
66	Vu01	17423601	19405901	2_39036	18413764	2_28909,2_31854,2_43193,2_55397,2_38340
17C	Vu01	17529253	17529253	2_44629	17529253	NA
66	Vu01	18413764	20361822	2_55397	19405901	2_31854
17C	Vu01	19882098	19882098	2_48564	19882098	NA
66	Vu01	21809150	21809150	2_41389	21809150	NA
17C	Vu01	21963108	21963108	2_06194	21963108	NA
74	Vu01	25565987	25565987	2_12571	25565987	NA
53	Vu01	26530691	26530691	2_52879	26530691	NA
66	Vu01	26574672	26787012	2_34968	26787012	2_34723
74	Vu01	27070239	27520011	2_39613	27070239	2_32694
54	Vu01	27324968	27324968	2_35114	27324968	NA
5C	Vu01	28115007	28115007	2_06648	28115007	NA
18C	Vu01	28942082	28942082	2_06426	28942082	NA
17C	Vu01	33242578	33514334	2_33296	33514334	NA
72	Vu01	33242578	33514334	2_40402	33242578	NA
54	Vu01	34310785	34310785	2_27029	34310785	NA
54	Vu01	34467818	34467818	2_37264	34467818	NA
53	Vu01	34955059	34955669	2_32154	34955059	2_33078
7C	Vu01	36448858	36448858	2_03380	36448858	NA
17C	Vu01	36939647	37576115	2_36079	36939647	2_35652
18C	Vu01	37144044	37144044	2_23971	37144044	NA
74	Vu01	37658772	37658772	2_32098	37658772	NA
54	Vu01	37876872	37876872	2_16106	37876872	NA
7C	Vu01	38278918	38278918	2_10794	38278918	NA
73	Vu01	38668453	38668453	2_27590	38668453	NA
74	Vu01	39103330	39103330	2_32907	39103330	NA
17C	Vu02	4516645	4598381	2_38564	4519790	2_38565,2_45349,2_13678,2_29501
73	Vu02	4973658	4973658	2_09767	4973658	NA
72	Vu02	7434623	7434623	2_42320	7434623	NA
15C	Vu02	7788062	7788062	2_51289	7788062	NA

74	Vu02	8179616	8179616	2_47115	8179616	NA
17C	Vu02	8787473	8787473	2_47523	8787473	NA
74	Vu02	9038955	10026276	2_51136	9038955	2_39399
74	Vu02	10026276	10134369	2_43091	10134369	2_39399,2_51136
66	Vu02	11490966	11490966	2_39018	11490966	NA
74	Vu02	13430605	14018731	2_43708	13430605	2_50950
74	Vu02	14669110	14669110	2_36387	14669110	NA
13C	Vu02	15108748	15108748	2_32499	15108748	NA
72	Vu02	20161289	20161289	2_38638	20161289	NA
74	Vu02	20498344	20498344	2_33063	20498344	NA
74	Vu02	21231492	21345696	2_47713	21265865	2_35755,2_36476,2_37255,2_54902
38C	Vu02	22270268	22270268	2_35150	22270268	NA
54	Vu02	23133650	23133650	2_50266	23133650	NA
38C	Vu02	23337673	23434197	2_15457	23434197	2_27578
71	Vu02	23572311	23572311	2_19074	23572311	NA
74	Vu02	24312031	24312031	2_04977	24312031	NA
74	Vu02	25619379	25619379	2_36398	25619379	NA
228	Vu02	27693476	27693476	2_11213	27693476	NA
14	Vu02	27983520	27983520	2_07802	27983520	NA
17C	Vu02	29352306	29352306	2_36331	29352306	NA
17C	Vu02	30920782	30929148	2_35680	30920782	2_36593
17C	Vu02	30948583	30948583	2_36254	30948583	NA
38C	Vu02	31050767	31061020	2_06097	31061020	2_20584
71	Vu02	31085090	31106855	2_24181	31085090	2_32324,2_26122,2_03873
74	Vu02	32261977	32261977	2_43076	32261977	NA
38C	Vu02	32646898	32646898	2_13647	32646898	NA
38C	Vu02	32935870	32945921	2_51840	32945921	2_26440
73	Vu02	33199525	33199525	2_36028	33199525	NA
53	Vu03	373172	373172	2_41560	373172	NA
17C	Vu03	2657043	2866839	2_28525	2863595	2_33713
72	Vu03	2657043	2866839	2_28525	2863595	2_30382,2_16935,2_33713,2_34441,2_30381,2_29506,2_03236
17C	Vu03	2959244	2959244	2_34404	2959244	NA
66	Vu03	3280997	3280997	2_28140	3280997	NA
17C	Vu03	4007485	4074456	2_46984	4007485	2_36421
66	Vu03	5119325	5119325	2_32652	5119325	NA
17C	Vu03	8040424	8040424	2_35275	8040424	NA
66	Vu03	8759438	8817999	2_27157	8817999	1_1349
2	Vu03	10061102	10069281	2_26803	10069281	2_33159
74	Vu03	10822597	10822597	2_54869	10822597	NA
21C	Vu03	10920429	11068119	2_03389	10933603	2_42885,2_10237,2_10236,2_02455,2_02456
21C	Vu03	10920429	11793024	2_10236	11477892	2_02456,2_42885,2_02455,2_39707,2_10237
22C	Vu03	10920429	11068119	2_03389	10933603	1_0511,2_05875,2_02455,2_02456,2_05876,1_07

						13,2_05872,2_14350,2_14469,2_18295,2_19120,2_23108,2_02742,2_03388,2_04622,2_27032,2_31916,2_32961,2_41315,2_42885,2_46858,2_50161,2_10236,2_03525,2_04454,2_04455,2_13898,2_14349,2_26432,2_06225,2_09682,2_09683,2_25974,2_23891,2_25906,2_13048,2_13049,2_26366,2_26367,2_25973,2_13119,2_10237,2_13120
21C	Vu03	10933603	11208404	2_20787	11068119	2_03389
22C	Vu03	10933603	11208404	2_20787	11068119	2_03388,2_03389,2_19120,2_25906,2_06159,2_41011
22C	Vu03	11049029	11208404	2_06159	11208404	2_41011
21C	Vu03	11059076	11793024	2_39707	11532668	NA
22C	Vu03	11059076	11793024	2_23320	11060686	2_09682,2_03525,2_04454,2_13898,2_06225,2_02456,2_04455,2_23321,2_02742,2_25973,2_14469,2_23891,2_02455,2_10237,2_14349,1_0713,2_04622,2_31916,2_13048,2_05876,2_10236,2_25974,2_32961,2_14350,2_05875,2_09683,2_03388,1_0511,2_13120,2_50161,2_05872,2_13049,2_41315,2_27032,2_26366,2_18295,2_26367,2_13119,2_23108,2_26432,2_46858,2_42885,2_13051,2_15637,2_15638,2_38811,2_48282,2_42976
22C	Vu03	11397547	11532668	2_13051	11453793	2_15638,2_38811,2_42976,2_23108,2_15637,2_48282
22C	Vu03	12610969	12610969	2_27583	12610969	NA
22C	Vu03	15556009	15556009	2_33523	15556009	NA
22C	Vu03	15569807	15569807	2_16725	15569807	NA
54	Vu03	16896211	16896211	2_46273	16896211	NA
66	Vu03	16981309	17127731	2_24497	17012661	2_41426,2_32660,2_51012,2_52190,2_16052,2_06381
20C	Vu03	18288186	18288186	2_37942	18288186	NA
7C	Vu03	22439854	22439854	2_49360	22439854	NA

20C	Vu03	23846717	23846717	2_40798	23846717	NA
13C	Vu03	34391012	34391012	2_36974	34391012	NA
17C	Vu03	34652166	35072129	2_30144	34652166	2_20397
73	Vu03	35724093	35724093	2_29952	35724093	NA
73	Vu03	35782403	35852891	2_04401	35851067	2_49010,2_19887,2_19888
31C	Vu03	36541369	36541369	2_53604	36541369	NA
38C	Vu03	42580534	42580534	2_36869	42580534	NA
33C	Vu03	44562080	44562080	2_27478	44562080	NA
38C	Vu03	46212581	46215125	2_04905	46215125	2_10498
17C	Vu03	47555896	48042739	2_10003	47926965	2_37428
72	Vu03	47555896	48042739	2_44674	47555896	2_50273
71	Vu03	48052890	48072785	2_19132	48052890	2_01311,2_01134
38C	Vu03	49889767	49889767	2_37286	49889767	NA
74	Vu03	50859638	51051007	2_32860	50859638	2_01927
66	Vu03	51769442	51769442	2_43372	51769442	NA
227	Vu03	51868542	51868542	2_36753	51868542	NA
71	Vu03	51868542	51868542	2_36753	51868542	NA
17C	Vu03	59333736	60331466	2_02163	60331466	NA
71	Vu03	59333736	60331466	2_19393	59333736	NA
28C	Vu03	60371237	60371237	2_52095	60371237	NA
7C	Vu03	60551379	60551379	2_13260	60551379	NA
17C	Vu03	61072482	61072482	2_35518	61072482	NA
1C	Vu03	61072482	61072482	2_35518	61072482	NA
18C	Vu03	62331002	62331002	2_32543	62331002	NA
66	Vu03	62787496	62787496	2_17764	62787496	NA
24C	Vu03	63328812	63499826	2_29516	63328812	2_32134
71	Vu03	63328812	63499826	2_13156	63499826	NA
73	Vu04	858655	858655	2_34652	858655	NA
72	Vu04	1938360	1938360	2_00096	1938360	NA
72	Vu04	2940793	2940793	2_33623	2940793	NA
228	Vu04	5782310	5785996	2_26059	5785996	2_23009
74	Vu04	7494017	7639403	2_51347	7494017	2_07551
74	Vu04	8720817	8720817	2_17131	8720817	NA
36C	Vu04	31212475	31212475	2_48221	31212475	NA
74	Vu04	36648989	36648989	2_35908	36648989	NA
74	Vu04	36935722	36935722	2_07604	36935722	NA
233	Vu04	38712786	38712786	2_35176	38712786	NA
66	Vu04	39042866	39042866	2_33190	39042866	NA
38C	Vu04	39560206	39560206	2_36916	39560206	NA
17C	Vu04	39769280	39769280	2_25893	39769280	NA
229	Vu04	41815430	41815430	2_26762	41815430	NA
71	Vu05	2063355	2063355	2_31962	2063355	NA
19C	Vu05	2338261	2338261	2_31973	2338261	NA
19C	Vu05	2992413	3002809	2_12036	2992413	2_29558
21C	Vu05	2992413	3002809	2_12036	2992413	NA
3C	Vu05	3069471	3316827	2_27750	3081526	2_09161,2_32646,2_27749,2_08149,2_08148

3C	Vu05	3078541	3347469	2_20420	3236339	2_08148,2_09161,2_08149,2_37210,2_45419,2_32646
3C	Vu05	3078541	3348824	2_37210	3347469	NA
19C	Vu05	3104538	3274155	2_15182	3225877	NA
19C	Vu05	3104538	3225877	2_19309	3104538	2_15182
21C	Vu05	3104538	3274155	2_15182	3225877	NA
21C	Vu05	3104538	3225877	2_19309	3104538	2_15182
3C	Vu05	3104538	3274155	2_15182	3225877	2_32646,2_15996,2_21972
3C	Vu05	3104538	3225877	2_19309	3104538	2_15182,2_15996,2_21972
3C	Vu05	3225877	3316827	2_15996	3267152	2_27749,2_21972,2_37210,2_09161,2_27750,2_20420,2_32646
19C	Vu05	3299310	3348824	2_36160	3299310	NA
1C	Vu05	3299310	3348824	2_36237	3329312	2_37209,2_35199
19C	Vu05	3667555	3950678	2_05741	3667555	2_12924,2_16071,2_08654,1_0928,2_16072,2_18148,2_18485,2_01821,2_19960,2_19602,2_25246,2_05074,2_20467,2_05742,2_32974,2_50691,2_53482,1_0357
72	Vu05	5136652	5136652	2_08287	5136652	NA
74	Vu05	5429041	5429041	2_26028	5429041	NA
66	Vu05	5962669	5962669	2_49991	5962669	NA
17C	Vu05	13274864	13274864	2_46385	13274864	NA
7	Vu05	14952849	14952849	2_31474	14952849	NA
74	Vu05	16253450	16253450	2_36666	16253450	NA
20C	Vu05	17992220	18944005	2_42412	18944005	NA
71	Vu05	17992220	18944005	2_41886	17992220	NA
17C	Vu05	19933485	19980733	2_36482	19933485	2_50120
7C	Vu05	21331496	21331496	2_28561	21331496	NA
17C	Vu05	21587997	21587997	2_49570	21587997	NA
28C	Vu05	23893330	23893330	2_42062	23893330	NA
17C	Vu05	24087579	24576080	2_35462	24576080	2_40414
17C	Vu05	26813700	26813700	2_44225	26813700	NA
229	Vu05	38880133	38880133	2_55422	38880133	NA
9	Vu05	39410260	39410260	2_48319	39410260	NA
229	Vu05	41448610	41448610	2_36667	41448610	NA
74	Vu05	41448610	41448610	2_36667	41448610	NA
72	Vu05	42362160	42362160	2_38667	42362160	NA
25C	Vu05	43464679	43464679	2_45241	43464679	NA
71	Vu05	45165695	45165695	2_19967	45165695	NA
17C	Vu05	45455480	45455480	2_21646	45455480	NA
227	Vu05	46363629	46363629	2_38635	46363629	NA
72	Vu05	47135991	47135991	2_33634	47135991	NA
74	Vu06	1663765	1663765	2_48489	1663765	NA

20C	Vu06	13491073	13645944	2_22603	13494129	2_39383,2_19089,2_43281
20C	Vu06	14788644	14788644	2_37276	14788644	NA
227	Vu06	20515970	20516279	2_23678	20516279	2_23679
2C	Vu06	22927963	22927963	2_09033	22927963	NA
228	Vu06	25452240	25460259	2_35123	25458657	2_35125,2_36698,2_42555
228	Vu06	26769861	26769861	2_20341	26769861	NA
7	Vu06	27608425	27608425	2_23061	27608425	NA
12C	Vu06	28355872	28355872	2_37184	28355872	NA
73	Vu06	28689352	28689352	2_35926	28689352	NA
19C	Vu06	29564076	29564076	2_21361	29564076	NA
24C	Vu06	31163890	31163890	2_49492	31163890	NA
229	Vu07	468215	498437	2_36310	498437	1_0268,2_47382
229	Vu07	563222	563222	2_02414	563222	NA
66	Vu07	3075360	3086611	2_00042	3085843	2_23291,2_00041
17C	Vu07	3995425	4015929	2_04669	3995425	NA
72	Vu07	3995425	4015929	2_08490	4015929	2_04669
233	Vu07	4155991	4155991	2_51127	4155991	NA
72	Vu07	6794667	6835562	2_13109	6794667	2_41770,2_25119,2_01552,2_52387
38C	Vu07	7848992	7868049	2_39375	7868049	2_52917
66	Vu07	8588523	9969321	2_38580	9278616	2_52241
2C	Vu07	8677078	8677078	2_37135	8677078	NA
13C	Vu07	8802148	9284925	2_50329	8802148	2_47859
17C	Vu07	8802148	9722084	2_38581	9284925	NA
38C	Vu07	9269258	9269258	2_34848	9269258	NA
66	Vu07	9278616	9969321	2_53451	9769401	2_46350,2_45765,2_37753,2_52241,2_38580
17C	Vu07	9284925	9722084	2_25879	9415859	2_38581
227	Vu07	9284925	9722084	2_52522	9722084	NA
7	Vu07	9463221	9769401	2_21244	9463221	NA
17C	Vu07	10558728	11791448	2_09701	11109263	NA
72	Vu07	10558728	11791448	2_09701	11109263	2_31420,2_03606
1C	Vu07	10637029	10637029	2_33257	10637029	NA
227	Vu07	11109263	12602283	2_25449	11791448	NA
24C	Vu07	11791448	12602283	2_31748	12602283	NA
13C	Vu07	12463387	12463387	2_39203	12463387	NA
13C	Vu07	12508907	12508907	2_53099	12508907	NA
24C	Vu07	13038056	13038056	2_44450	13038056	NA
2C	Vu07	13038056	13038056	2_44450	13038056	NA
66	Vu07	13038056	13038056	2_44450	13038056	NA
66	Vu07	13169280	13169280	2_34260	13169280	NA
72	Vu07	13969059	13969059	2_54739	13969059	NA
24C	Vu07	14142086	14142086	2_53170	14142086	NA
2C	Vu07	14142086	14142086	2_53170	14142086	NA
66	Vu07	14142086	14142086	2_53170	14142086	NA
66	Vu07	14811786	14811786	2_24463	14811786	NA
73	Vu07	14993939	14993939	2_36956	14993939	NA

97	Vu07	15343135	15343135	2_17872	15343135	NA
16C	Vu07	18764426	18764426	2_42383	18764426	NA
66	Vu07	18771369	20315347	2_44003	19512947	2_38668,2_49475,2_54930,2_38669
17C	Vu07	19399611	20178630	2_24958	20178630	2_32758,2_40805
66	Vu07	19399611	20315347	2_32831	19905277	NA
17C	Vu07	19512947	20315347	2_40805	20092363	2_32758
66	Vu07	19512947	20315347	2_07322	19811099	2_22869,2_55172,2_37522
66	Vu07	19512947	21103695	2_12938	20315347	1_0585
66	Vu07	19512947	20315347	2_38448	19979921	2_44003,2_54930,2_02041,2_39620,2_40444,2_40805,2_49475,2_32831,2_37522,2_38669,2_38668,2_38447,2_12938,2_07322,2_24322,2_55172,1_0585
66	Vu07	19512947	20315347	2_40805	20092363	NA
66	Vu07	19811099	20542488	2_55172	20295282	2_22869
13C	Vu07	20111663	20542488	2_09639	20542488	NA
73	Vu07	20298425	20298425	2_36046	20298425	NA
66	Vu07	20337425	20337425	2_06974	20337425	NA
233	Vu07	20974225	20974225	2_46826	20974225	NA
229	Vu07	21754743	21839244	2_32469	21798274	2_05211,2_26671,2_46429
17C	Vu07	22812185	23501697	2_42790	23499288	2_54601,2_49642
66	Vu07	22812185	23501697	2_43700	22864558	2_04854,2_18561,2_24385,2_04853,2_04851,2_24384,2_18562
71	Vu07	23426186	23426186	2_28739	23426186	NA
17C	Vu07	23458194	23501697	2_03004	23458194	2_54601,2_42790,2_49642
66	Vu07	23815918	23815918	2_33151	23815918	NA
66	Vu07	24689051	24729093	2_54497	24698211	2_24386,2_21627,2_24387
2C	Vu07	24715771	25076677	2_05371	24715771	NA
66	Vu07	24715771	25076677	2_05371	24715771	2_12044,2_01769,2_01768
66	Vu07	25115089	25115089	2_12852	25115089	NA
17C	Vu07	25898418	25898418	2_45477	25898418	NA
2C	Vu07	25947911	25947911	2_05822	25947911	NA
66	Vu07	25947911	25947911	2_05822	25947911	NA
72	Vu07	26902692	26902692	2_02060	26902692	NA
66	Vu07	27370207	27370207	2_25944	27370207	NA
233	Vu07	28628551	28628551	2_22377	28628551	NA
228	Vu07	31395692	31428762	2_33527	31420273	2_32900
27C	Vu07	31395692	31428762	2_32900	31404706	2_33527,2_28878,2_26289,2_23609
228	Vu07	32994678	32994678	2_32943	32994678	NA

74	Vu07	36273903	36273903	2_36018	36273903	NA
74	Vu08	263699	263699	1_0684	263699	NA
74	Vu08	4654798	4777414	2_33499	4665481	2_20571,2_20548,2_20570,2_39146,2_32851
17C	Vu08	8426891	8626988	2_44089	8626988	2_30051
233	Vu08	14252443	14252443	2_41801	14252443	NA
74	Vu08	14252443	14252443	2_41801	14252443	NA
233	Vu08	16017206	16113931	2_49480	16017206	NA
74	Vu08	16017206	16113931	2_49480	16017206	2_40079
73	Vu08	17114311	17114311	2_41242	17114311	NA
17C	Vu08	19095243	20379344	2_44306	19876001	2_44181,2_38468
74	Vu08	21313967	21774870	2_54107	21774870	2_47620
17C	Vu08	21848948	23633007	2_26268	22749755	NA
26C	Vu08	21848948	22749755	2_39672	21848948	NA
17C	Vu08	22749755	24177813	2_48479	23579937	2_05677,2_29438,2_46315,2_26268,2_32996,2_42443,2_45104,2_32818
26C	Vu08	23579937	24177813	2_49817	24076163	NA
18C	Vu08	27112841	27112841	2_46783	27112841	NA
17C	Vu08	27325676	28130075	2_06875	27588186	2_36542
17C	Vu08	27588186	28130075	2_25113	28130075	2_06875,2_36542
17C	Vu08	29335519	29335519	2_10185	29335519	NA
227	Vu08	30115958	30115958	2_07752	30115958	NA
71	Vu08	32511062	32530164	2_35895	32511062	2_46426
72	Vu08	32511062	32530164	2_35895	32511062	NA
8C	Vu08	33031296	33031296	1_0205	33031296	NA
17C	Vu08	33809265	33809265	2_03607	33809265	NA
17C	Vu08	35583293	35583293	2_35319	35583293	NA
17C	Vu09	306753	315359	2_43551	306753	2_28785,2_28786
17C	Vu09	342959	352803	2_02481	351217	2_02482,2_30763
66	Vu09	643886	643886	2_11217	643886	NA
17C	Vu09	1305294	1305294	2_51126	1305294	NA
228	Vu09	1305294	1305294	2_51126	1305294	NA
54	Vu09	1502699	1502699	2_07223	1502699	NA
74	Vu09	2084981	2084981	2_36247	2084981	NA
38C	Vu09	2156441	2246970	2_19831	2175870	2_19832,2_50454,2_12553,2_31010,2_11488,2_12552,2_07782
72	Vu09	2806376	2806376	2_47664	2806376	NA
18C	Vu09	3355272	3362624	2_35427	3362624	2_52637
7C	Vu09	4679853	4959818	2_21235	4959818	2_11646
71	Vu09	6819459	6855744	2_38895	6819459	2_47305,2_34794
66	Vu09	6903155	6903155	2_27778	6903155	NA
66	Vu09	9360132	9360132	2_34467	9360132	NA
66	Vu09	13312511	14023956	2_26926	14023956	2_55298
74	Vu09	15063241	15063241	2_24619	15063241	NA
16C	Vu09	26515879	26515879	2_21477	26515879	NA
74	Vu09	27317242	27317786	2_15349	27317786	2_15350
72	Vu09	28509305	28509305	2_10716	28509305	NA

16C	Vu09	29225905	29225905	2_48310	29225905	NA
15C	Vu09	29622192	30710002	2_26717	30559985	2_27900
16C	Vu09	29622192	30572856	2_54462	29622192	2_09945
18C	Vu09	29622192	30710002	2_33224	30209393	2_13517,2_51640,2_17818,2_26080,2_13518
14C	Vu09	29985905	29994227	2_34650	29985905	2_23984
14C	Vu09	30035583	31416843	2_01960	30428852	2_33606,2_12304
14C	Vu09	30035583	30428852	2_22961	30035583	2_01960,2_12304,2_33606
15C	Vu09	30035583	31416843	2_01960	30428852	2_52510,2_23057,2_12692
16C	Vu09	30035583	31416843	2_01960	30428852	2_12692,2_52510,2_14668
18C	Vu09	30035583	31416843	2_01960	30428852	2_22961
28C	Vu09	30035583	31302906	2_12692	30376117	2_52510,2_14668
97	Vu09	30035583	31416843	2_01960	30428852	2_52510,2_12692
14C	Vu09	30083632	30572856	2_09945	30285477	NA
16C	Vu09	30083632	30572856	2_09945	30285477	NA
97	Vu09	30112817	30710002	2_11533	30665041	2_27426,2_03159,2_24952,2_11532,2_24953,2_18373
14C	Vu09	30428852	31846740	2_33606	31416843	2_12304
15C	Vu09	31121793	31416843	2_23057	31121793	NA
28C	Vu09	31302906	31846740	2_14668	31846740	NA
71	Vu09	31427308	31427308	2_36594	31427308	NA
16C	Vu09	31838872	31846740	2_14669	31844731	2_14668,2_22544,2_22543
54	Vu09	32264253	32264253	2_18534	32264253	NA
15C	Vu09	32927959	33029738	2_01338	33016441	2_08608,2_41781,2_02530,2_49578,2_31005,2_08225,2_04797,2_04798,2_49727,2_05304,2_05954,2_05955,2_05303,2_26706,2_26705,2_10585,2_10586,2_18205,2_19696
72	Vu09	33282881	33282881	2_30768	33282881	NA
228	Vu09	33520567	33568294	2_46834	33565907	2_28569
38C	Vu09	33520567	33568294	2_50679	33520567	NA
15C	Vu09	34064769	34187745	2_26718	34064769	2_43656
7C	Vu09	34064769	34187745	2_43656	34187745	NA
38C	Vu09	34536874	34542158	2_36118	34542158	2_36177
228	Vu09	34900740	34978188	2_17754	34900740	NA
54	Vu09	34900740	34978188	2_55289	34978188	NA
54	Vu09	35105190	35105190	2_20569	35105190	NA
16C	Vu09	35387032	35501467	2_16803	35387032	2_32790
7C	Vu09	35387032	35501467	2_16803	35387032	NA
228	Vu09	37278391	37279943	2_18476	37278699	2_29757,2_18475
229	Vu09	37987642	37987642	2_40524	37987642	NA
227	Vu09	40355252	40355252	2_36142	40355252	NA

17C	Vu09	40365271	40429159	2_54627	40429159	NA
71	Vu09	40365271	40429159	2_28114	40365271	NA
229	Vu09	41585431	41585431	2_37293	41585431	NA
17C	Vu09	43224047	43538365	2_05228	43538365	2_05229,2_13284
73	Vu09	43649766	43649766	2_36716	43649766	NA
66	Vu10	279688	279688	2_15378	279688	NA
17C	Vu10	3989649	3989649	2_45162	3989649	NA
74	Vu10	5433654	5433654	2_03471	5433654	NA
229	Vu10	7419407	7419407	2_16371	7419407	NA
74	Vu10	31187705	31224378	2_23127	31224378	2_31446
74	Vu10	32788513	32788513	2_07906	32788513	NA
17C	Vu10	34240565	34240565	2_14358	34240565	NA
71	Vu10	35632133	35632133	2_14331	35632133	NA
8	Vu10	37318410	37348580	2_47599	37334571	2_28454,2_28453,2_16784,2_28456
16C	Vu10	37534007	37534007	2_15395	37534007	NA
14C	Vu10	38454572	38458993	2_13095	38454820	NA
17C	Vu10	38454572	38458993	2_13095	38454820	2_31919,2_13094
18C	Vu10	38454572	38458993	2_13095	38454820	2_55456,2_32426
18C	Vu10	38454572	38547774	2_32426	38468485	2_55456
24C	Vu10	38454572	38468485	2_55456	38467161	2_32426
28C	Vu10	38454572	38458993	2_13095	38454820	NA
71	Vu10	38454572	38468485	2_55456	38467161	2_32426
97	Vu10	38454572	38458993	2_13095	38454820	2_32426,2_13094,2_55456
97	Vu10	38454572	38547774	2_32426	38468485	2_13094,2_55456
14C	Vu10	38454820	38467161	2_31919	38458993	2_13095
17C	Vu10	38454820	38467161	2_31919	38458993	2_13094
18C	Vu10	38454820	38467161	2_31919	38458993	2_55456,2_13095,2_32426
24C	Vu10	38454820	38467161	2_31919	38458993	2_55456,2_32426
28C	Vu10	38454820	38467161	2_31919	38458993	2_13095
71	Vu10	38454820	38467161	2_31919	38458993	2_55456,2_32426
72	Vu10	38454820	38467161	2_31919	38458993	NA
97	Vu10	38454820	38467161	2_31919	38458993	2_13094,2_13095,2_55456,2_32426
17C	Vu10	38468485	38547774	2_01024	38547774	2_13094,2_16251,2_31224,2_18494,2_18495,2_16252
24C	Vu10	38468485	38547774	2_01024	38547774	2_16252,2_18494,2_32426,2_55456,2_16251,2_18495,2_31224
71	Vu10	38468485	38547774	2_01024	38547774	2_32426,2_55456
72	Vu10	38468485	38547774	2_01024	38547774	NA
16C	Vu10	39254984	39254984	2_32602	39254984	NA
26C	Vu10	39307602	39307602	2_10935	39307602	NA
14	Vu10	40286217	40286217	2_37116	40286217	NA
15C	Vu10	40363326	40363326	2_31092	40363326	NA
38C	Vu10	40942089	40942089	2_35738	40942089	NA

16C	Vu10	41100865	41290623	2_07834	41100865	2_05889,2_39017,2_40530,2_49802,2_15994,2_02838,2_05888,2_24173,2_19471,2_21273,2_52016,2_24174,2_29434,2_30390
14	Vu11	947008	971434	2_44459	971434	2_42822
66	Vu11	3304839	3304839	2_24220	3304839	NA
74	Vu11	3975217	3975217	2_37059	3975217	NA
28C	Vu11	4850940	4850940	2_36641	4850940	NA
227	Vu11	6144549	6144549	2_53332	6144549	NA
14	Vu11	6473263	6496934	2_50657	6496934	2_23669
233	Vu11	7719370	7719370	2_38154	7719370	NA
71	Vu11	9832429	9832429	2_47497	9832429	NA
71	Vu11	10542213	10693514	2_26393	10542213	2_46962
17C	Vu11	13319514	13319514	2_36583	13319514	NA
71	Vu11	16091288	16091288	2_25859	16091288	NA
72	Vu11	16842008	16842008	2_47299	16842008	NA
71	Vu11	24527942	24530008	2_50559	24527942	2_27491
71	Vu11	25936381	25936381	2_52373	25936381	NA
34C	Vu11	27691973	27691973	2_02302	27691973	NA
15C	Vu11	30747805	31673951	2_09976	30747805	NA
4C	Vu11	30747805	32037759	2_18437	31657191	2_23597,2_18358,2_38719,2_46026
229	Vu11	33288049	33418153	2_11629	33412532	2_02808,1_0480,2_01366,2_28201,2_28884,2_28885,2_32304,2_02809,2_02866,2_20835,2_16426,2_28202,2_03695,2_09623
17C	Vu11	34113329	34119337	2_27979	34113329	2_29439,2_08870,2_13488
74	Vu11	34314577	34376811	2_19159	34376784	2_33347,2_06098,2_06099,2_07731
17C	Vu11	34975478	34975478	2_45786	34975478	NA
72	Vu11	37231065	37253742	2_23412	37253742	2_22531
74	Vu11	38464264	38464264	1_0795	38464264	NA
14	Vu11	39998160	39998160	2_27132	39998160	NA

Conclusion

In this dissertation, I presented three chapters that each examine a different question under the general topic of the causes and consequences of plant genome evolution. In Chapter 1, I developed a novel K-mer based method to estimate sequence copy number variation and used the method to study variation in over 1,000 sequenced genomes of *A. thaliana.* I showed that variation in genome content in *A. thaliana* is primarily explained by copy number variation of repetitive sequences present in the centromere and pericentromere. Further, I mapped the genetic basis of multiple repeat classes to genes enriched for involvement in DNA replication and DNA repair, highlighting the importance of these processes in regulating sequence copy number in different contexts across the genome. Finally, I showed that loci affecting sequence copy number are under strong purifying selection, but persist in some populations on the fringes of the species range due to genetic drift.

In Chapter 2, I leveraged novel genome assemblies of *C. bursa-pastoris*, *C. orientalis*, and *C. rubella* to examine the evolution of the two subgenomes in *C. bursa-pastoris*. I found that the evolution of the two subgenomes was defined by thousands of small structural variants and did not involve large scale genomic rearrangements. My analysis of population structure of a global sampling of *C. bursa-pastoris* showed that the global pattern of polymorphism is best explained by two subpopulations strongly differentiated by both geography and climate. Finally, I showed that the ability of *C. bursa-pastoris* to adapt to different environments was probably due to modulation of flowering time.

In Chapter 3, I described the genetic variation and population structure of a global sample of cowpea, a drought tolerant crop native to West Africa that is grown for both food and fodder. My work suggests that population structure in cowpea is best described using two subpopulations corresponding to Western and Southeastern Africa, respectively. I also demonstrated the utility of this resource for genome-wide association mapping and proposed candidate genes that appear to control the red and blue seed color phenotypes.

The code to generate all main figures and major analyses described in this Dissertation is available at https://github.com/cjfiscus/2022_Fiscus_Dissertation and has been archived using zenodo (https://doi.org/10.5281/zenodo.7051833).